Phylogeny-aware metrics for microbial community surveys

Msc. Biomedical Engineering
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Contents

Abstract

The microbial community studied in this article comes from dug hole of pit latrines in Tanzania and Vietnam. The purpose of studying these microbes is to improve the use of basic sanitation facilities. If the rate and extent of fecal decomposition in basic sanitation facilities (such as pit latrines) can be improved, it will benefit approximately 1.7 billion users worldwide. Use pyrosequencing of 16S rRNA genes to detect the microbial community in pit latrines from Tanzania and Vietnam. At the same time, it combines other environmental factors (such as temperature, pH, geographic factors, location selection, etc.) on the diversity and diversity of these microbial communities. The composition structure is analyzed. The reason for choosing 16S rRNA is because it gives species level discretization. At the same time, 16Sr RNA gene has the functional constancy and highly conserved nature, which can be used as an important indicator of phylogeny. The main motivation behind this project is to add to existing knowledge about pit latrines, especially in view of the dataset that was available and the recent advances in phylogeny metrics that became available. We have extensively analysed the dataset based on operational taxonomic unit (OTU) to give an account of differences between microbial ecology between countries (hypothesis1) and in terms of depth (hypothesis2) in these pit latrines. Our results show community assemblage processes as well as peculiarities in terms of patterns in microbial signature.

Introduction

The improvement of infrastructure and basic living conditions can greatly improve the lives of ordinary people. Data show that every year by improving basic sanitation conditions, approximately 2.4 million people worldwide can avoid death (Torondel et al, 2016). Although the current measures have been very effective, due to technical limitations, for the poor, they sometimes cannot afford the cost of improving sanitary conditions, which is about 2.6 billion (Torondel et al, 2016). Pit latrines are still used in many areas. Compared with modern toilets, pit latrines are not hygienic and will affect the environment and human health. When the pit latrines are filled, they need to be emptied or landfilled, which will bring economic pressure and health risks to users. In theory, suitable microbial communities and environmental conditions can make the decomposition rate of pit latrines higher than the filling rate (Torondel et al, 2016). Therefore, it is necessary to understand which structure of the microbial communities in the two places affects the decomposition rate of pit latrines. Promote. It is currently believed that the composition of the microbial community will be affected by the ecological environment and the microbes themselves, and that changes in the composition of the microbial community will also affect the external ecological environment and the health of the human system. Therefore, selecting the appropriate phylogeny analysis method and appropriate phylogeny-aware metrics can be used to indicate the appropriate changes in the microbial community development structure.

Analysis of phylogeny in microbiomes can clarify the mechanism based on community assembly, diversity-process relationships, and ecosystem responses to environmental change (Martiny et al,2015). Phylogeny analysis in microbiomes can explain the variation of microbial community and its connection with the health and function of environment, engineering and human systems. It helps to reveal the aggregation mechanism of communities, the relationship between biodiversity and ecosystem functions, and the impact of environmental changes on microbial community (Martiny et al, 2016).

A diversity index is a quantitative measure that reflects how many different types (such as species) there are in a dataset, and simultaneously takes into account how evenly the basic entities (such as individuals) are distributed among those types. The value of a diversity index increases both when the number of types increases and when evenness increases. For a given number of types, the value of a diversity index is maximized when all types are equally abundant.

In the process of microbial community surveys, its biodiversity (such as phylogenetic diversity and functional diversity) will change, and there are many indicators that can be used to assess the phylogeny of the microbial community in terms of underlying processes to give mechanistic underpinnings. The phylogeny methods used in this thesis for microbial community investigation Net Relatedness Index (NRI), Nearest Taxon Index (NTI), and Quantitative Process Estimates (QPE). For sake of completion, we have also included alpha diversity and beta diversity metrics.

Alpha diversity（α-diversity）

A measurement used to measure the number of biological species in a community and the relative abundance of biological species. It reflects the results of coexistence between species in the community through competition for resources or the use of the same habitat. There are many types of alpha diversity indices, the one more commonly used include: species richness index; species evenness index; and species diversity index. The purpose is to use a common diversity index to measure the distribution of taxa in the sample, and then compare the specified groups or conditions through analysis of variance.

The details are as follows. The number of species in a community is characterized by a community richness index, which reflects the abundance of organisms in a certain spatial range. The evenness index (community evenness) is used to describe the relative density of each species in the community. The community diversity index (community diversity) is a function that combines species diversity and species abundance. The higher the diversity index, the ecological advantage the smaller the degree, the higher the uniformity index.

RH Whittaker believes that Alpha diversity (α-diversity) refers to the average diversity of species in different locations or different ecological environments within a local area. It can also be said to be the diversity that exists in a single ecosystem or sample. The simplest measure of alpha diversity is the abundance, species, or number of OTUs observed in the sample （allassignmenthelp，2019）.

Simpson index is used to describe the number of species present in the community and their relative abundance; Shannon is a commonly used index to characterize species diversity; Pielou's evenness is used to measure the intimacy of each species; Fisher alpha is a parametric index of diversity that models species as logseries distribution.

Beta diversity （β-diversity）

Beta diversity is a popular metric used to find the difference in either distribution or phylogeny between multiple samples. Additionally, there are multivariate tests, such as PERMANOVA, and PERMDISP to explore the sources of variation in beta diversity based on extrinsic parameters. Often, the value of β-diversity is constrained between 0 and 1. If the beta diversity value is closer to 0, the community structure is assumed to be similar. On the other hand, a value closer to 1 suggests a dissimilar community structure.

There are different methods that are often utilized to assess beta diversity: Bray-Curtis distance (that takes into account the distribution of microbial species count); Unweighted UniFrac distance (that takes into account proportion of branch length shared on a phylogeny between two samples) and Weighted UniFrac distance (that combines both phylogeny and abundances).

NRI （Net Relatedness Index）/ NTI （Nearest Taxon Index）

The NRI is a standardized effect size (SES) for the MPD metric (Swenson, 2014). In R when the observed MPD is larger than the mean of the null distribution, the NRI is positive. NTI is the comparison of the average nearest neighbor distance within the community and the random construction of the zero model of the community. In order to characterize the composition of the system development (the unique point in space and time) within each sample, we use "MNTD" to quantify the mean-nearest-taxon-distance and the nearest-taxon-index (NTI). Note that NTI is a negative number output by "ses.mntd"， occurrence distance. Then, the abundance obtained at these systematic occurrence distances exceeds the expected range (Stegen et al,2012). If NRI and NTI are greater than 0, it means that the species in the plot has a higher phylogenetic aggregation degree than the community randomly sampled from the species library, indicating that the developmental structure of the community system is more concentrated, more affected by environmental pressure; if the NRI/NTI is less than 0, then It indicates that the inter-species genetic relationship is more divergent than the community formed by random sampling from the species library, more affected by competitive exclusion principle; NRI/NTI is equal to 0, indicating that the inter-species genetic relationship is the same as the community formed by random sampling from the species library, and the community becomes a random phylogenetic structure .

NRI (Net relatedness index) and NTI (Nearest taxon index) can be used to represent the phylogenetic diversity of the microbial community (Ackerly,2011).

NRI (Net Relatedness Index) is defined as:

$$NRI = -1 * \frac{MPDobs - mn(MPDexp)}{sd(MPDexp)}, \tag{1}$$

where mn and sd are the mean and standard deviation of MPD values obtained from a large number (usually 999+) of random draws. For the clustered communities, NRI is positive and it is negative for the evenly spread communities. The significance of NRI can be determined by comparing the distribution of the observed value with the null value.

Want to know that the observed community is phylogenetically clustered or conversely, you need to calculate the mean MPD across a large number of random draws. MPD (mean phylogenetic distance) can be used to determine a particular plot are more closely related than expected by chance or not, it can be calculated as the sum of the pairwise phyletic distances among all pairs of taxa in the community (Ackerly,2011).

$$MPD = \frac{\sum_{i=1}^{N-1}\sum_{j=i+1}^{N} di,j\ pi\ pj}{\sum_{i=1}^{N-1}\sum_{j=i+1}^{N} pi\ pj}, \tag{2}$$

where $d_{i,j}$ is phyletic distance between taxa i and j. When p_i,p_j is 0, it means that the species exists; when p_i,p_j is 1, it means that the species does not exist. Relative abundance can also be used for p_i values, the numerator alone is then known as Rao's entropy, it is closely related to the Simpson diversity index used in ecology.

To obtain the value of NTI (nearest taxon index), you need to compare the mean nearest neighbor distance with the expected distribution under a null model.

$$NTI = -1 * \frac{NNPDobs - mn(NNPDexp)}{sd(NNPDexp)}, \tag{3}$$

When the NTI value is positive, it means that species co-occur with more closely related species than expected. When the NTI value is negative, it indicates that closely related species do not co-occur.

By calculating the mean nearest neighbor distance can determine the genus ratios. The genus ratio is another measure of the community phylogenetic structure is whether the most closely related co-occurring species in a community is more or less closely related than expected. It is more directly related to the calculation of species and focuses on whether closely related species tend to co-occur or not.

$$NNPD = \frac{\sum_{i=1}^{N} \min\left(\sum_{j=1}^{N(j \neq i)} di,j\ pi\ p\ j\right)}{N}, \tag{4}$$

QPE (quantitative process estimate)

Quantitative process estimates (QPE) is a method used to quantify the relative importance of potential species sorting, dispersal limitation, drift and mass effects. This method requires an index that can reflect the difference in ecological niches where different microbial communities are located. This index is the phylogenetic distances (PD) among taxa (Vass et al,2020). Máté et al. found that niche differences caused by most of the environmental variables that structured communities according to the RDA (redundancy analysis) results could induce turnover in phylogenetic community composition.

Specifically, combines a null model approaches based on phylogeny and abundance (Raup-Crick) β diversity (β_{RCbray}) measures to quantitatively estimate the relative importance of processes, such as selection, drift, dispersal limitation, and mass effects. In addition, this quantitative process estimation (QPE) method also distinguishes heterogeneous/variable (ie, β diversity enhancement) and homogeneous (ie, β diversity decreasing) selection processes. The main process in QPE is divided into two steps, Step 1: Calculate βNTI (pairwise comparison). If the value of ｜βNTI｜ is greater than 2, that means fraction with non-significant betaNTI value; if the value of ｜βNTI｜ is less than 2, that means fraction with significant βNTI value. This can help us determine that the selection procss is variable or homogeneous. Step 2: Calculate the β_{RCbray} (Bray-Curtis-based pairwise comparison). If β_{RCbray} is greater than +0.95, this shows that dispersal limitation coupled with drift and 'true' effects of dispersal limitation and/or historical contingency. If β_{RCbray} is less than -0.95, this shows that it is homogenizing dispersal (= mass effect) and if the ｜β_{RCbray}｜ is less than 0.95, this shows random processes acting alone (eccological drift) (Vass et al,2020).

Use the observed βMNTD value (β-mean-nearest-taxon-distance) which deviated from the mean of the null distribution and use the β Nearest Taxon Index (βNTI; difference between observed βMNTD and the mean of the null distribution in units of SDs) to evaluate the significance, you can perform the quantitative process estimates (Vass et al,2020). If the observed βMNTD value is significantly greater than the null expectation (βNTI> 2), it means that the community is assembled by variable. If the observed βMNTD value is significantly smaller than the null expectation (βNTI<-2), it indicates that the community is homogeneous selection (Vass et al,2020). If there is no significant deviation between the observed βMNTD and the null expectation, then the observed difference in phylogenetic community composition should be the result of dispersion limitation, homogeneous dispersion (mass effect) or random drift (Vass et al,2020). In the second step, the abundance-based (Raup-Crick) beta-diversity is calculated by using pairwise Bray-Curtis dissimilarity (β_{RCbray}) to estimate the relative importance of the one-step process. When there is no significant difference between βRC and 0, the community is considered to be randomly selected. When the value of βRC is close to -1, it is considered that this community is deterministically assembled and more similar to each other than expected by chance. When the value of βRC is close to +1, it indicates that deterministic processes favor dissimilar communities (Vass et al,2020). Based on the calculated β_{RCbray}, we can assume that the communities in the first step are structured by three different reasons that have not been randomly selected. In the first case, if β_{RCbray}> 0.95, this means that the change of the community is affected by dispersal limitation coupled with drift. The second case, if β_{RCbray} <−0.95, means that the change in the community is affected by homogenizing dispersal. The third case, if β_{RCbray} falls in between −0.95 and 0.95 (0.95<β_{RCbray}<0.95), which means random processes acting alone (drift) (Vass et al,2020). When β_{RCbray}> 0.95, the first situation, it may either indicate 'true' effects of dispersal limitation and/or historical contingency that both result in more dissimilar communities than expected by chance (Vass et al,2020).

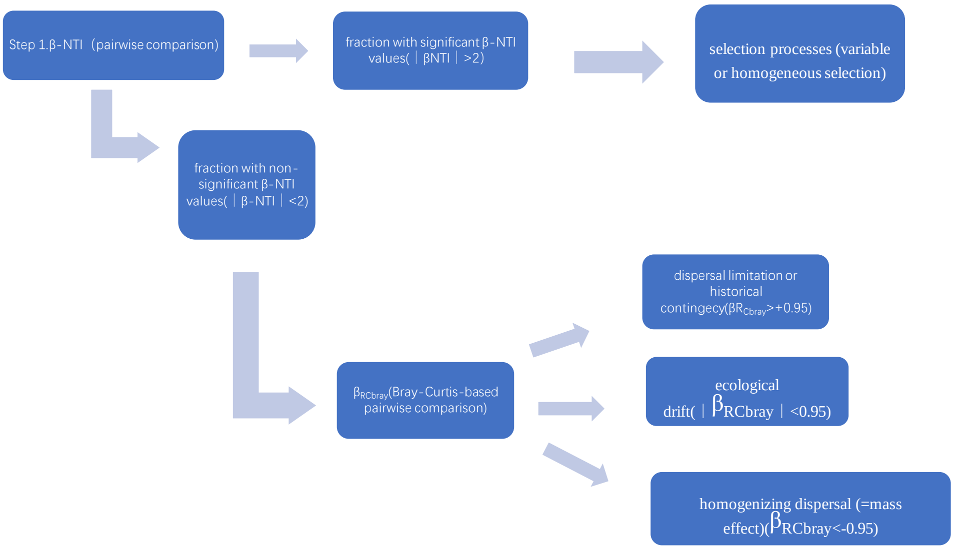

Figure 1: The flow chart of QPE (quantitative process estimates).

Use Evloview to visualize subtrees

EvolView is a web application for visualizing, annotating and managing phylogenetic trees, it is a system tree browser and customization tool; it can visualize phylogenetic trees in various formats and customize these phylogenetic trees through built-in functions (Zhang et al,2012). Secondly, EvolView is a tree and dataset management tool. Users can easily organize related trees into different projects, add new datasets to the tree, and edit and manage existing trees and datasets (Zhang et al,2012).

The "BVSTEP" routine has be used in this article, it is very important for phylogeny analysis and it is also a very common routine for bioinformation. Through permuting through 2n-1 possible combinations of features in the variable dataset, an algorithm that searches for highest correlation (Mantel test) between dissimilarities of a fixed and variable multivariate datasets using bvStep() from sinkr package (Ijaz et al, 2018). Testing all feature combinations is unrealistic and computationally intractable when the feature space is high (999 OTUs in our case). Thus, we used the abundance table with 1000 most abundant OTUs (with the premise that the most abundant species that may have a significant role to play) to best correlate with the overall similarities given all the OTUs (999 in our case). This analysis is complimentary to the differential analysis and identified the OTUs that were causing the major shifts in beta diversity.

Material and method

Data collection

We have used the dataset from the microbial communities in pit toilets collected from Tanzania in South Africa (the toilets in the villages of Sululu and Signali in the Kilombero Valley in the town of Ifakara in the Morogoro region of south-central Tanzania) were selected. Most of the residents are engaged in subsistence agriculture and their diet is mainly vegetarian. The toilets are located in the courtyard and built in the soil with an average depth of 2 m) and Vietnam in Southeast Asia（Neighbouring communes in Hoang Tay and Nhat Tan, Henan Province，about 60 kilometers south of central Hanoi. In order to collect the manure for agriculture, the volume of the pit dug in Vietnam is much smaller than usual in Tanzania, and the maximum depth of the vault is 1 meter）, which is also the source of data for this article (Torondel et al, 2016).

In addition, the climate and living habits of the residents are also different in the two places. Tanzania has a tropical climate. Usually, the rainy season is short, from November to December. Rainfall is heavy from April to May and the average daily temperature ranges from 19°C to 32°C (Torondel et al,2016).

The average daily temperature in Vietnam ranges from 3°C to 38°C. The residents of Tanzania are engaged in subsistence agriculture and their diet is mainly vegetarian and they use water for cleaning after going to the toilet (Torondel et al,2016). In Vietnam, it is mainly agriculture, intensive rice cultivation and animal husbandry. The local people’s eating habits are diverse, often including rice, noodles, various green vegetables, and meat or poultry. They are accustomed to using paper towels for cleaning and using lime to cover up the smell（Torondel et al,2016）.

They found that these microorganisms are a mixture of microbial populations in human feces and environmental microbial populations. Due to the local climate, residents’ eating habits, and different cleaning methods, the microorganisms in the pit toilets obtained The composition of the community is also different, and it is believed that the local environmental conditions have a greater impact on the structure of the microbial community (Torondel et al, 2016).

Analysis method

During the development of the microbial community, its own composition and structure will change, for example, biodiversity will change. At the same time, the process of microbial community surveys will be affected by relatively deterministic and random factors (Stegen et al, 2012). Deterministic factors include non-biological environment ("environmental filtration") and antagonism and synergy between species the choice imposed by sexual interaction (Stegen et al, 2012). Random factors include unpredictable interference, scattered probability, and random birth and death events. They combine phylogenetic community composition and null models to characterize random processes and certainty How does the influence of the process on the structure of the microbial community change with environmental changes (Stegen et al,2012). This paper also adopted this method to obtain the proportion of the number of microorganisms affected by different conditions in the total community, thus showing the factor that has the greatest influence on the composition of the microbial community.

Alpha diversity: The measure of alpha diversity can weigh the rare and abundant species with different ways. Through the measure of the richness, the number of species or OTUs which are observed within the sample, we can get the alpha diversity and refers to the diversity in a single ecosystem or sample (allassignmenthelp, 2019).

Beta diversity: It uses the evolutionary relationship and abundance information of each sample sequence to calculate the distance between samples, so as to compare the diversity of different samples, thereby reflecting whether there are significant differences in microbial communities between samples. There are two methods for calculating beta diversity. The first is the community comparison method based on bray Curtis distance, and the second is the Unifrac distance method. The first method is simple to calculate but does not consider the impact of evolution. The second method is to compare according to the phylogenetic tree which are obtained after aligning OTUs. We have used the second method. The distance matrix between samples (Unifrac distance matrix) can be obtained. The Unifrac distance matrix is divided into two types, weighted and Unweighted. Unweighted only considers the change of species. The Weighted Unifrac distance matrix considers both the presence or absence of species and changes in species abundance. When the number of the Weighted Unifrac distance matrix is 0, it indicates that the types and numbers of OTUs in the communities are the same (Swenson, 2014).

NRI/NTI: The Net Relatedness Index can be calculated using equation (1). The MPD (the mean phylognetic distance) in formula (1) is the sum of the pairwise phyletic distances among all pairs of taxa in the community, it can determine whether species in a particular area are more closely related than expected by chance (Ackerly, 2011). Extracting communities with the same richness and calculating mean MPD randomly, then get the expected MPD value. Compare the observed MPD (MPD_{obs}) and the expected MPD (MPD_{exp}). If MPDobs < MPDexp, then the observed community is phylogenetically clustered, and conversely if MPDobs > MPDexp (David, 2011). NTI can be calculated by equation (3). NNPD in equation (3) is the mean nearest neighbor distance. When the value of NTI is positive, it means that species co-occur with more closely related species than expected. On the contrary, when the value of NTI is negative, it means that closely related species do not co-occur (Ackerly,2011).

QPE: In the first step of QPE, the observed differences in phylogenetic community composition can be determined by which factors are affected and restricted by calculating the βMNTD and βNTI. In the second step, the abundance-based (Raup-Crick) beta-diversity is calculated using pairwise Bray-Curtis dissimilarity (βRCbray). Through the value of βRCbray to judge the observed differences in phylogenetic community composition by which factors are affected and restricted (Vass et al,2020).

This article uses R function to analyze the data and output related charts, it can help us to find the microbiome community survey model and the composition of the sample.

At the same time, use Evolview to annotate the phylogenetic tree to get a more intuitive chart. Before using Evolview for analysis, you need to extract a subset of the original phylogenetic tree by pruning particular taxa out of the phylogeny. We do not analyze the entire phylogeny because it contains too many species. We only analyze the selected community. Therefore, it is necessary to establish a subtree and conduct a subset analysis. In R, we can use the subtrees()

function to extract individual clades from our phylogeny. This function takes an input phylogeny and produce a list. In this list, each element is a phylogeny object. Each element contains a phylogeny object (Swenson, 2014). After getting the subtree, upload it to web application-Evolview for analysis. We uploaded data for bar plot, heatmap and group label separately, and output bar plot, heatmap and group label images respectively. Obtain the ratio of different OTUs in their respective communities and be able to show the difference between the same OTU in different communities. In the view of Evolview, the pink bar plots indicate the proportion of each OTUs in the microbial communities in Tanzania and Vietnam; the heatmap shows the abundance of each OTUs in the communities of the two places; the group label refers to each OUT Corresponding microorganism types.

Results

Alpha diversity

alpha diversity of hypothesis 1

It can be seen from figure 2 that Tanzania's Fisher alpha index and Richness are both higher than Vietnam, which shows that the species richness of the microbial community in pit toilets in Tanzania is higher than that in Vietnam, but the gap is not big. And Vietnam's Pielou's evenness, Shannon index and Simpson index are higher than Tanzania, which means that Vietnam's microbial community has a higher number of species, species relative abundance, species diversity and species intimacy.

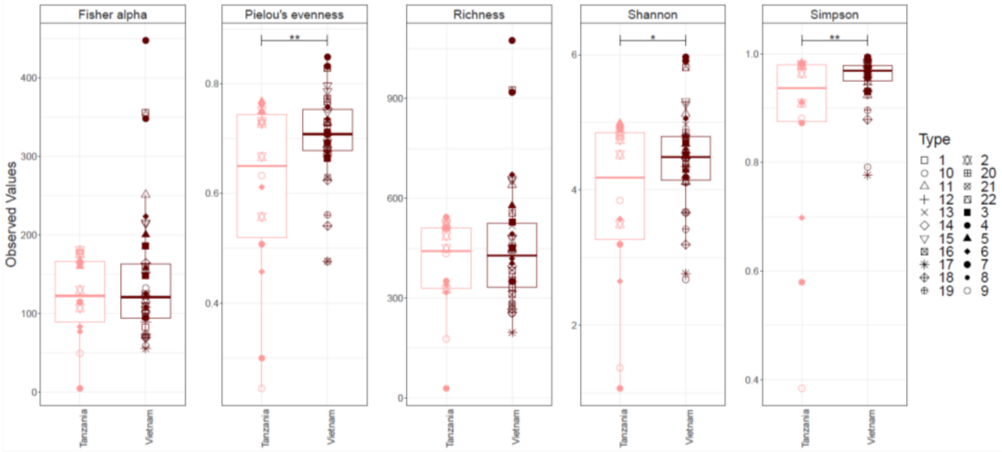

Figure 2: alpha diversity of Vietnam and Tanzania.

alpha diversity of hypothesis 2

It can be seen from Figure 3 that with Fisher alpha as the index, depth 3 has the highest diversity, followed by depth 4, and then depth 2, and depth 1 has the lowest diversity.

When considering Pielou's evenness, depth3 has the highest inter-species intimacy, followed by depth2, and then depth1 and depth4 have the lowest species intimacy. For the four different depths, the richness of the microbial community is sorted from high to low: depth3>depth4>depth2>depth1. If Shannon is used as the index, then the species diversity of the microbial community is sorted from high to low: depth3> depth2>depth1>depth4. When considering the Simpson index, the number of species present in the community and their relative abundance is ranked from high to low: depth3>depth1>depth2>depth4.

This shows that when the depth is set to depth3, the number of species, the relative abundance, species diversity, the intimacy of each species, richness and diversity of the microbial community are all the highest.

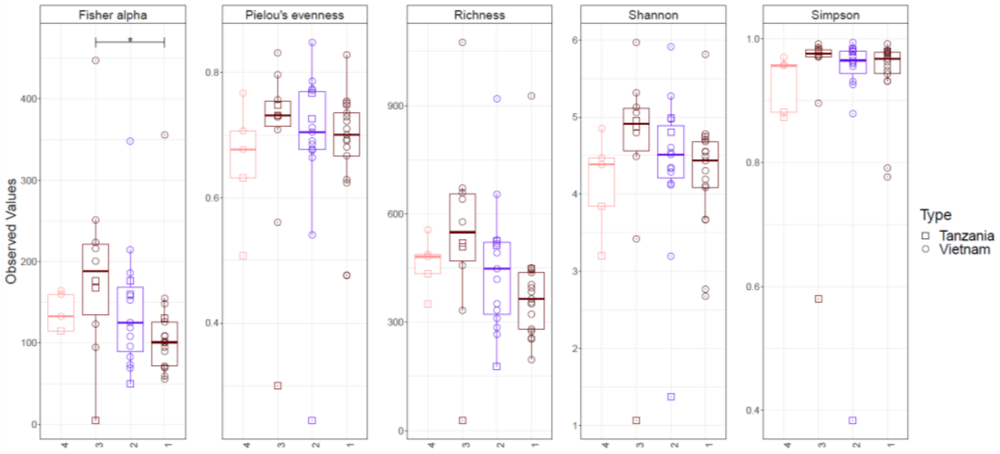

Figure 3: alpha diversity of 4 different depths.

Beta diversity

beta diversity of hypothesis 1

It can be seen in figure 4 that for the PCOA chart of hypothesis1, using group (country) the X-axis explains 21.39% variability whilst the Y-axis can explain 13.14% variability. We can see two distinct clusters suggesting that microbial community structure is different between the two countries.

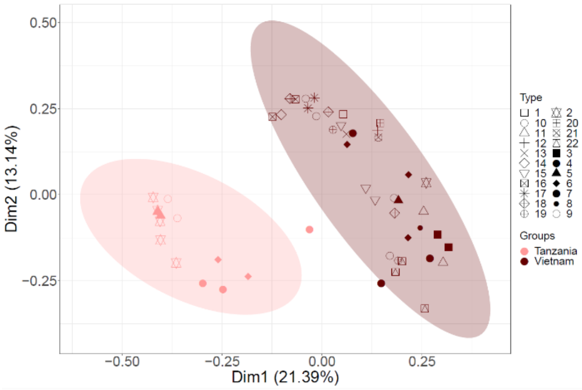

Figure 4: beta diversity of Vietnam and Tanzania.

beta diversity for hypothesis 2

It can be seen in figure 4 that for the PCOA chart of hypothesis1, using group (country) the X-axis explains 21.28% variability whilst the Y-axis can explain 12.82% variability. We can see four distinct clusters suggesting that microbial community structure is different between the four depths.

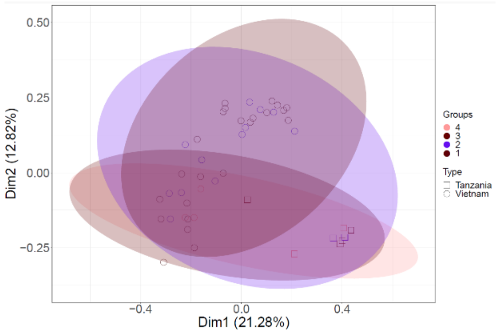

Figure 5: beta diversity of 4 different depths.

NRI/NTI

NRI/NTI of hypothesis1

Select ‘Country’ as the community's operational taxonomic unit, use R.Studio for data analysis and plot the figure6. It can be seen from the figure that when Country is selected as the operational taxonomic unit, the mean value of NRI of ‘Vietnam’ and 'Tanzania' are both greater than 0. It shows that the community structure tends to cluster together similarly related species. In the NTI graph, the mean value of the NTI of 'Vietnam' and 'Tanzania' are both greater than +2. This means that the individual communities are significantly phylogenetically clustered in groups 'Vietnam' and 'Tanzania'. This means that coexisting taxa are more closely related than expected by chance (phylogenetic clustering) for these two communities (Stegen et al, 2012) and community of 'Vietnam' has a greater degree of phylogenetic clustering.

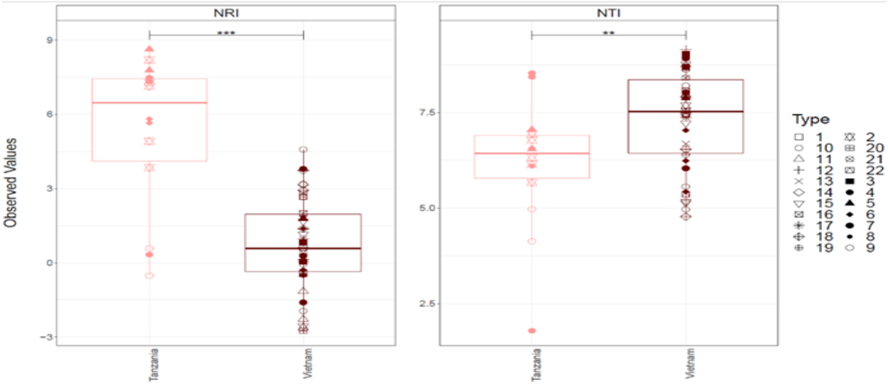

Figure6: NRI/NTI of Vietnam and Tanzania.

NRI/NTI of hypothesis 2 (depth)

Select 'Depth' as the operational taxonomic unit of the community, and use R.Studio for data analysis. From figure7, when ‘Depth’ is selected as the operational taxonomic unit, the mean value of the NRI of community 1, 2, 3 and 4 are all greater than 0. It shows that the community structure at this time also tends to gather together species with similar genetic relationships. In the NTI graph, the mean value of NTI for community 1, 2, 3 and 4 is all greater than +2. This means that the individual communities are significantly phylogenetically clustered in groups '1','2','3' and '4'. This means The coexisting taxa are more closely related than expected by chance (phylogenetic clustering) for these 4 communities (Stegen et al,2012) and community of '1','2','3' and '4' Decrease, the phylogenetic aggregation degree of community '1' is the highest, and community '4' is the lowest.

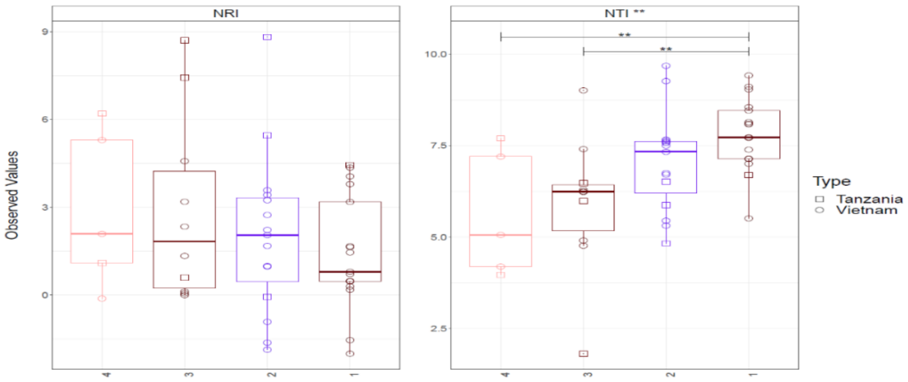

Figure 7: NRI/NTI of 4 different depths.

QPE

QPE of hypothesis1

From figure8, the reasons for the changes in the structural composition of the microbial community in Vietnam and Tanzania can be drawn. For Vietnam, the change in the structure of the microbial community in this area is mainly affected by the dispersal limitation. The proportion affected by this is 51.35%, which is more than half of the total. Secondly, it is affected by the variable selection, which accounts for 28.45%. The proportion affected by the ecological drift was 14.94%, and the proportion affected by homogenizing selection was 4.27%. The proportion affected by the homogenizing dispersal is the smallest, only 1%. For the microbial community in Tanzania, the change in its structural composition is mainly affected by the variable selection, accounting for 46.15%. The second is affected by the dispersal limitation, accounting for 28.57%. The proportion affected by the Ecological Drift was 21.98%, and the proportion affected by homogenizing dispersal was 2.20%. The proportion affected by the homogenizing selection is the smallest, only 1.10%.

Therefore, it can be concluded that for the microbial communities in Tanzania and Vietnam, changes in their composition and structure are more likely to be affected by ecological drift, dispersion limitation and variable selection, while homogenizing selection and homogenizing dispersal affect the microbial communities in the two places. The degree of influence of changes in the composition structure is very small. At the same time, the microbial community of Tazania is more prone to structural changes due to the influence of ecological drift and variable selection than the microbial community of Vietnam. Vietnam's microbial community is more prone to structural changes due to dispersion limitation than Tanzania's microbial community.

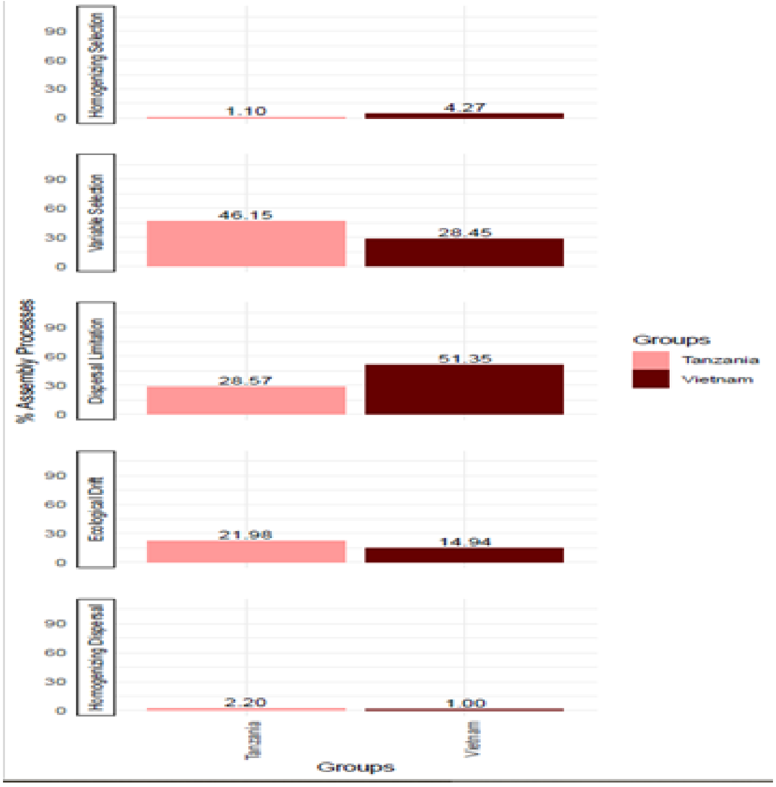

Figure 8: QPE of Vietnam and Tanzania.

QPE of hypothesis2

From figure9, the reasons for the changes in the structural composition of the microbial community in four different depths can be drawn. For depth 4, the change in the structure of the microbial community here is only affected by dispersal limitation and variable selection, and the percentages are 60.00% and 40.00% respectively, and will not be affected by ecological drift, homogenizing selection and homogenizing dispersal influences. For the microbial community at depth 3, the change in its composition is mainly affected by variable selection, which accounts for 40.00%. The second is affected by dispersal limitation, which accounts for 33.33%. The influence of ecological drift accounts for 24.44%, and the influence of homogenizing selection accounts for 2.22%. The microbial community at depth 3 will not be affected by homogenizing dispersal. For the microbial community at depth 2, variable selection is most likely to affect the changes in its composition, accounting for 49.52%, which is close to half. The second is affected by dispersal limitation, which accounts for 29.52%. The influence of ecological drift accounts for 17.14%, and the influence of homogenizing selection accounts for 3.81%. The homogenizing dispersal will not affect the composition of the microbial community at depth 2. For the microbial community at depth 1, these five influencing factors will all affect the composition of the community. Among them, the dispersal limitation has the greatest impact on the composition of the community, and the affected part accounts for 44.12% of the total community. The second is variable selection, which can affect the 32.35% portion. The percentage of parts affected by dispersal limitation is 16.18%, and the percentage of parts affected by dispersal limitation is 6.62%. Homogenizing dispersal has the smallest degree of impact and can only affect the part accounting for 0.74%. It can be seen that for different depths, the change in the composition of the microbial community is mainly affected by dispersal limitation and variable selection, and the sum of the two exceeds 70%.

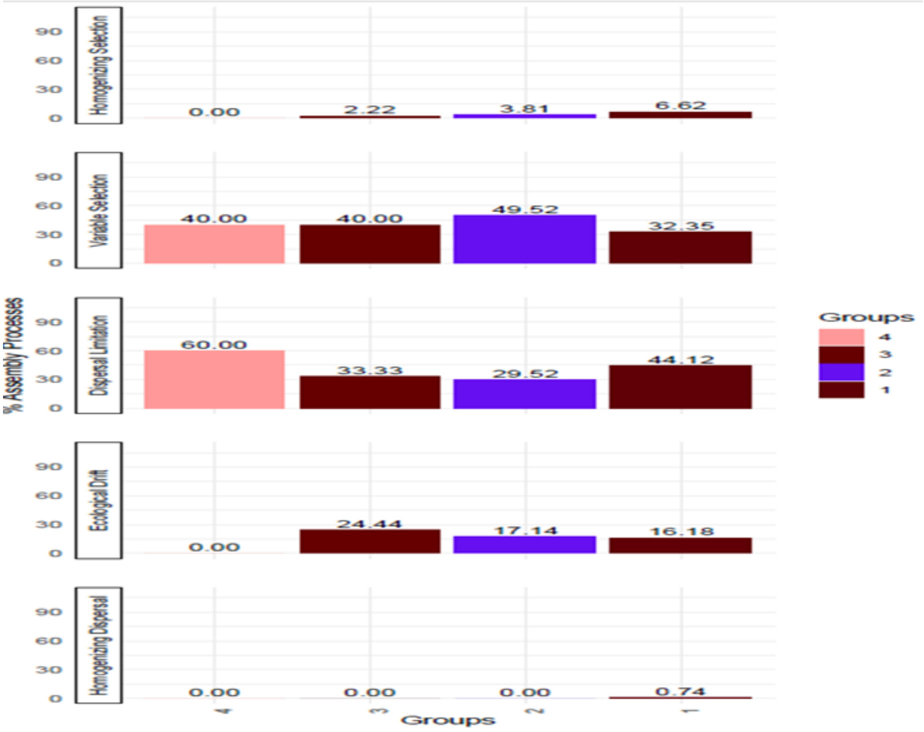

Figure 9: QPE of 4 different depths.

Subtree after visualization with Evolview

visualize phylogenetic trees of hypothesis1

In R, use subtree() function to trim the phylogenetic tree based on the hypothesis 1 community. Obtain subtrees with OTUs C8, C9, C10, C12, C13, and C14. After uploading data for bar plot, data for heatmap and data for group label in Evolview respectively, subanalysis charts of the microbial communities in Tanzania and Vietnam are obtained.

The group label of C8 is Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Ruminococcaceae UCG-005. At this time, the microorganisms contained in C8 accounted for 15.75% of the microbial community in Tanzania and the same microorganisms accounted for 6.22% of the microbial community in Vietnam. The heatmap of C8 shows that the average abundance of this OTU in the microbial community of Tanzania is higher than that of Vietnam.

The group label of C9 is Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae 1; Clostridium sensu stricto 1. At this time, the microorganisms contained in C9 accounted for 12.40% of the microbial community in Tanzania and the same microorganisms accounted for 58.93% of the microbial community in Vietnam. The heatmap of C9 shows that the average abundance of this OTU in the microbial community of Tanzania is lower than that of Vietnam.

The group label of C10 is Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilus; Haemophilus influenzae. At this time, the microorganisms contained in C10 accounted for 19.73% of the microbial community in Tanzania and the same microorganisms accounted for 0% of the microbial community in Vietnam. The heatmap also shows that the abundance of C8 in the microbial community of Tanzania is higher than that of Vietnam. The heatmap of C10 shows that the average abundance of this OTU in the microbial community of Tanzania is higher than that of Vietnam. The mean abundance of C10 in Vietnam is 0.

The group label of C12 is Bacteria; Firmicutes; Clostridia; Clostridiales; Christensenellaceae; Christensenellaceae R-7 group. At this time, the microorganisms contained in C12 accounted for 24.34% of the microbial community in Tanzania and the same microorganisms accounted for 0% of the microbial community in Vietnam. The heatmap of C12 shows that the average abundance of this OTU in the microbial community of Tanzania is higher than that of Vietnam. The mean abundance of C12 in Vietnam is 0.

The group label of C13 is Bacteria; Firmicutes; Clostridia; Clostridiales; Christensenellaceae; Christensenellaceae R-7 group. At this time, the microorganisms contained in C13 accounted for 13.70% of the microbial community in Tanzania and the same microorganisms accounted for 8.19% of the microbial community in Vietnam. The heatmap of C13 shows that the average abundance of this OTU in the microbial community of Tanzania is higher than that of Vietnam.

The group label of C14 is Bacteria; Firmicutes; Clostridia; Clostridiales; Christensenellaceae; Christensenellaceae R-7 group. At this time, the microorganisms contained in C14 accounted for 6.88% of the microbial community in Tanzania, and the same microorganisms accounted for 24.02% of the microbial community in Vietnam.

Figure 10: visualize phylogenetic trees of Vietnam and Tanzania.

Heatmap can show the mean abundance of different OTUs in the same country or the same depth (vertical) according to the color of the graph and can also show the mean abundance of the same OTU in different countries or different depths (horizontal). The red squares and text in the next column indicate that these OTUs are derived from the subtree（Ijaz et al,2018）.

According to the horizontal order, we can find that the mean abundance of Tanzania's C9 and C14 is lower than that of Vietnam. In the microbial community of Tanzania, the mean abundance of C8; C10; C12 and C13 is higher than that of Vietnam. According to the vertical order, we can find that the mean abundance of OTUs in Tanzania is from high to low: C12>C10>C8>C13>C9>C14. At the same time, the mean abundance of OTUs in Vietnam is from high to low. The low order is: C9>C14>C13>C8>C10=C12. Among them, C14 in Vietnam has the highest mean abundance, exceeding 50%, and C10 and C12 have the lowest mean abundance, only 0. This shows that C10 and C12 microorganisms are not distributed in Vietnam, which may be related to the climate of different regions and the living habits of local residents.

visualize phylogenetic trees of hypothesis 2.

The pink histogram represents the mean abundance of different OTUs at depth 4. The blue histogram represents the mean abundance of different OTUs at depth 3. The brown histogram represents the mean abundance of different OTUs at depth2. The purple histogram represents the mean abundance of different OTUs at depth 1.

The mean abundance of the microorganisms contained in C8 is 7.54% at depth 4; the mean abundance at depth 3 is 4.31%; at depth 2, the mean abundance is 14.44%; at depth 1, the mean abundance is 8.42%.

For the microorganism represented by C9, its mean abundance at depth 4 is 55.42%; at depth 3, the mean abundance of C9 is 62.06%; at depth 2 the mean abundance of C9 is 51.97%; at depth 1 The mean abundance of C9 is 38.45%.

The mean abundance of the microorganism represented by C10 is 10.04% at depth 4; its mean abundance is only 0% at depth 3; at depth 2, the mean abundance of C 10 is 1.38%; at depth 1, C10 mean abundance is 0%.

The mean abundance of the microorganism represented by C12 is 9.13% at depth 4; the mean abundance of C12 is 0% at depth 3; at depth 2, the mean abundance of C12 is 1.38%; at depth 1, the mean abundance of C12 is 0.58%.

The mean abundance of the microorganism represented by C13 is 17.05% at depth 4; the mean abundance of C13 is 8.50% at depth 3; at depth 2, the mean abundance of C13 is 2.31%; at depth 1, the mean abundance of C13 is 10.13% of the total.

The mean abundance of the microorganism represented by C14 is 0.82% at depth 4; the mean abundance of C14 is 6.80% at depth 3; at depth 2, the mean abundance of C14 is 12.87%; at depth 1, the mean abundance of C14 is Is 42.42%.

Figure 11: visualize phylogenetic trees of 4 different depths.

Through the comparison of the graphics colors in the heatmap, in the horizontal order, you will find that the mean abundance of C10 is sorted from the highest at the four depths as follows: depth 4>depth 2>depth 3=depth1; the mean abundance of C12 is in the four depths The order from high to low is: depth 4>depth 3>depth 2>depth 1; the order of C8 mean abundance in the four depths from high to low: depth 2>depth 1>depth 4>depth 3; C9 The order of mean abundance in the four depths from high to low is: depth 3>depth 4>depth 2>depth 1; the order of C14’s mean abundance in the four depths from high to low is: depth 1>depth 2>depth 3 >depth 4; The order of C13's mean abundance in the four depths from high to low is: depth 4>depth 2>depth 1>depth 3. According to the vertical order, it can be found that for depth 4, mean abundance is from high to low The order is: C9>C13>C10>C12>C8>C14; for depth 3, the order of mean abundance from high to low is: C9>C13>C12>C14>C8>C10; for depth 2, The order of mean abundance from high to low is: C9>C8>C14>C13>C12>C10; for depth 1, the order of mean abundance from high to low is: C14>C9>C13>C8>C12>C10.

From the information contained in the heatmap, it is not difficult to find that in the four different depths, the mean abundance of C9 is very high. For depth 2; depth 3 and depth 4, the mean abundance of C9 is the highest among the six OTUs. Even at depth 1, the mean abundance of C9 is close to 40%. The mean abundance of C10 is only 0 at depth 3 and depth 2, which means that the microorganism represented by C10 is not distributed at depth 3 and depth 1.

Discussion

From the results obtained, because the selected microbial community is in different regions (country) and location (depth), the structural composition of the microbial community will also vary. Different phylogeny-aware metrics can show different characteristics of microbial community.

Metrics of hypothesis1 (country)

Alpha diversity indicates that the species richness of the microbial community in pit toilets in Tanzania is higher than that in Vietnam. The number of species, species relative abundance, species diversity and species intimacy of the microbial community in the pit toilets in Vietnam are all higher than the microbial community in Tanzania.

When the microbial communities in pit toilets are distinguished by the country, the beta diversity can show that there is a 21.39% difference between the microbial communities in the two places.

The NRI/NTI image shows that for the microbial communities in Tanzania and Vietnam, they tend to cluster similar species, and the degree of aggregation of microbial community in Vietnam is higher than that in Tanzania.

QPE shows that the microbial communities in Tanzania and Vietnam, changes in their composition and structure are more likely to be affected by ecological drift, dispersion limitation and variable selection, while the degree of influence of changes in the composition structure of homogenizing selection and homogenizing dispersal affect the microbial communities in the two places is very small. At the same time, the microbial community of Tanzania is more prone to structural changes due to the influence of ecological drift and variable selection than the microbial community of Vietnam. Vietnam's microbial community is more prone to structural changes due to dispersion limitation than Tanzania's microbial community.

Metrics of hypothesis2 (depth)

Alpha diversity shows that when the depth is set to depth3, the number of species, the relative abundance, species diversity, the intimacy of each species, richness and diversity of the microbial community are all the highest.

When the microbial communities in pit toilets are distinguished by the depth, the beta diversity can show that there are approximately 21.28% differences in microbial communities with different depths.

The NRI/NTI images show that even at different depths, the selected communities tend to cluster similar species. As the depth increases, the degree of aggregation of the microbial community decreases, the phylogenetic aggregation degree of community '1' is the highest, and community '4' is the lowest. (depth1>depth2>depth3>depth4).

The QPE image shows that for communities with different depths, the change in the composition of the microbial community is mainly affected by dispersal limitation and variable selection, and the sum of the two exceeds 70%.

Conclusion and future direction

At present, the detection method can detect the biological diversity of the sample itself and between different samples. At the same time, it can also express the expression difference of the sample between different operational taxonomic units and detect the co-occurrence pattern of the community level. Analyze the relationship between environments.

During the testing process, we found that sometimes it takes a long time due to too many samples. Therefore, the workflow can be optimized in the future to reduce the time required. At the same time, other software packages can also be developed to combine with existing functions to explore the influence of the internal composition of the sample on the survival mode of the community.

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Appendix

Appendix A

The R script and data below are related to alpha diversity calculations.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to "To Source File Location"
#Script for calculation of diversity indices, and also supports paired data
#v1.2 (All metrics are now being saved)

library(phyloseq)
library(stringr)
library(data.table)
library(vegan)
library(ggplot2)
library(grid) #We need grid to draw the arrows

#PARAMETERS ##########################
which_level="Otus" #Otus Genus Family Order Class Phylum
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
text_size=16
axis_text_size=14
strip_text_size=18
increment_divider=3
exclude_pvalues_text_from_drawing=FALSE
legends_position_bottom=FALSE
exclude_legends=TRUE #FALSE
pairwise_text_size=7
number_of_rows=1
legend_text_size=20
legend_title_size=22
axis_title_size=20
height_image=9
width_image=20
smoothing_alpha=0.3
use_provided_colors=TRUE
turn_smoothing_on=FALSE
#/PARAMETERS ##########################

abund_table<-otu_table(physeq)
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]
```

```
OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment", and
"non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") |
OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") |
OTU_taxonomy$Family %in% c("Mitochondria"))]


#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
#when reducing the abund_table, there is a high likelihood that an OTU was only present in a
sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their
dimensions should match
#/DATA IMPORT############################################################

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE############################
#In the hypothesis space, all you need is to select the rows in meta_table you are interested in
```

```
#and then allocate a column to meta_table$Groups that you want to use.

label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
"Tanzania",
"Vietnam"
))
colours <- c(
  "#ff9999",
  "#660000",
    #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1
000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Latrine))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
  #Cross-sectional comparisons
  combn(c( "Tanzania",
           "Vietnam"),2)
)

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
  "4",
  "3",
  "2",
  "1"
))
colours <- c(
  "#ff9999",
  "#660000",
  "#660FF0",
  "#600006",
  #Next colors are for lines mainly used in the PCoA script
```

```
"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1
000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Country))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
   #Cross-sectional comparisons
   combn(c( "1",
            "2",
            "3",
            "4"),2)
)
#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE#############################

#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]
#Adjust OTU taxonomy
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#COLLATE OTUS AT A PARTICULAR LEVEL#######################################
new_abund_table<-NULL
if(which_level=="Otus"){
   new_abund_table<-abund_table
} else {
   list<-unique(OTU_taxonomy[,which_level])
   new_abund_table<-NULL
   for(i in list){
      tmp<-
data.frame(rowSums(abund_table[,rownames(OTU_taxonomy)[OTU_taxonomy[,which_level]==
i],drop=FALSE]))
      if(i==""){colnames(tmp)<-c("__Unknowns__")} else {
         #colnames(tmp)<-paste("",i,sep="")
         colnames(tmp)<-
gsub(";+$","",paste(sapply(OTU_taxonomy[OTU_taxonomy[,which_level]==i,][1,1:which(colna
mes(OTU_taxonomy)==which_level)],as.character),collapse=";"))
      }
      if(is.null(new_abund_table)){new_abund_table<-tmp} else {new_abund_table<-
cbind(tmp,new_abund_table)}
   }
}
```

```
new_abund_table<-as.data.frame(as(new_abund_table,"matrix"))
abund_table<-new_abund_table
#/COLLATE OTUS AT A PARTICULAR
LEVEL###########################################

grouping_column<-"Groups" #"Groups

#Calculate Richness
R<-vegan::rarefy(abund_table,min(rowSums(abund_table)))
df_R<-data.frame(sample=names(R),value=R,measure=rep("Richness",length(R)))

#Calculate Shannon entropy
H<-vegan::diversity(abund_table)
df_H<-data.frame(sample=names(H),value=H,measure=rep("Shannon",length(H)))

#Calculate Simpson diversity index
simp <- vegan::diversity(abund_table, "simpson")
df_simp<-data.frame(sample=names(simp),value=simp,measure=rep("Simpson",length(simp)))

#Calculate Fisher alpha
alpha <- vegan::fisher.alpha(abund_table)
df_alpha<-data.frame(sample=names(alpha),value=alpha,measure=rep("Fisher
alpha",length(alpha)))

#Calculate Pielou's evenness
S <- vegan::specnumber(abund_table)
J <- H/log(S)
df_J<-data.frame(sample=names(J),value=J,measure=rep("Pielou's evenness",length(J)))

#Uncomment to retain everything
df<-rbind(df_R,df_H,df_J,df_alpha,df_simp)

#Write all the metrics in a file for further analyses elsewhere
data_to_write<-
data.frame(df_R[,"value",drop=F],df_H[,"value",drop=F],df_simp[,"value",drop=F],df_alpha[,"va
lue",drop=F],df_J[,"value",drop=F])
colnames(data_to_write)<-c("Richness","Shannon","Simpson","FisherAlpha","PielouEvenness")
write.csv(data_to_write,paste("Diversity_",which_level,"_",label,".csv",sep=""))
#/Write all the metrics in a file for further analyses else where

rownames(df)<-NULL

#Incorporate categorical data in df
```

```
df<-data.frame(df,meta_table[as.character(df$sample),])

#To do anova, we will convert our data.frame to data.table

#Since we can't pass a formula to data.table, I am creating
#a dummy column .group. so that I don't change names in the formula
dt<-data.table(data.frame(df,.group.=df[,grouping_column]))

#I am also specifying a p-value cutoff for the ggplot2 strips
pValueCutoff<-0.05
pval<-dt[, list(pvalue = sprintf("%.2g",
                                                  tryCatch(summary(aov(value
~ .group.))[[1]][["Pr(>F)"]][1],error=function(e) NULL))),
          by=list(measure)]

#Filter out pvals that we don't want
pval<-pval[!pval$pvalue=="",]
pval<-pval[as.numeric(pval$pvalue)<=pValueCutoff,]

#I am using sapply to generate significances for pval$pvalue using the cut function.
pval$pvalue<-sapply(as.numeric(pval$pvalue),function(x){as.character(cut(x,breaks=c(-Inf,
0.001, 0.01, 0.05, Inf),label=c("***", "**", "*", "")))})

#Update df$measure to change the measure names if the grouping_column has more than three
classes
if(length(unique(as.character(meta_table[,grouping_column])))>2){
  df$measure<-as.character(df$measure)
  if(dim(pval)[1]>0){
    for(i in seq(1:dim(pval)[1])){

df[df$measure==as.character(pval[i,measure]),"measure"]=paste(as.character(pval[i,measure]),as.
character(pval[i,pvalue]))
    }
  }
  df$measure<-as.factor(df$measure)
}

#Get all possible combination of values in the grouping_column
s<-NULL
if(provide_your_own_pvalue_combinations){
  s<-provided_combination
} else{
  s<-combn(unique(as.character(df[,grouping_column])),2)
}
```

```
#df_pw will store the pair-wise p-values
df_pw<-NULL
for(k in unique(as.character(df$measure))){
   #We need to calculate the coordinate to draw pair-wise significance lines
   #for this we calculate bas as the maximum value
   bas<-max(df[(df$measure==k),"value"])

   #Calculate increments as % of the maximum values
   inc<-0.05*(bas-min(df[(df$measure==k),"value"]))

   #Give an initial increment
   bas<-bas+inc
   for(l in 1:dim(s)[2]){

      #Do a pair-wise anova
      tmp<-
c(k,s[1,l],s[2,l],bas,paste(sprintf("%.2g",tryCatch(summary(aov(as.formula(paste("value
~",grouping_column)),data=df[(df$measure==k) & (df[,grouping_column]==s[1,l] |
df[,grouping_column]==s[2,l]),] ))[[1]][["Pr(>F)"]][1],error=function(e) NULL)),"",sep=""))

      #Ignore if anova fails
      if(!is.na(as.numeric(tmp[length(tmp)]))){

         #Only retain those pairs where the p-values are significant
         if(as.numeric(tmp[length(tmp)])<0.05){
            if(is.null(df_pw)){df_pw<-tmp}else{df_pw<-rbind(df_pw,tmp)}

            #Generate the next position
            bas<-bas+inc
         }
      }
   }
}

if(!is.null(df_pw)){
   if(class(df_pw)=="character"){
      df_pw<-t(as.matrix(df_pw))
   }
   df_pw<-data.frame(row.names=NULL,df_pw)
   names(df_pw)<-c("measure","from","to","y","p")
}


#Draw the boxplots
```

```
p<-ggplot(aes_string(x=grouping_column,y="value",color=grouping_column,group=grouping_column,shape="Type"),data=df)
if(turn_smoothing_on){
p<-p + geom_smooth(aes(x=Groups,y=value,fill=Type,group=Type),method=loess,linetype=0,alpha=smoothing_alpha)
}
p<-p+geom_boxplot(outlier.size=0,show.legend=FALSE,position="identity")+geom_jitter(position = position_jitter(height = 0, width=0), size=4)
p<-p+theme_bw()
p<-p+facet_wrap(~measure,scales="free_y",nrow=number_of_rows)+ylab("Observed Values")+xlab("Samples")

if(!is.null(df_pw)){
   #This loop will generate the lines and signficances
   for(i in 1:dim(df_pw)[1]){
      p<-p+geom_path(inherit.aes=F,aes(x,y),data = data.frame(x = c(which(levels(df[,grouping_column])==as.character(df_pw[i,"from"])),which(levels(df[,grouping_column])==as.character(df_pw[i,"to"]))), y = c(as.numeric(as.character(df_pw[i,"y"])),as.numeric(as.character(df_pw[i,"y"]))), measure=c(as.character(df_pw[i,"measure"]),as.character(df_pw[i,"measure"]))), color="black",lineend = "butt",arrow = arrow(angle = 90, ends = "both", length = unit(0.1, "inches")))
      p<-p+geom_text(inherit.aes=F,aes(x=x,y=y,label=label),data=data.frame(x=(which(levels(df[,grouping_column])==as.character(df_pw[i,"from"]))+which(levels(df[,grouping_column])==as.character(df_pw[i,"to"])))/2,y=as.numeric(as.character(df_pw[i,"y"])),measure=as.character(df_pw[i,"measure"]),label=as.character(cut(as.numeric(as.character(df_pw[i,"p"])),breaks=c(-Inf, 0.001, 0.01, 0.05, Inf),label=c("***", "**", "*", ""))))),size=pairwise_text_size)
      if(exclude_pvalues_text_from_drawing){
         p<-p+geom_text(inherit.aes=F,aes(x=x,y=y,label=label),data=data.frame(x=(which(levels(df[,grouping_column])==as.character(df_pw[i,"from"]))+which(levels(df[,grouping_column])==as.character(df_pw[i,"to"])))/2,y=as.numeric(as.character(df_pw[i,"y"])),measure=as.character(df_pw[i,"measure"]),label=paste("p=",as.character(as.numeric(as.character(df_pw[i,"p"]))),sep="")),size=pairwise_text_size,vjust=-1)
      }
   }
}
if(use_provided_colors){
   p<-p+scale_color_manual(grouping_column,values=colours)
} else {
```

```
    #coloring function
    gg_color_hue<-function(n){
        hues=seq(15,375,length=n+1)
        hcl(h=hues,l=65,c=100)[1:n]
    }
    cols=gg_color_hue(length(unique(df$Groups)))
}

if(!is.null(meta_table$Type)){
    p<-p+scale_shape_manual("Type",values=c(c(0:25),c(33:127)))
}
#if crashes at panel.margin change it to panel.spacing, if crashes at panel.spacing, change it to
panel.margin
p<-p+theme(strip.background = element_rect(fill="white"))+theme(panel.spacing = unit(2,
"lines"),
                                                                  strip.text =
element_text(size=strip_text_size),

legend.text=element_text(size=legend_text_size),
                                                                  legend.title =
element_text(size=legend_title_size),
                                                                  text =
element_text(size=text_size),

axis.text=element_text(size=axis_text_size),

axis.title=element_text(size=axis_title_size),
                                                                  axis.text.x =
element_text(angle = 90, hjust = 1))
if(legends_position_bottom){
    p<-p+theme(legend.key = element_blank(),    #removes the box around each legend item
                     legend.position = "bottom", #legend at the bottom
                     legend.direction = "horizontal",
                     legend.box = "horizontal",
                     legend.box.just = "centre")
}
if(exclude_legends){
    p<-p+guides(colour=FALSE) #FALSE
}



p<-p+theme(axis.title.x=element_blank(),
                 axis.ticks.x=element_blank())
```

```
pdf(paste("ANOVA_diversity_",which_level,"_",label,".pdf",sep=""),height=height_image,width=
width_image)
print(p)
dev.off()
```

Script 1: R script of alpha diversity

	Richness	Shannon	Simpson	FisherAlpha	PielouEvenness
T_2_1	449.2653	4.741917	0.980577	130.1139	0.750426
T_2_2	525.3553	4.807072	0.978827	176.4877	0.726723
T_2_3	520.5388	4.871195	0.978955	176.0201	0.731488
T_2_6	326.1779	3.499647	0.909362	106.9549	0.557234
T_2_9	486.7575	4.524742	0.963702	180.4262	0.666263
T_4_3	28.2139	1.065357	0.579689	4.67454	0.299649
T_4_4	351.031	3.197922	0.872765	114.7983	0.507248
T_4_5	543.4738	4.900875	0.980826	163.1753	0.762222
T_5_2	512.6365	4.990983	0.98358	160.0756	0.767514
T_5_3	508.6471	4.956303	0.982165	167.4995	0.74748
T_6_7	339.7311	3.572436	0.910936	83.11349	0.611045
T_6_8	316.97	2.651065	0.698376	76.92259	0.457152
T_9_2	177.6799	1.369945	0.384067	49.42801	0.244541
T_9_4	433.7617	3.847577	0.881188	114.3626	0.632121
V_1_2	333.5641	4.539315	0.979227	82.88091	0.771556
V_2_2	448	4.136829	0.926071	118.7353	0.677636
V_3_1	450.4903	4.701335	0.972341	148.0704	0.710021
V_3_2	528.0645	4.513771	0.931026	185.9699	0.6641
V_5_3	577.9602	4.795788	0.970263	200.4835	0.708787
V_6_1	404.4312	4.489656	0.975291	108.2721	0.735163
V_6_2	418.8888	4.287008	0.955349	125.0997	0.675584
V_6_3	671.6831	5.058678	0.971862	223.697	0.756482
V_7_1	350.7265	4.192944	0.962733	94.77042	0.693079
V_7_2	918.8326	5.912294	0.994107	348.1533	0.848046
V_7_3	1074.988	5.968914	0.991565	447.5365	0.831317
V_8_2	492.2567	4.605841	0.970967	157.9509	0.70477
V_9_1	253.1531	2.676255	0.791378	59.12163	0.475862
V_9_2	285.5638	4.116913	0.959728	68.98385	0.712177
V_9_4	481.5035	4.383577	0.958293	132.5403	0.706739
V_10_1	275.6518	4.110519	0.955727	69.79384	0.690769
V_11_1	444.5748	4.681562	0.977508	154.8492	0.700612
V_11_3	640.7377	5.128601	0.981626	251.1666	0.728893
V_12_1	322.1944	4.085974	0.943286	89.4499	0.667132
V_13_2	517.564	4.97117	0.98086	152.6249	0.773739
V_14_1	395.3303	4.549382	0.976139	102.4113	0.754372

V_15_1	437.548	4.781685	0.980293	125.8202	0.747887
V_15_2	654.3319	5.271775	0.984126	214.4333	0.786027
V_15_3	658.8982	5.314558	0.985706	216.126	0.796392
V_16_1	383.9916	4.304126	0.948408	108.8638	0.68095
V_16_2	310.8446	4.331835	0.964942	95.96992	0.690566
V_17_1	196.4128	2.76711	0.776936	55.47467	0.476419
V_17_2	351.1639	4.346329	0.962001	108.0569	0.685311
V_18_1	256.4041	3.667531	0.931623	69.32915	0.623673
V_18_2	266.5111	3.194834	0.879042	73.16197	0.540756
V_18_4	487.794	4.470636	0.956625	164.3228	0.677243
V_19_1	364.6542	4.434614	0.967588	100.6594	0.722263
V_19_3	332.7562	3.419945	0.89607	94.58136	0.560617
V_20_1	354.7424	4.555448	0.978843	99.86476	0.729326
V_21_1	281.3664	3.673005	0.931429	71.49202	0.62887
V_22_1	926.6679	5.8134	0.99172	355.7207	0.828097
V_22_3	457.416	4.488633	0.973241	123.1797	0.730805
V_22_4	555.6948	4.851534	0.970001	159.7057	0.767119

Table 1： Diversity of different OTUs in hypothesis 1.

	Richness	Shannon	Simpson	FisherAlpha	PielouEvenness
T_2_1	449.2653	4.741917	0.980577	130.1139	0.750426
T_2_2	525.3553	4.807072	0.978827	176.4877	0.726723
T_2_3	520.5388	4.871195	0.978955	176.0201	0.731488
T_4_3	28.2139	1.065357	0.579689	4.67454	0.299649
T_4_4	351.031	3.197922	0.872765	114.7983	0.507248
T_5_2	512.6365	4.990983	0.98358	160.0756	0.767514
T_5_3	508.6471	4.956303	0.982165	167.4995	0.74748
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T_9_4	433.7617	3.847577	0.881188	114.3626	0.632121
V_1_2	333.5641	4.539315	0.979227	82.88091	0.771556
V_2_2	448	4.136829	0.926071	118.7353	0.677636
V_3_1	450.4903	4.701335	0.972341	148.0704	0.710021
V_3_2	528.0645	4.513771	0.931026	185.9699	0.6641
V_5_3	577.9602	4.795788	0.970263	200.4835	0.708787
V_6_1	404.4312	4.489656	0.975291	108.2721	0.735163
V_6_2	418.8888	4.287008	0.955349	125.0997	0.675584
V_6_3	671.6831	5.058678	0.971862	223.697	0.756482
V_7_1	350.7265	4.192944	0.962733	94.77042	0.693079
V_7_2	918.8326	5.912294	0.994107	348.1533	0.848046
V_7_3	1074.988	5.968914	0.991565	447.5365	0.831317
V_8_2	492.2567	4.605841	0.970967	157.9509	0.70477
V_9_1	253.1531	2.676255	0.791378	59.12163	0.475862
V_9_2	285.5638	4.116913	0.959728	68.98385	0.712177
V_9_4	481.5035	4.383577	0.958293	132.5403	0.706739

V_10_1	275.6518	4.110519	0.955727	69.79384	0.690769
V_11_1	444.5748	4.681562	0.977508	154.8492	0.700612
V_11_3	640.7377	5.128601	0.981626	251.1666	0.728893
V_12_1	322.1944	4.085974	0.943286	89.4499	0.667132
V_13_2	517.564	4.97117	0.98086	152.6249	0.773739
V_14_1	395.3303	4.549382	0.976139	102.4113	0.754372
V_15_1	437.548	4.781685	0.980293	125.8202	0.747887
V_15_2	654.3319	5.271775	0.984126	214.4333	0.786027
V_15_3	658.8982	5.314558	0.985706	216.126	0.796392
V_16_1	383.9916	4.304126	0.948408	108.8638	0.68095
V_16_2	310.8446	4.331835	0.964942	95.96992	0.690566
V_17_1	196.4128	2.76711	0.776936	55.47467	0.476419
V_17_2	351.1639	4.346329	0.962001	108.0569	0.685311
V_18_1	256.4041	3.667531	0.931623	69.32915	0.623673
V_18_2	266.5111	3.194834	0.879042	73.16197	0.540756
V_18_4	487.794	4.470636	0.956625	164.3228	0.677243
V_19_1	364.6542	4.434614	0.967588	100.6594	0.722263
V_19_3	332.7562	3.419945	0.89607	94.58136	0.560617
V_20_1	354.7424	4.555448	0.978843	99.86476	0.729326
V_21_1	281.3664	3.673005	0.931429	71.49202	0.62887
V_22_1	926.6679	5.8134	0.99172	355.7207	0.828097
V_22_3	457.416	4.488633	0.973241	123.1797	0.730805
V_22_4	555.6948	4.851534	0.970001	159.7057	0.767119

Table 2：Diversity of different OTUs in hypothesis 2

Appendix B

The R script and data below are related to beta diversity calculations.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to "To Source File Location"
#Script for calculation of beta diversity (Principle Coordinate Analysis)

#Sometimes bray-curtis distance doesn't work with the newer version of phyloseq
#install it using:
#library("devtools")
#install_github("joey711/phyloseq")


library(phyloseq)
library(vegan)
library(ggplot2)
library(ape)
library(phangorn)
library(stringr)
```

```
library(grid)

#PARAMETERS ###########################
which_level<-"Otus" #Phylum Class Order Family Genus Otus
kind <- "sd" #sd se (sd is for drawing ellipse based on sd, se is for drawing ellipse based on standard errors)
which_distance<-"unifrac" #bray unifrac wunifrac
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
#Load the tree using ape package
OTU_tree <- read.tree("../../Data/tree.nwk")


exclude_legends=FALSE
draw_mean_values_text=FALSE
point_size=6
point_opacity=1
draw_glow=FALSE
point_glow_opacity=0.2
point_glow_differential=3
mean_values_text_size=8
mean_values_text_opacity=1
draw_confidence_intervals=TRUE
draw_ellipses_and_not_polygons=FALSE
pairwise_connections_and_not_longitudinal_connections=FALSE#FALSE
should_connections_end_in_arrows=TRUE
should_we_reverse_direction_of_arrows=TRUE
opacity_ellipses_polygons=0.25
linesize_ellipses_polygons=0.8
linetype_ellipses_polygons="blank" #blank solid dashed dotted dotdash longdash twodash
linking_samples_line_size=1
linking_samples_line_opacity=1.0
linking_samples_linetype="solid" #blank solid dashed dotted dotdash longdash twodash
legend_text_size=20
legend_title_size=20
axis_title_size=30
text_size=30
axis_text_size=26
height_image=10 #15
width_image=15
use_provided_colors=TRUE
#/PARAMETERS ###########################

abund_table<-otu_table(physeq)
```

```
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]


OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment",
and "non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") |
OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") |
OTU_taxonomy$Family %in% c("Mitochondria"))]


#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
#when reducing the abund_table, there is a high likelihood that an OTU was only present in
a sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their
dimensions should match
#/DATA
IMPORT############################################################
```

```
#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE############################
#In the hypothesis space, all you need is to select the rows in meta_table you are interested in
#and then allocate a column to meta_table$Groups that you want to use, meta_table$Connections to connect them
#additionally if you provide a second meta_table$Subconnections, it will connect the group averages
#You can use meta_table$Type to assign shape and PERMANOVA_variables to give variables

label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "Tanzania",
   "Vietnam"
))
colours <- c(
   "#ff9999",
   "#660000",
   #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Latrine))
meta_table$Connections<-NULL
meta_table$Subconnections<-NULL
PERMANOVA_variables<-c("Country","Latrine","Depth")

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "4",
   "3",
   "2",
   "1"
```

```
))
colours <- c(
  "#ff9999",
  "#660000",
  "#660FF0",
  "#600006",
  #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Country))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
  #Cross-sectional comparisons
  combn(c( "1",
           "2",
           "3",
           "4"),2)
)

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE############################

#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]
#Adjust OTU taxonomy
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]


#COLLATE OTUS AT A PARTICULAR LEVEL#######################################
new_abund_table<-NULL
if(which_level=="Otus"){
  new_abund_table<-abund_table
} else {
  list<-unique(OTU_taxonomy[,which_level])
  new_abund_table<-NULL
  for(i in list){
    tmp<-
data.frame(rowSums(abund_table[,rownames(OTU_taxonomy)[OTU_taxonomy[,which_level]==i],drop=FALSE]))
```

```
      if(i==""){colnames(tmp)<-c("__Unknowns__")} else {
         #colnames(tmp)<-paste("",i,sep="")
         colnames(tmp)<-gsub(";+$","",paste(sapply(OTU_taxonomy[OTU_taxonomy[,which_level]==i,][1,1:which(colnames(OTU_taxonomy)==which_level)],as.character),collapse=";"))
      }
      if(is.null(new_abund_table)){new_abund_table<-tmp} else {new_abund_table<-cbind(tmp,new_abund_table)}
   }
}

new_abund_table<-as.data.frame(as(new_abund_table,"matrix"))
abund_table<-new_abund_table
#/COLLATE OTUS AT A PARTICULAR LEVEL#######################################


#Convert the data to phyloseq format
OTU = otu_table(as.matrix(abund_table), taxa_are_rows = FALSE)
TAX = tax_table(as.matrix(OTU_taxonomy))
SAM = sample_data(meta_table)

physeq<-NULL
if(which_level=="Otus"){
   physeq<-merge_phyloseq(phyloseq(OTU, TAX),SAM,OTU_tree)
} else {
   physeq<-merge_phyloseq(phyloseq(OTU),SAM)
}
```

Script 2: R script of beta diversity.

Appendix c

The R script and data below are related to the value of NRI/NTI calculations.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to "To Source File Location"
#Script for calculation of phylogenetic alpha diversity metrics such as NRI/NTI
#to give an account of stochastic versus deterministic nature of microbial communities
#v1.2 (All metrics are now being saved)

library(phyloseq)
library(ape)
library(picante)
library(data.table)
```

```
#PARAMETERS ###########################
runs=999
iterations=1000
Top_N_abundant_OTUs=2000
abundance.weighted = FALSE
null.model= "richness" #taxa.labels richness    frequency sample.pool phylogeny.pool independentswap trialswap
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
#Load the tree using ape package
OTU_tree <- read.tree("../../Data/tree.nwk")
text_size=16
axis_text_size=14
strip_text_size=18
increment_divider=2
exclude_pvalues_text_from_drawing=FALSE
legends_position_bottom=FALSE
exclude_legends=TRUE
pairwise_text_size=7
number_of_rows=1
legend_text_size=20
legend_title_size=22
axis_title_size=20
height_image=9
width_image=15
smoothing_alpha=0.3
use_provided_colors=TRUE
turn_smoothing_on=FALSE
#PARAMETERS ###########################

abund_table<-otu_table(physeq)
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]

OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
```

```
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment",
and "non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") |
OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") |
OTU_taxonomy$Family %in% c("Mitochondria"))]

#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
#when reducing the abund_table, there is a high likelihood that an OTU was only present in
a sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their
dimensions should match
#/DATA
IMPORT############################################################

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE############################
#In the hypothesis space, all you need is to select the rows in meta_table you are interested
in
#and then allocate a column to meta_table$Groups that you want to use.
#
label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "Tanzania",
   "Vietnam"
```

```
))
colours <- c(
   "#ff9999",
   "#660000",
   #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(100
0));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Latrine))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
   #Cross-sectional comparisons
   combn(c( "Tanzania",
                "Vietnam"),2)
)

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "4",
   "3",
   "2",
   "1"
))
colours <- c(
   "#ff9999",
   "#660000",
   "#660FF0",
   "#600006",
   #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(100
0));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Country))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
   #Cross-sectional comparisons
   combn(c( "1",
                "2",
```

```
                    "3",
                    "4"),2)
)
# PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE##############################



second_label="Unweighted"
if(abundance.weighted){
   second_label="Weighted"
}

#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]

#We extract N most abundant OTUs
abund_table<-
abund_table[,order(colSums(abund_table),decreasing=TRUE)][,1:min(Top_N_abundant_OTUs
,dim(abund_table)[2])]

#Adjust OTU_tree
OTU_tree<-drop.tip(OTU_tree,OTU_tree$tip.label[!OTU_tree$tip.label %in%
colnames(abund_table)])

#There is a bug in adespatial as it doesn't like phyloseq's class and won't calculate
#the values, so I am forcing it to become matrix
abund_table<-as(abund_table,"matrix")

#Reference http://kembellab.ca/r-workshop/biodivR/SK_Biodiversity_R.html
abund_table.sesmpd <- ses.mpd(abund_table, cophenetic(OTU_tree),   null.model =
null.model, abundance.weighted = abundance.weighted,
                                runs = runs, iterations=iterations)
abund_table.sesmntd <- ses.mntd(abund_table, cophenetic(OTU_tree),   null.model =
null.model, abundance.weighted = abundance.weighted,
                                    runs = runs, iterations=iterations)

#Write all the metrics in a file for further analyses elsewhere
data_to_write<-
data.frame(abund_table.sesmpd[,"mpd.obs.z",drop=F],abund_table.sesmntd[,"mntd.obs.z",d
rop=F])
#Convert SES scores to NRI/NTI
```

```
data_to_write<-data_to_write*-1
colnames(data_to_write)<-c("NRI","NTI")
write.csv(data_to_write,file=paste("Environmental_Filtering","_",second_label,"_",label,"_",null.
model,".csv",sep=""))
#/Write all the metrics in a file for further analyses elsewhere

#Positive SES values (abund_table.sesmpd$mpd.obs.z > 0) and high quantiles
(abund_table.sesmpd$mpd.obs.p > 0.95)
#indicate phylogenetic evenness, while negative SES values and low quantiles
(abund_table.sesmpd$mpd.obs.p < 0.05)
#indicate phylogenetic clustering, relative to the null model. MPD is generally thought to be
more sensitive to
#tree-wide patterns of phylogenetic clustering and eveness, while MNTD is more sensitive
to patterns of evenness
#and clustering closer to the tips of the phylogeny.
df<-rbind(data.frame(value=-
1*abund_table.sesmpd$mpd.obs.z,meta_table,measure="NRI"),
          data.frame(value=-
1*abund_table.sesmntd$mntd.obs.z,meta_table,measure="NTI"))

#To do anova, we will convert our data.frame to data.table
library(data.table)
grouping_column="Groups"
#Since we can't pass a formula to data.table, I am creating
#a dummy column .group. so that I don't change names in the formula
dt<-data.table(data.frame(df,.group.=df[,grouping_column]))

#I am also specifying a p-value cutoff for the ggplot2 strips
pValueCutoff<-0.05
pval<-dt[, list(pvalue = sprintf("%.2g",
                              tryCatch(summary(aov(value
~ .group.))[[1]][["Pr(>F)"]][1],error=function(e) NULL))),
         by=list(measure)]

#Filter out pvals that we don't want
pval<-pval[!pval$pvalue=="",]
pval<-pval[as.numeric(pval$pvalue)<=pValueCutoff,]

#I am using sapply to generate significances for pval$pvalue using the cut function.
pval$pvalue<-sapply(as.numeric(pval$pvalue),function(x){as.character(cut(x,breaks=c(-Inf,
0.001, 0.01, 0.05, Inf),label=c("***", "**", "*", "")))})

#Update df$measure to change the measure names if the grouping_column has more than
three classes
```

```
if(length(unique(as.character(df[,grouping_column])))>2){
   df$measure<-as.character(df$measure)
   if(dim(pval)[1]>0){
      for(i in seq(1:dim(pval)[1])){

df[df$measure==as.character(pval[i,measure]),"measure"]=paste(as.character(pval[i,measure
]),as.character(pval[i,pvalue]))
      }
   }
   df$measure<-as.factor(df$measure)
}

#Get all possible combination of values in the grouping_column
s<-NULL
if(provide_your_own_pvalue_combinations){
   s<-provided_combination
} else{
   s<-combn(unique(as.character(df[,grouping_column])),2)
}

#df_pw will store the pair-wise p-values
df_pw<-NULL
for(k in unique(as.character(df$measure))){
   #We need to calculate the coordinate to draw pair-wise significance lines
   #for this we calculate bas as the maximum value
   bas<-max(df[(df$measure==k),"value"])

   #Calculate increments as % of the maximum values
   inc<-0.05*(bas-min(df[(df$measure==k),"value"]))

   #Give an initial increment
   bas<-bas+inc
   for(l in 1:dim(s)[2]){

      #Do a pair-wise anova
      tmp<-
c(k,s[1,l],s[2,l],bas,paste(sprintf("%.2g",tryCatch(summary(aov(as.formula(paste("value
~",grouping_column)),data=df[(df$measure==k) & (df[,grouping_column]==s[1,l] |
df[,grouping_column]==s[2,l]),] ))[[1]][["Pr(>F)"]][1],error=function(e) NULL)),"",sep=""))

      #Ignore if anova fails
      if(!is.na(as.numeric(tmp[length(tmp)]))){

         #Only retain those pairs where the p-values are significant
```

```
            if(as.numeric(tmp[length(tmp)])<0.05){
                if(is.null(df_pw)){df_pw<-tmp}else{df_pw<-rbind(df_pw,tmp)}

                #Generate the next position
                bas<-bas+inc
            }
        }
    }
}

if(!is.null(df_pw)){
    if(class(df_pw)=="character"){
        df_pw<-t(as.matrix(df_pw))
    }
    df_pw<-data.frame(row.names=NULL,df_pw)
    names(df_pw)<-c("measure","from","to","y","p")
}

library(ggplot2)

#We need grid to draw the arrows
library(grid)
#Get rid of NA columns
df<-df[complete.cases(df$value),]

#Draw the boxplots
p<-ggplot(aes_string(x=grouping_column,y="value",color=grouping_column,group=grouping_column,shape="Type"),data=df)
if(turn_smoothing_on){
p<-p + geom_smooth(aes(x=Groups,y=value,fill=Type,group=Type),method=loess,linetype=0,alpha=smoothing_alpha)
}
p<-p+geom_boxplot(outlier.size=0,show.legend=FALSE,position="identity")+geom_jitter(position = position_jitter(height = 0, width=0), size=4)
p<-p+theme_bw()


p<-p+facet_wrap(~measure,scales="free_y",nrow=number_of_rows)+ylab("Observed Values\n")+xlab("\nSamples")

if(!is.null(df_pw)){
```

```
    #This loop will generate the lines and signficances
    for(i in 1:dim(df_pw)[1]){
        p<-p+geom_path(inherit.aes=F,aes(x,y),data = data.frame(x =
c(which(levels(df[,grouping_column])==as.character(df_pw[i,"from"])),which(levels(df[,groupi
ng_column])==as.character(df_pw[i,"to"]))), y =
c(as.numeric(as.character(df_pw[i,"y"])),as.numeric(as.character(df_pw[i,"y"]))),
measure=c(as.character(df_pw[i,"measure"]),as.character(df_pw[i,"measure"]))),
color="black",lineend = "butt",arrow = arrow(angle = 90, ends = "both", length = unit(0.1,
"inches")))
        p<-
p+geom_text(inherit.aes=F,aes(x=x,y=y,label=label),data=data.frame(x=(which(levels(df[,gro
uping_column])==as.character(df_pw[i,"from"]))+which(levels(df[,grouping_column])==as.ch
aracter(df_pw[i,"to"])))/2,y=as.numeric(as.character(df_pw[i,"y"])),measure=as.character(df_p
w[i,"measure"]),label=as.character(cut(as.numeric(as.character(df_pw[i,"p"])),breaks=c(-Inf,
0.001, 0.01, 0.05, Inf),label=c("***", "**", "*", ""))))),size=pairwise_text_size)
        if(exclude_pvalues_text_from_drawing){
            p<-
p+geom_text(inherit.aes=F,aes(x=x,y=y,label=label),data=data.frame(x=(which(levels(df[,gro
uping_column])==as.character(df_pw[i,"from"]))+which(levels(df[,grouping_column])==as.ch
aracter(df_pw[i,"to"])))/2,y=as.numeric(as.character(df_pw[i,"y"])),measure=as.character(df_p
w[i,"measure"]),label=paste("p=",as.character(as.numeric(as.character(df_pw[i,"p"])))),sep="")),
size=pairwise_text_size,vjust=-1)
        }
    }
}
if(use_provided_colors){
    p<-p+scale_color_manual(grouping_column,values=colours)
}

if(!is.null(meta_table$Type)){
    p<-p+scale_shape_manual("Type",values=c(c(0:25),c(33:127)))
}

#if crashes at panel.margin change it to panel.spacing, if crashes at panel.spacing, change it
to panel.margin
p<-p+theme(strip.background = element_rect(fill="white"))+theme(panel.spacing = unit(2,
"lines"),
                                                                  strip.text =
element_text(size=strip_text_size),

legend.text=element_text(size=legend_text_size),
                                                                  legend.title =
element_text(size=legend_title_size),
                                                                  text =
```

```
element_text(size=text_size),

axis.text=element_text(size=axis_text_size),

axis.title=element_text(size=axis_title_size),
                                                                              axis.text.x =
element_text(angle = 90, hjust = 1))
if(legends_position_bottom){
  p<-p+theme(legend.key = element_blank(),   #removes the box around each legend
item
             legend.position = "bottom", #legend at the bottom
             legend.direction = "horizontal",
             legend.box = "horizontal",
             legend.box.just = "centre")
}
if(exclude_legends){
  p<-p+guides(colour=FALSE)
}

p<-p+theme(axis.title.x=element_blank(),
           #axis.text.x=element_blank(),
           axis.ticks.x=element_blank())

pdf(paste("PC_vs_OD","_",second_label,"_",label,"_",null.model,".pdf",sep=""),height=height_i
mage,width=width_image)
print(p)
dev.off()
```

Script 3: R script of NRI/NTI

	NRI	NTI
T_2_1	3.845057	6.935214
T_2_2	4.909081	5.664437
T_2_3	7.130528	6.322857
T_2_6	8.190531	6.775391
T_2_9	7.295184	6.138107
T_4_3	0.329542	1.783808
T_4_4	7.332925	8.434502
T_4_5	7.475298	8.531849
T_5_2	8.623363	6.54462
T_5_3	7.77714	7.053118
T_6_7	5.808864	6.569973
T_6_8	5.649985	6.10038
T_9_2	-0.51721	4.967308
T_9_4	0.583104	4.128598

V_1_2	2.668164	9.033791
V_2_2	-2.59084	7.679408
V_3_1	0.826848	8.700525
V_3_2	0.045941	9.041407
V_5_3	1.783831	7.884012
V_6_1	-0.28639	7.034421
V_6_2	1.379832	5.425554
V_6_3	-0.50976	6.235372
V_7_1	0.285013	8.921781
V_7_2	-1.60118	8.029974
V_7_3	3.790993	6.03822
V_8_2	1.85427	7.903377
V_9_1	0.374151	5.558546
V_9_2	-1.94519	7.402462
V_9_4	4.575878	4.961922
V_10_1	3.179037	8.205818
V_11_1	-2.28112	8.852302
V_11_3	-1.15316	8.753426
V_12_1	0.038198	9.15578
V_13_2	0.229193	6.682426
V_14_1	3.158316	7.460852
V_15_1	1.157071	7.221521
V_15_2	1.679147	5.167956
V_15_3	0.548396	5.130229
V_16_1	1.996733	7.898132
V_16_2	2.820094	8.07112
V_17_1	0.137038	7.500397
V_17_2	0.961429	7.376089
V_18_1	3.732864	7.90673
V_18_2	2.928977	6.537826
V_18_4	1.380278	4.772604
V_19_1	-0.05403	8.621909
V_19_3	2.654637	6.395657
V_20_1	-2.74528	8.666107
V_21_1	-0.38418	8.410149
V_22_1	0.604463	7.551052
V_22_3	-0.39524	5.358477
V_22_4	-0.46138	7.462683

Table 3： NRI/NTI of hypothesis 1.

	NRI	NTI
T_2_1	4.445458	6.699261
T_2_2	5.45279	5.876561

T_2_3	7.43337	5.985757
T_4_3	0.599443	1.817555
T_4_4	6.202035	7.700354
T_5_2	8.823179	6.520504
T_5_3	8.705303	6.481279
T_9_2	-0.06037	4.829443
T_9_4	1.098666	3.972081
V_1_2	3.240939	9.263716
V_2_2	-1.87136	7.572567
V_3_1	1.637676	9.038842
V_3_2	0.974098	9.683856
V_5_3	2.337852	7.406061
V_6_1	0.293122	7.389244
V_6_2	2.046531	5.317272
V_6_3	-0.00287	6.249354
V_7_1	0.713179	9.109753
V_7_2	-0.91903	7.333793
V_7_3	4.577433	6.29139
V_8_2	2.734216	7.598753
V_9_1	0.473221	5.513401
V_9_2	-1.62999	7.503693
V_9_4	5.298608	5.061919
V_10_1	4.05727	8.083371
V_11_1	-1.54128	8.553111
V_11_3	0.052106	9.012462
V_12_1	0.46573	9.417509
V_13_2	0.990931	6.752877
V_14_1	3.792841	7.144873
V_15_1	1.667152	7.008651
V_15_2	2.225954	5.451503
V_15_3	1.33368	4.769537
V_16_1	3.180233	8.141802
V_16_2	3.579895	7.666763
V_17_1	0.793731	7.136733
V_17_2	1.679033	7.630259
V_18_1	4.356683	7.724908
V_18_2	3.41854	6.709737
V_18_4	2.09065	4.198334
V_19_1	0.475506	7.723208
V_19_3	3.189744	6.235478
V_20_1	-2.00794	8.105097
V_21_1	0.180719	8.46152
V_22_1	1.456292	7.715093

V_22_3	0.120759	4.909991
V_22_4	-0.12161	7.202116

Table 4： NRI/NTI of hypothesis 2.

Appendix d

The R script and data below are related to the value of QPE.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to "To Source File Location"
#Script for null modelling (beta NTI, Raup-Crick Beta-Diversity, and Elements of Metacommunity)
#Reference: http://uu.diva-portal.org/smash/get/diva2:1373632/DATASET09.txt
#v1.0 (All metrics are now being saved)
#v1.1 (Found a serious bug as Raup-Crick Beta-Diversity can be used in both incidence and Bray-Curtis model)

library(phyloseq)
library(vegan)
library(ape)
library(picante)
library(ecodist)
library(metacom)

#PARAMETERS ############################
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
#Load the tree using ape package
OTU_tree <- read.tree("../../Data/tree.nwk")
#/PARAMETERS ############################

abund_table<-otu_table(physeq)
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]


OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
```

```
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment",
and "non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") |
OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") |
OTU_taxonomy$Family %in% c("Mitochondria"))]


#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
#when reducing the abund_table, there is a high likelihood that an OTU was only present in
a sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their
dimensions should match
#/DATA
IMPORT###############################################################

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE############################
#In the hypothesis space, all you need is to select the rows in meta_table you are interested
in
#and then allocate a column to meta_table$Groups that you want to use.

label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
"Tanzania",
```

```
"Vietnam"
))

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "4",
   "3",
   "2",
   "1"
))
colours <- c(
   "#ff9999",
   "#660000",
   "#660FF0",
   "#600006",
   #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Country))
provide_your_own_pvalue_combinations<-TRUE
provided_combination<-cbind(
   #Cross-sectional comparisons
   combn(c( "1",
            "2",
            "3",
            "4"),2)
)

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE############################

#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]
#Adjust OTU taxonomy
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
```

```
#Convert the data to phyloseq format
OTU = otu_table(as.matrix(abund_table), taxa_are_rows = FALSE)
TAX = tax_table(as.matrix(OTU_taxonomy))
SAM = sample_data(meta_table)

physeq<-merge_phyloseq(phyloseq(OTU, TAX),SAM,OTU_tree)

#Pruning and subsampling
physeq<-prune_taxa(taxa_sums(physeq)>10, physeq)

#Rarefy to minimum sample size
physeq_rel = rarefy_even_depth(physeq, sample.size = min(sample_sums(physeq)))


#incidence_based Raup_Crick:
https://github.com/jfq3/QsNullModels/blob/master/R/raup_crick.R
raup_crick=function(spXsite, plot_names_in_col1=FALSE, classic_metric=FALSE,
                    split_ties=TRUE, reps=999, set_all_species_equal=FALSE,
                    as.distance.matrix=TRUE, report_similarity=FALSE){

  # expects a species by site matrix for spXsite, with row names for plots,
  # or optionally plots named in column 1.  By default calculates a modification
  # of the Raup-Crick metric (standardizing the metric to range from -1 to 1
  # instead of 0 to 1). Specifying classic_metric=TRUE instead calculates the
  # original Raup-Crick metric that ranges from 0 to 1. The option split_ties
  # (defaults to TRUE) adds half of the number of null observations that are
  # equal to the observed number of shared species to the calculation- this
  # is highly recommended.  The argument report_similarity defaults to FALSE
  # so the function reports a dissimilarity (which is appropriate as a measure
  # of beta diversity).  Setting report_similarity=TRUE returns a measure of
  # similarity, as Raup and Crick originally specified.  If ties are split
  # (as we recommend) the dissimilarity (default) and similarity (set
  # report_similarity=TRUE) calculations can be flipped by multiplying by -1
  # (for our modification, which ranges from -1 to 1) or by subtracting the
  # metric from 1 (for the classic metric which ranges from 0 to 1). If ties
  # are not split (and there are ties between the observed and expected shared
  # number of species) this conversion will not work. The argument reps specifies
  # the number of randomizations (a minimum of 999 is recommended- default was
  # 9999).  set_all_species_equal weights all species equally in the null model
  # instead of weighting species by frequency of occupancy.

  # Note that the choice of how many plots (rows) to include has a real impact
  # on the metric, as species and their occurrence frequencies across the set
  # of plots is used to determine gamma and the frequency with which each
```

```
# species is drawn from the null model

# this section moves plot names in column 1 (if specified as being present)
# into the row names of the matrix and drops the column of names
if(plot_names_in_col1){
   row.names(spXsite)<-spXsite[,1]
   spXsite<-spXsite[,-1]
}

# count number of sites and total species richness across all plots (gamma)
n_sites<-nrow(spXsite)
gamma<-ncol(spXsite)

# make the spXsite matrix into a pres/abs. (overwrites initial spXsite matrix):
ceiling(spXsite/max(spXsite))->spXsite

# create an occurrence vector- used to give more weight to widely distributed
# species in the null model:
occur<-apply(spXsite, MARGIN=2, FUN=sum)

# NOT recommended- this is a non-trivial change to the metric:
# sets all species to occur with equal frequency in the null model
# e.g.- discards any occupancy frequency information
if(set_all_species_equal){
   occur<-rep(1,gamma)
}

# determine how many unique species richness values are in the dataset
# this is used to limit the number of null communities that have to be
# calculated
alpha_levels<-sort(unique(apply(spXsite, MARGIN=1, FUN=sum)))

# make_null:

# alpha_table is used as a lookup to help identify which null distribution
# to use for the tests later.   It contains one row for each combination of
# alpha richness levels.

alpha_table<-data.frame(c(NA), c(NA))
names(alpha_table)<-c("smaller_alpha", "bigger_alpha")
col_count<-1

# null_array will hold the actual null distribution values.   Each element
# of the array corresponds to a null distribution for each combination of
```

```
  # alpha values.  The alpha_table is used to point to the correct null
  # distribution- the row numbers of alpha_table correspond to the [[x]]
  # indices of the null_array.  Later the function will find the row of
  # alpha_table with the right combination of alpha values.  That row number
  # is used to identify the element of null_array that contains the correct
  # null distribution for that combination of alpha levels.

  null_array<-list()

  # looping over each combination of alpha levels:

  for(a1 in 1:length(alpha_levels)){
    for(a2 in a1:length(alpha_levels)){

      # build a null distribution of the number of shared species for a
      # pair of alpha values:
      null_shared_spp<-NULL
      for(i in 1:reps){

        # two empty null communities of size gamma:
        com1<-rep(0,gamma)
        com2<-rep(0,gamma)

        # add alpha1 number of species to com1, weighting by species occurrence
frequencies:
        com1[sample(1:gamma, alpha_levels[a1], replace=FALSE, prob=occur)]<-1

        # same for com2:
        com2[sample(1:gamma, alpha_levels[a2], replace=FALSE, prob=occur)]<-1

        # how many species are shared in common?
        null_shared_spp[i]<-sum((com1+com2)>1)

      }

      # store null distribution, record values for alpha 1 and 2 in the alpha_table to
      # help find the correct null distribution later:
      null_array[[col_count]]<-null_shared_spp

      alpha_table[col_count, which(names(alpha_table)=="smaller_alpha")]<-
alpha_levels[a1]
      alpha_table[col_count, which(names(alpha_table)=="bigger_alpha")]<-
alpha_levels[a2]
```

```
      # increment the counter for the columns of the alpha table/ elements of the null array
      col_count<-col_count+1

    }

  }

  # create a new column with both alpha levels to match on:
  alpha_table$matching<-paste(alpha_table[,1], alpha_table[,2], sep="_")

  ######################
  # do the test:

  # build a site by site matrix for the results, with the names of the sites in the row and col
names:
  results<-matrix(data=NA, nrow=n_sites, ncol=n_sites, dimnames=list(row.names(spXsite),
row.names(spXsite)))

  # for each pair of sites (duplicates effort now to make a full matrix instead
  # of a half one- but this part should be minimal time as compared to the null
  # model building)
  for(i in 1:n_sites){
    for(j in 1:n_sites){

      # how many species are shared between the two sites:
      n_shared_obs<-sum((spXsite[i,]+spXsite[j,])>1)

      # what was the observed richness of each site?
      obs_a1<-sum(spXsite[i,])
      obs_a2<-sum(spXsite[j,])

      # place these alphas into an object to match against alpha_table (sort so
      # smaller alpha is first)
      obs_a_pair<-sort(c(obs_a1, obs_a2))

      # match against the alpha table- row index identifies which element of the
      # null array contains the correct null distribution for the observed
      # combination of alpha values:
      null_index<-which(alpha_table$matching==paste(obs_a_pair[1], obs_a_pair[2],
sep="_"))

      # how many null observations is the observed value tied with?
      num_exact_matching_in_null<-sum(null_array[[null_index]]==n_shared_obs)
```

```
            # how many null values are bigger than the observed value?
            num_greater_in_null<-sum(null_array[[null_index]]>n_shared_obs)

            rc<-(num_greater_in_null)/reps

            if(split_ties){

                rc<-((num_greater_in_null+(num_exact_matching_in_null)/2)/reps)
            }

            if(!classic_metric){

                # our modification of raup crick standardizes the metric to range
                # from -1 to 1 instead of 0 to 1

                rc<-(rc-.5)*2
            }

            #   at this point rc represents an index of dissimilarity- multiply by -1
            # to convert to a similarity as specified in the original 1979 Raup Crick paper
            if(report_similarity & !classic_metric){
                rc<- rc*-1
            }

            # the switch to similarity is done differently if the original 0 to 1 range
            # of the metric is used:
            if(report_similarity & classic_metric){
                rc<- 1-rc
            }

            # store the metric in the results matrix:
            results[i,j]<-round(rc, digits=2)

        }
    }

    if(as.distance.matrix){
        results<-as.dist(results)
    }

    return(results)

}
```

```
# Second step of the QPE approach (abundance-based Raup-Crick beta-diversity)
raup_crick_abundance = function(spXsite, plot_names_in_col1=TRUE, classic_metric=FALSE,
split_ties=TRUE, reps=9999, set_all_species_equal=FALSE, as.distance.matrix=TRUE,
report_similarity=FALSE){

  ##expects a species by site matrix for spXsite, with row names for plots, or optionally plots
named in column 1.  By default calculates a modification of the Raup-Crick metric
(standardizing the metric to range from -1 to 1 instead of 0 to 1). Specifying
classic_metric=TRUE instead calculates the original Raup-Crick metric that ranges from 0 to
1. The option split_ties (defaults to TRUE) adds half of the number of null observations that
are equal to the observed number of shared species to the calculation- this is highly
recommended.  The argument report_similarity defaults to FALSE so the function reports a
dissimilarity (which is appropriate as a measure of beta diversity).  Setting
report_similarity=TRUE returns a measure of similarity, as Raup and Crick originally specified.
If ties are split (as we recommend) the dissimilarity (default) and similarity (set
report_similarity=TRUE) calculations can be flipped by multiplying by -1 (for our modification,
which ranges from -1 to 1) or by subtracting the metric from 1 (for the classic metric which
ranges from 0 to 1). If ties are not split (and there are ties between the observed and expected
shared number of species) this conversion will not work. The argument reps specifies the
number of randomizations (a minimum of 999 is recommended- default is 9999).
set_all_species_equal weights all species equally in the null model instead of weighting species
by frequency of occupancy.


  ##Note that the choice of how many plots (rows) to include has a real impact on the metric,
as species and their occurrence frequencies across the set of plots is used to determine
gamma and the frequency with which each species is drawn from the null model


  ##this section moves plot names in column 1 (if specified as being present) into the row
names of the matrix and drops the column of names
  if(plot_names_in_col1){
    row.names(spXsite)<-spXsite[,1]
    spXsite<-spXsite[,-1]
  }


  ## count number of sites and total species richness across all plots (gamma)
  n_sites<-nrow(spXsite)
  gamma<-ncol(spXsite)
```

```
  ##build a site by site matrix for the results, with the names of the sites in the row and col
names:
  results<-matrix(data=NA, nrow=n_sites, ncol=n_sites, dimnames=list(row.names(spXsite),
row.names(spXsite)))

  ##make the spXsite matrix into a new, pres/abs. matrix:
  ceiling(spXsite/max(spXsite))->spXsite.inc

  ##create an occurrence vector- used to give more weight to widely distributed species in
the null model:
  occur<-apply(spXsite.inc, MARGIN=2, FUN=sum)

  ##create an abundance vector- used to give more weight to abundant species in the
second step of the null model:
  abundance<-apply(spXsite, MARGIN=2, FUN=sum)

  ##make_null:

  ##looping over each pairwise community combination:

  for(null.one in 1:(nrow(spXsite)-1)){
    for(null.two in (null.one+1):nrow(spXsite)){

      null_bray_curtis<-NULL
      for(i in 1:reps){

        ##two empty null communities of size gamma:
        com1<-rep(0,gamma)
        com2<-rep(0,gamma)

        ##add observed number of species to com1, weighting by species occurrence
frequencies:
        com1[sample(1:gamma, sum(spXsite.inc[null.one,]), replace=FALSE,
prob=occur)]<-1
        com1.samp.sp = sample(which(com1>0),(sum(spXsite[null.one,])-
sum(com1)),replace=TRUE,prob=abundance[which(com1>0)]);
        com1.samp.sp = cbind(com1.samp.sp,1); # head(com1.samp.sp);
        com1.sp.counts =
as.data.frame(tapply(com1.samp.sp[,2],com1.samp.sp[,1],FUN=sum));
colnames(com1.sp.counts) = 'counts'; # head(com1.sp.counts);
        com1.sp.counts$sp = as.numeric(rownames(com1.sp.counts)); #
head(com1.sp.counts);
        com1[com1.sp.counts$sp] = com1[com1.sp.counts$sp] + com1.sp.counts$counts; #
```

```
com1;
        #sum(com1) - sum(spXsite[null.one,]); ## this should be zero if everything work
properly
        rm('com1.samp.sp','com1.sp.counts');

        ##same for com2:
        com2[sample(1:gamma, sum(spXsite.inc[null.two,]), replace=FALSE, prob=occur)]<-
1
        com2.samp.sp = sample(which(com2>0),(sum(spXsite[null.two,])-
sum(com2)),replace=TRUE,prob=abundance[which(com2>0)]);
        com2.samp.sp = cbind(com2.samp.sp,1); # head(com2.samp.sp);
        com2.sp.counts =
as.data.frame(tapply(com2.samp.sp[,2],com2.samp.sp[,1],FUN=sum));
colnames(com2.sp.counts) = 'counts'; # head(com2.sp.counts);
        com2.sp.counts$sp = as.numeric(rownames(com2.sp.counts)); #
head(com2.sp.counts);
        com2[com2.sp.counts$sp] = com2[com2.sp.counts$sp] + com2.sp.counts$counts; #
com2;
        # sum(com2) - sum(spXsite[null.two,]); ## this should be zero if everything work
properly
        rm('com2.samp.sp','com2.sp.counts');

        null.spXsite = rbind(com1,com2); # null.spXsite;

        ##calculate null bray curtis
        null_bray_curtis[i] = ecodist::distance(null.spXsite,method='bray-curtis');

      }; # end reps loop

      ## empirically observed bray curtis
      obs.bray = ecodist::distance(spXsite[c(null.one,null.two),],method='bray-curtis');

      ##how many null observations is the observed value tied with?
      num_exact_matching_in_null = sum(null_bray_curtis==obs.bray);

      ##how many null values are smaller than the observed *dissimilarity*?
      num_less_than_in_null = sum(null_bray_curtis<obs.bray);

      rc = (num_less_than_in_null )/reps; # rc;

      if(split_ties){

        rc = ((num_less_than_in_null +(num_exact_matching_in_null)/2)/reps)
      };
```

```
      if(!classic_metric){

        ##our modification of raup crick standardizes the metric to range from -1 to 1 instead of 0 to 1

        rc = (rc-.5)*2
      };

      results[null.two,null.one] = round(rc,digits=2); ##store the metric in the results matrix

      print(c(null.one,null.two,date()));

    }; ## end null.two loop

  }; ## end null.one loop

  if(as.distance.matrix){ ## return as distance matrix if so desired
    results<-as.dist(results)
  }

  return(results)

}; ## end function


summarySE <- function(data=NULL, measurevar, groupvars=NULL, na.rm=FALSE,
                      conf.interval=.95, .drop=TRUE) {
  library(plyr)

  # New version of length which can handle NA's: if na.rm==T, don't count them
  length2 <- function (x, na.rm=FALSE) {
    if (na.rm) sum(!is.na(x))
    else       length(x)
  }

  # This does the summary. For each group's data frame, return a vector with
  # N, mean, and sd
  datac <- ddply(data, groupvars, .drop=.drop,
                 .fun = function(xx, col) {
                   c(N    = length2(xx[[col]], na.rm=na.rm),
                     mean = mean   (xx[[col]], na.rm=na.rm),
                     sd   = sd     (xx[[col]], na.rm=na.rm)
```

```
                                    )
                                }, 
                                measurevar
    )

    # Rename the "mean" column
    datac <- rename(datac, c("mean" = measurevar))

    datac$se <- datac$sd / sqrt(datac$N)  # Calculate standard error of the mean

    # Confidence interval multiplier for standard error
    # Calculate t-statistic for confidence interval: 
    # e.g., if conf.interval is .95, use .975 (above/below), and use df=N-1
    ciMult <- qt(conf.interval/2 + .5, datac$N-1)
    datac$ci <- datac$se * ciMult

    return(datac)
}


abund_table_ems<-otu_table(physeq_rel)
meta_table_ems<-sample_data(physeq_rel)

collated_coherence<-NULL
collated_turnover<-NULL
collated_boundary<-NULL
collated_sitescores<-NULL
collated_pairwise_RC_abundance<-NULL
collated_pairwise_RC_incidence<-NULL
collated_pairwise_bNTI<-NULL

for(i in 1:nlevels(meta_table_ems$Groups)){
    abund_table_ems_group<-
abund_table_ems[meta_table_ems$Groups==levels(meta_table_ems$Groups)[i],,drop=F]
    abund_table_ems_group =
abund_table_ems_group[,which(colSums(abund_table_ems_group) != 0)]

    #Now calculate Elements of Metacommunity
    met_ems_group=Metacommunity( abund_table_ems_group, scores = 1, method = "r1",
sims = 999, order = T, binary = F, verbose=T, allowEmpty=T)
    om_ems_group=OrderMatrix(abund_table_ems_group, outputScores=T, binary=F)

    coherence<-t(data.frame(row.names=met_ems_group$Coherence[-
nrow(met_ems_group$Coherence),1],stats=met_ems_group$Coherence[-
```

```
nrow(met_ems_group$Coherence),2]))
  rownames(coherence)<-levels(meta_table$Groups)[i]

  turnover<-t(data.frame(row.names=met_ems_group$Turnover[-
nrow(met_ems_group$Turnover),1],stats=met_ems_group$Turnover[-
nrow(met_ems_group$Turnover),2]))
  rownames(turnover)<-levels(meta_table$Groups)[i]

  boundary<-
t(data.frame(row.names=met_ems_group$Boundary[,1],stats=met_ems_group$Boundary[,2]
))
  rownames(boundary)<-levels(meta_table$Groups)[i]

  sitescores<-data.frame(om_ems_group$sitescores)
  colnames(sitescores)<-c("sitescores")
  sitescores$Groups<-levels(meta_table_ems$Groups)[i]

  #Now calculate Raup-Crick abundance based
  results=raup_crick_abundance(abund_table_ems_group, set_all_species_equal = F,
plot_names_in_col1 = F, reps=999)
  pairwise_RC_abundance<-reshape2::melt(as.matrix(results))
  pairwise_RC_abundance$Groups<-levels(meta_table_ems$Groups)[i]


  #Now calculate Raup-Crick incidence based
  results=raup_crick(abund_table_ems_group,plot_names_in_col1 = F, reps = 999,
as.distance.matrix = T, set_all_species_equal = F)
  pairwise_RC_incidence<-reshape2::melt(as.matrix(results))
  pairwise_RC_incidence$Groups<-levels(meta_table_ems$Groups)[i]


  #Now calculate betaMNTD
  m=match.phylo.data(OTU_tree, t(abund_table_ems_group)) #Extract subtree for each
group
  OTU_tree_ems_group=m$phy

  abund_table_ems_group<-t(abund_table_ems_group)

  beta.mntd.weighted =
as.matrix(comdistnt(t(abund_table_ems_group),cophenetic(OTU_tree_ems_group),abundanc
e.weighted=T));


  beta.reps = 999;
```

```
    rand.weighted.bMNTD.comp = array(c(-
999),dim=c(ncol(abund_table_ems_group),ncol(abund_table_ems_group),beta.reps));
    dim(rand.weighted.bMNTD.comp);

    for (rep in 1:beta.reps) {

        rand.weighted.bMNTD.comp[,,rep] =
as.matrix(comdistnt(t(abund_table_ems_group),taxaShuffle(cophenetic(OTU_tree_ems_group
)),abundance.weighted=T,exclude.conspecifics = F));

        print(c(date(),rep));

    }

    weighted.bNTI =
matrix(c(NA),nrow=ncol(abund_table_ems_group),ncol=ncol(abund_table_ems_group));
    dim(weighted.bNTI);

    for (columns in 1:(ncol(abund_table_ems_group)-1)) {
        for (rows in (columns+1):ncol(abund_table_ems_group)) {

            rand.vals = rand.weighted.bMNTD.comp[rows,columns,];
            weighted.bNTI[rows,columns] = (beta.mntd.weighted[rows,columns] -
mean(rand.vals)) / sd(rand.vals);
            rm("rand.vals");

        };
    };
    rownames(weighted.bNTI) = colnames(abund_table_ems_group);
    colnames(weighted.bNTI) = colnames(abund_table_ems_group);
    pairwise_bNTI<-reshape2::melt(as.matrix(weighted.bNTI))
    pairwise_bNTI$Groups<-levels(meta_table_ems$Groups)[i]

    #Now collate all the statistics together
    if(is.null(collated_coherence)){collated_coherence<-coherence} else
{collated_coherence<-rbind(collated_coherence,coherence)}
    if(is.null(collated_boundary)){collated_boundary<-boundary} else {collated_boundary<-
rbind(collated_boundary,boundary)}
    if(is.null(collated_turnover)){collated_turnover<-turnover} else {collated_turnover<-
rbind(collated_turnover,turnover)}
    if(is.null(collated_sitescores)){collated_sitescores<-sitescores} else {collated_sitescores<-
rbind(collated_sitescores,sitescores)}
    if(is.null(collated_pairwise_RC_abundance)){collated_pairwise_RC_abundance<-
pairwise_RC_abundance} else {collated_pairwise_RC_abundance<-
```

```
rbind(collated_pairwise_RC_abundance,pairwise_RC_abundance)}
  if(is.null(collated_pairwise_RC_incidence)){collated_pairwise_RC_incidence<-
pairwise_RC_incidence} else {collated_pairwise_RC_incidence<-
rbind(collated_pairwise_RC_incidence,pairwise_RC_incidence)}
  if(is.null(collated_pairwise_bNTI)){collated_pairwise_bNTI<-pairwise_bNTI} else
{collated_pairwise_bNTI<-rbind(collated_pairwise_bNTI,pairwise_bNTI)}


}

collated_RC<-summarySE(collated_pairwise_RC_incidence, measurevar = "value", groupvars
= "Groups")
rownames(collated_RC)<-collated_RC[,1]
collated_RC<-collated_RC[,-1]
collated_bNTI<-summarySE(collated_pairwise_bNTI, measurevar = "value", groupvars =
"Groups")
rownames(collated_bNTI)<-collated_bNTI[,1]
collated_bNTI<-collated_bNTI[,-1]

write.csv(collated_coherence,file=paste("Coherence_",label,".csv",sep=""))
write.csv(collated_boundary,file=paste("Boundary_",label,".csv",sep=""))
write.csv(collated_turnover,file=paste("Turnover_",label,".csv",sep=""))
write.csv(collated_sitescores,file=paste("Sitescores_",label,".csv",sep=""))
write.csv(collated_pairwise_RC_abundance,file=paste("PairwiseRC_",label,".csv",sep=""))
write.csv(collated_pairwise_bNTI,file=paste("PairwisebNTI_",label,".csv",sep=""))
write.csv(collated_RC,file=paste("RC_",label,".csv",sep=""))
write.csv(collated_bNTI,file=paste("bNTI_",label,".csv",sep=""))
```

Script 4: R script about the work flow of QPE.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to
"To Source File Location"
#Script for visualisation of null modelling (beta NTI, Raup-Crick Beta-Diversity, and
Elements of Metacommunity)
#Reference: http://uu.diva-portal.org/smash/get/diva2:1373632/DATASET09.txt
#Authors: Umer, Anna, and Simon
#Versions: 1.1 (fixed ordering issue)

library(ggplot2)

#PARAMETERS ###########################
label="Hypothesis1  "
PairwisebNTI<-read.csv("PairwisebNTI_Hypothesis1.csv",header=T,row.names=1)
PairwiseRC<-read.csv("PairwiseRC_Hypothesis1.csv",header=T,row.names=1)
RC<-read.csv("RC_Hypothesis1.csv",header=T,row.names=1)
```

```
Coherence<-read.csv("Coherence_Hypothesis1.csv",header=T,row.names=1)
BoundaryClump<-read.csv("Boundary_Hypothesis1.csv",header=T,row.names=1)
Turnover<-read.csv("Turnover_Hypothesis1.csv",header=T,row.names=1)
ordering<-c(
  "Tanzania",
  "Vietnam"
)
colours <- c(
  "#ff9999",
  "#660000",
  #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1000));
QPE_height=10
QPE_width=5
EMS_height=7
EMS_width=5
RC_height=7
RC_width=5

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
  "4",
  "3",
  "2",
  "1"
))
colours <- c(
  "#ff9999",
  "#660000",
  "#660FF0",
  "#600006",
  #Next colors are for lines mainly used in the PCoA script

"#000080","#4876FF","#CAE1FF","#9FB6CD","#1E90FF","#00F5FF","#00C957",grey.colors(1000));
#meta_table$Type is for shapes
meta_table$Type<-as.factor(as.character(meta_table$Country))
provide_your_own_pvalue_combinations<-TRUE
```

```
provided_combination<-cbind(
   #Cross-sectional comparisons
   combn(c( "1",
                 "2",
                 "3",
                 "4"),2)
)
# #/PARAMETERS ###########################

QPE_table<-cbind(Var1=as.character(PairwiseRC$Var1),
Var2=as.character(PairwiseRC$Var2),bNTI=PairwisebNTI[,"value",drop=F],
RC=PairwiseRC[,"value",drop=F], Groups=PairwiseRC[,"Groups",drop=F])
#Now we want to get rid of any rows that have NA there to get the comparisons from
# N x N to N (N-1)/2. A way to do this to use complete.cases
QPE_table<-QPE_table[complete.cases(QPE_table),]
names(QPE_table)<-c("Var1","Var2","bNTI","RC","Groups")

QPE_df<-NULL

for(i in levels(QPE_table$Groups)){
   tmp<-QPE_table[QPE_table$Groups==i,]
   sp_mask<-abs(tmp$bNTI)>2
   hs_count<-sum(tmp$bNTI[sp_mask]<2)
   vs_count<-sum(tmp$bNTI[sp_mask]>2)
   sig_count<-sum(sp_mask)
   total_count<-nrow(tmp)
   nonsig_count<-nrow(tmp[!sp_mask,])
   dl_count<-sum(tmp[!sp_mask,"RC"]>0.95)
   hd_count<-sum(tmp[!sp_mask,"RC"]<(-0.95))
   ed_count<-nonsig_count-dl_count-hd_count
   tmp2<-data.frame(measure="Homogenizing
Selection",value=(hs_count/total_count*100),Groups=i)
   tmp2<-rbind(tmp2,data.frame(measure="Variable
Selection",value=(vs_count/total_count*100),Groups=i))
   tmp2<-rbind(tmp2,data.frame(measure="Dispersal
Limitation",value=(dl_count/total_count*100),Groups=i))
   tmp2<-rbind(tmp2,data.frame(measure="Ecological
Drift",value=(ed_count/total_count*100),Groups=i))
   tmp2<-rbind(tmp2,data.frame(measure="Homogenizing
Dispersal",value=(hd_count/total_count*100),Groups=i))
   if(is.null(QPE_df)){QPE_df<-tmp2} else {QPE_df<-rbind(QPE_df,tmp2)}
}

#Change the orderign of the Groups
```

```
QPE_df$Groups<-factor(as.character(QPE_df$Groups),levels=ordering)
pdf(paste("QPE_",label,".pdf",sep=""),width=QPE_width,height=QPE_height)
p<-ggplot(QPE_df, aes(x=Groups, y=value, fill=Groups))
p<-p+geom_bar(stat="identity")+theme_minimal()
p<-p+geom_text(aes(label=sprintf("%0.2f", round(value, digits = 2))), vjust=-0.3, size=3.5)
p<-p+facet_wrap(~measure, strip.position="left", ncol=1,scales="free_y")
p<-p+scale_fill_manual(values=colours)
p<-p+ylim(0,110)
p<-p+ylab("% Assembly Processes")
p<-p+theme(strip.background = element_rect(fill="white"))+theme(panel.spacing = unit(2,
"lines"),
                                                                                   axis.text.x =
element_text(angle = 90, hjust = 1))
print(p)
dev.off()

#We move on to EMS (Elements of Metacommunity Structure)
collated_community_types<-NULL
for(i in rownames(Coherence)){
    community_type="Random"
    if(Coherence[i,"p"]<0.05){
        #Top left figure
        if(Coherence[i,"z"]<(-1.96)){
            community_type="Checkerboard"
        } else if(Coherence[i,"z"]>1.96) {
                #Top middle left
                    if(Turnover[i,"z"]<(-1.96)){
                        if(BoundaryClump[i,"p"]<0.05){
                            if(BoundaryClump[i,"index"]<0){
                                community_type="Nested Hyperdispersed species loss"
                            } else {
                                community_type="Nested Clumped species loss"
                            }
                        }
                        else{
                            community_type="Nested Random species loss"
                        }
                    }
                    #Top middle right
                      else if(Turnover[i,"z"]>1.96)
                        {
                            if(BoundaryClump[i,"p"]<0.05){
                                if(BoundaryClump[i,"index"]<0){
                                    community_type="Evenly spaced"
```

```
                  } else {
                    community_type="Clementsian"
                  }
                }
                else{
                  community_type="Gleasonian"
                }
          }
        if(Turnover[i,"p"]>0.05){
          community_type=paste("Quasi-structure",community_type)
        }
      }

  }
  #Collate all the information together
  if(is.null(collated_community_types)){collated_community_types<-community_type} else
{collated_community_types<-c(collated_community_types,community_type)}
}

EMS<-
cbind(Coherence,Turnover,BoundaryClump,Metacommunity=collated_community_types)
names(EMS)<-
c("Coherence_Abs","Coherence_z","Coherence_p","Coherence_simMean","Coherence_simVa
riance",

"Turnover_turn","Turnover_z","Turnover_p","Turnover_simMean","Turnover_simVariance",
              "Clumping_index","Clumping_p","Clumping_df","Metacommunity")
write.csv(EMS,file=paste("EMS_",label,".csv",sep=""))

EMS<-cbind(EMS,Groups=rownames(EMS))
#Change the ordering of the Groups
EMS$Groups<-factor(as.character(EMS$Groups),levels=ordering)
pdf(paste("EMS_",label,".pdf",sep=""),width=EMS_width,height=EMS_height)
p<-
ggplot(EMS,aes(Groups,Coherence_z,color=Turnover_z,size=Clumping_index,shape=Metac
ommunity))
p<-p+geom_point()
p <- p + geom_hline(yintercept = 1.96,linetype="dotted")
p <-p +geom_text(aes(x=1,y=1.96, label="1.96\n"), colour="blue",size=2)

p <- p + geom_hline(yintercept = -1.96,linetype="dotted")
p <-p +geom_text(aes(x=1,y=-1.96, label="\n-1.96"), colour="blue",size=2)

p <- p + ylab("Coherence (z-value)")
```

```
p <- p + scale_color_continuous("Turnover (z-value)")
p <- p + scale_size_continuous("Boundary clumping (Morisita's index)")
p<-p+theme(strip.background = element_rect(fill="white"))+theme(panel.spacing = unit(2,
"lines"),
                                                                          axis.text.x =
element_text(angle = 90, hjust = 1))

p<-p+theme_minimal()
print(p)
dev.off()

RC<-cbind(RC,Groups=rownames(RC))
#Change the ordering of the Groups
RC$Groups<-factor(as.character(RC$Groups),levels=ordering)
pdf(paste("RC_",label,".pdf",sep=""),width=RC_width,height=RC_height)
p<-ggplot(RC,aes(Groups,value,colour=Groups))
p<-p+geom_errorbar(aes(ymin=value-se, ymax=value+se), width=.1, lty=1)+
  geom_point(size=5)

p <- p + geom_hline(yintercept = 0,linetype="dotted")
p <-p +geom_text(aes(x=1,y=0, label="0\n"), colour="blue",size=2)

p <- p + geom_hline(yintercept = 1,linetype="dotted")
p <-p +geom_text(aes(x=1,y=1, label="+1\n"), colour="blue",size=2)

p <- p + geom_hline(yintercept = -1,linetype="dotted")
p <-p +geom_text(aes(x=1,y=-1, label="\n-1"), colour="blue",size=2)

p<-p+theme_minimal()
p<-p+scale_colour_manual(values=colours)
p<-p+ylab("Incidence-based beta-diversity (卤 SE)")
p<-p+theme(strip.background = element_rect(fill="white"))+theme(panel.spacing = unit(2,
"lines"),
                                                                          axis.text.x =
element_text(angle = 90, hjust = 1))

print(p)
dev.off()
```

Script 5: visualize the QPE.

	N	value	sd	se	ci
Tanzania	196	NA	NA	NA	NA
Vietnam	1444	NA	NA	NA	NA

Table 5：βNTI of hypothesis 1.

	N	value	sd	se	ci
1	289	NA	NA	NA	NA
2	225	NA	NA	NA	NA
3	100	NA	NA	NA	NA
4	25	NA	NA	NA	NA

Table 6： βNTI of hypothesis 2.

	Var1	Var2	value	Groups
1	T_2_1	T_2_1	NA	Tanzania
2	T_2_2	T_2_1	-0.46307	Tanzania
3	T_2_3	T_2_1	1.412288	Tanzania
4	T_2_6	T_2_1	4.374059	Tanzania
5	T_2_9	T_2_1	3.686981	Tanzania
6	T_4_3	T_2_1	3.14511	Tanzania
7	T_4_4	T_2_1	5.415596	Tanzania
8	T_4_5	T_2_1	7.30777	Tanzania
9	T_5_2	T_2_1	2.739074	Tanzania
10	T_5_3	T_2_1	2.929192	Tanzania
11	T_6_7	T_2_1	5.153634	Tanzania
12	T_6_8	T_2_1	2.27384	Tanzania
13	T_9_2	T_2_1	-0.45815	Tanzania
14	T_9_4	T_2_1	1.154654	Tanzania
15	T_2_1	T_2_2	NA	Tanzania
16	T_2_2	T_2_2	NA	Tanzania
17	T_2_3	T_2_2	-0.99808	Tanzania
18	T_2_6	T_2_2	3.224812	Tanzania
19	T_2_9	T_2_2	2.695094	Tanzania
20	T_4_3	T_2_2	1.081058	Tanzania
21	T_4_4	T_2_2	4.203045	Tanzania
22	T_4_5	T_2_2	4.721139	Tanzania
23	T_5_2	T_2_2	1.208184	Tanzania
24	T_5_3	T_2_2	1.220019	Tanzania
25	T_6_7	T_2_2	2.257954	Tanzania
26	T_6_8	T_2_2	1.012088	Tanzania
27	T_9_2	T_2_2	-0.48442	Tanzania
28	T_9_4	T_2_2	0.024609	Tanzania
29	T_2_1	T_2_3	NA	Tanzania
30	T_2_2	T_2_3	NA	Tanzania
31	T_2_3	T_2_3	NA	Tanzania
32	T_2_6	T_2_3	3.436154	Tanzania
33	T_2_9	T_2_3	2.739412	Tanzania
34	T_4_3	T_2_3	1.00819	Tanzania

35	T_4_4	T_2_3	4.377449	Tanzania
36	T_4_5	T_2_3	4.136756	Tanzania
37	T_5_2	T_2_3	0.617939	Tanzania
38	T_5_3	T_2_3	0.675665	Tanzania
39	T_6_7	T_2_3	2.162887	Tanzania
40	T_6_8	T_2_3	3.844239	Tanzania
41	T_9_2	T_2_3	0.045319	Tanzania
42	T_9_4	T_2_3	0.637019	Tanzania
43	T_2_1	T_2_6	NA	Tanzania
44	T_2_2	T_2_6	NA	Tanzania
45	T_2_3	T_2_6	NA	Tanzania
46	T_2_6	T_2_6	NA	Tanzania
47	T_2_9	T_2_6	3.223872	Tanzania
48	T_4_3	T_2_6	2.68064	Tanzania
49	T_4_4	T_2_6	2.124947	Tanzania
50	T_4_5	T_2_6	1.609148	Tanzania
51	T_5_2	T_2_6	4.967761	Tanzania
52	T_5_3	T_2_6	4.134722	Tanzania
53	T_6_7	T_2_6	1.017225	Tanzania
54	T_6_8	T_2_6	2.830418	Tanzania
55	T_9_2	T_2_6	-0.45103	Tanzania
56	T_9_4	T_2_6	1.367743	Tanzania
57	T_2_1	T_2_9	NA	Tanzania
58	T_2_2	T_2_9	NA	Tanzania
59	T_2_3	T_2_9	NA	Tanzania
60	T_2_6	T_2_9	NA	Tanzania
61	T_2_9	T_2_9	NA	Tanzania
62	T_4_3	T_2_9	0.064183	Tanzania
63	T_4_4	T_2_9	0.754144	Tanzania
64	T_4_5	T_2_9	0.296687	Tanzania
65	T_5_2	T_2_9	3.139779	Tanzania
66	T_5_3	T_2_9	2.91126	Tanzania
67	T_6_7	T_2_9	0.267331	Tanzania
68	T_6_8	T_2_9	0.049475	Tanzania
69	T_9_2	T_2_9	0.35992	Tanzania
70	T_9_4	T_2_9	0.764855	Tanzania
71	T_2_1	T_4_3	NA	Tanzania
72	T_2_2	T_4_3	NA	Tanzania
73	T_2_3	T_4_3	NA	Tanzania
74	T_2_6	T_4_3	NA	Tanzania
75	T_2_9	T_4_3	NA	Tanzania
76	T_4_3	T_4_3	NA	Tanzania
77	T_4_4	T_4_3	-1.92162	Tanzania

78	T_4_5	T_4_3	-1.39979	Tanzania
79	T_5_2	T_4_3	4.047574	Tanzania
80	T_5_3	T_4_3	1.704074	Tanzania
81	T_6_7	T_4_3	-0.82064	Tanzania
82	T_6_8	T_4_3	-0.82802	Tanzania
83	T_9_2	T_4_3	3.727312	Tanzania
84	T_9_4	T_4_3	4.664182	Tanzania
85	T_2_1	T_4_4	NA	Tanzania
86	T_2_2	T_4_4	NA	Tanzania
87	T_2_3	T_4_4	NA	Tanzania
88	T_2_6	T_4_4	NA	Tanzania
89	T_2_9	T_4_4	NA	Tanzania
90	T_4_3	T_4_4	NA	Tanzania
91	T_4_4	T_4_4	NA	Tanzania
92	T_4_5	T_4_4	-0.73042	Tanzania
93	T_5_2	T_4_4	3.973584	Tanzania
94	T_5_3	T_4_4	2.836243	Tanzania
95	T_6_7	T_4_4	-1.15361	Tanzania
96	T_6_8	T_4_4	-0.63685	Tanzania
97	T_9_2	T_4_4	-0.66383	Tanzania
98	T_9_4	T_4_4	0.598972	Tanzania
99	T_2_1	T_4_5	NA	Tanzania
100	T_2_2	T_4_5	NA	Tanzania
101	T_2_3	T_4_5	NA	Tanzania
102	T_2_6	T_4_5	NA	Tanzania
103	T_2_9	T_4_5	NA	Tanzania
104	T_4_3	T_4_5	NA	Tanzania
105	T_4_4	T_4_5	NA	Tanzania
106	T_4_5	T_4_5	NA	Tanzania
107	T_5_2	T_4_5	5.797159	Tanzania
108	T_5_3	T_4_5	3.092542	Tanzania
109	T_6_7	T_4_5	-1.64496	Tanzania
110	T_6_8	T_4_5	-0.93441	Tanzania
111	T_9_2	T_4_5	4.31401	Tanzania
112	T_9_4	T_4_5	4.821172	Tanzania
113	T_2_1	T_5_2	NA	Tanzania
114	T_2_2	T_5_2	NA	Tanzania
115	T_2_3	T_5_2	NA	Tanzania
116	T_2_6	T_5_2	NA	Tanzania
117	T_2_9	T_5_2	NA	Tanzania
118	T_4_3	T_5_2	NA	Tanzania
119	T_4_4	T_5_2	NA	Tanzania
120	T_4_5	T_5_2	NA	Tanzania

121	T_5_2	T_5_2	NA	Tanzania
122	T_5_3	T_5_2	0.107416	Tanzania
123	T_6_7	T_5_2	2.905166	Tanzania
124	T_6_8	T_5_2	3.740128	Tanzania
125	T_9_2	T_5_2	-0.26077	Tanzania
126	T_9_4	T_5_2	-0.13868	Tanzania
127	T_2_1	T_5_3	NA	Tanzania
128	T_2_2	T_5_3	NA	Tanzania
129	T_2_3	T_5_3	NA	Tanzania
130	T_2_6	T_5_3	NA	Tanzania
131	T_2_9	T_5_3	NA	Tanzania
132	T_4_3	T_5_3	NA	Tanzania
133	T_4_4	T_5_3	NA	Tanzania
134	T_4_5	T_5_3	NA	Tanzania
135	T_5_2	T_5_3	NA	Tanzania
136	T_5_3	T_5_3	NA	Tanzania
137	T_6_7	T_5_3	2.640825	Tanzania
138	T_6_8	T_5_3	3.296048	Tanzania
139	T_9_2	T_5_3	-0.10097	Tanzania
140	T_9_4	T_5_3	0.144174	Tanzania
141	T_2_1	T_6_7	NA	Tanzania
142	T_2_2	T_6_7	NA	Tanzania
143	T_2_3	T_6_7	NA	Tanzania
144	T_2_6	T_6_7	NA	Tanzania
145	T_2_9	T_6_7	NA	Tanzania
146	T_4_3	T_6_7	NA	Tanzania
147	T_4_4	T_6_7	NA	Tanzania
148	T_4_5	T_6_7	NA	Tanzania
149	T_5_2	T_6_7	NA	Tanzania
150	T_5_3	T_6_7	NA	Tanzania
151	T_6_7	T_6_7	NA	Tanzania
152	T_6_8	T_6_7	0.549696	Tanzania
153	T_9_2	T_6_7	-0.7215	Tanzania
154	T_9_4	T_6_7	1.968603	Tanzania
155	T_2_1	T_6_8	NA	Tanzania
156	T_2_2	T_6_8	NA	Tanzania
157	T_2_3	T_6_8	NA	Tanzania
158	T_2_6	T_6_8	NA	Tanzania
159	T_2_9	T_6_8	NA	Tanzania
160	T_4_3	T_6_8	NA	Tanzania
161	T_4_4	T_6_8	NA	Tanzania
162	T_4_5	T_6_8	NA	Tanzania
163	T_5_2	T_6_8	NA	Tanzania

164	T_5_3	T_6_8	NA	Tanzania
165	T_6_7	T_6_8	NA	Tanzania
166	T_6_8	T_6_8	NA	Tanzania
167	T_9_2	T_6_8	2.200971	Tanzania
168	T_9_4	T_6_8	1.83708	Tanzania
169	T_2_1	T_9_2	NA	Tanzania
170	T_2_2	T_9_2	NA	Tanzania
171	T_2_3	T_9_2	NA	Tanzania
172	T_2_6	T_9_2	NA	Tanzania
173	T_2_9	T_9_2	NA	Tanzania
174	T_4_3	T_9_2	NA	Tanzania
175	T_4_4	T_9_2	NA	Tanzania
176	T_4_5	T_9_2	NA	Tanzania
177	T_5_2	T_9_2	NA	Tanzania
178	T_5_3	T_9_2	NA	Tanzania
179	T_6_7	T_9_2	NA	Tanzania
180	T_6_8	T_9_2	NA	Tanzania
181	T_9_2	T_9_2	NA	Tanzania
182	T_9_4	T_9_2	0.360704	Tanzania
183	T_2_1	T_9_4	NA	Tanzania
184	T_2_2	T_9_4	NA	Tanzania
185	T_2_3	T_9_4	NA	Tanzania
186	T_2_6	T_9_4	NA	Tanzania
187	T_2_9	T_9_4	NA	Tanzania
188	T_4_3	T_9_4	NA	Tanzania
189	T_4_4	T_9_4	NA	Tanzania
190	T_4_5	T_9_4	NA	Tanzania
191	T_5_2	T_9_4	NA	Tanzania
192	T_5_3	T_9_4	NA	Tanzania
193	T_6_7	T_9_4	NA	Tanzania
194	T_6_8	T_9_4	NA	Tanzania
195	T_9_2	T_9_4	NA	Tanzania
196	T_9_4	T_9_4	NA	Tanzania
197	V_1_2	V_1_2	NA	Vietnam
198	V_2_2	V_1_2	-0.78513	Vietnam
199	V_3_1	V_1_2	4.483408	Vietnam
200	V_3_2	V_1_2	2.449176	Vietnam
201	V_5_3	V_1_2	0.569868	Vietnam
202	V_6_1	V_1_2	0.797287	Vietnam
203	V_6_2	V_1_2	-1.43566	Vietnam
204	V_6_3	V_1_2	0.977819	Vietnam
205	V_7_1	V_1_2	-0.76543	Vietnam
206	V_7_2	V_1_2	4.695998	Vietnam

207	V_7_3	V_1_2	5.036322	Vietnam
208	V_8_2	V_1_2	1.285258	Vietnam
209	V_9_1	V_1_2	0.746797	Vietnam
210	V_9_2	V_1_2	1.154746	Vietnam
211	V_9_4	V_1_2	2.088651	Vietnam
212	V_10_1	V_1_2	-0.07511	Vietnam
213	V_11_1	V_1_2	1.481253	Vietnam
214	V_11_3	V_1_2	1.648727	Vietnam
215	V_12_1	V_1_2	-1.79636	Vietnam
216	V_13_2	V_1_2	-0.65507	Vietnam
217	V_14_1	V_1_2	-1.35013	Vietnam
218	V_15_1	V_1_2	-0.20659	Vietnam
219	V_15_2	V_1_2	3.340749	Vietnam
220	V_15_3	V_1_2	5.390758	Vietnam
221	V_16_1	V_1_2	1.322927	Vietnam
222	V_16_2	V_1_2	2.246453	Vietnam
223	V_17_1	V_1_2	0.375479	Vietnam
224	V_17_2	V_1_2	-1.33105	Vietnam
225	V_18_1	V_1_2	-1.73676	Vietnam
226	V_18_2	V_1_2	-2.37706	Vietnam
227	V_18_4	V_1_2	3.233715	Vietnam
228	V_19_1	V_1_2	0.08586	Vietnam
229	V_19_3	V_1_2	1.862975	Vietnam
230	V_20_1	V_1_2	-1.60778	Vietnam
231	V_21_1	V_1_2	-2.6834	Vietnam
232	V_22_1	V_1_2	9.375953	Vietnam
233	V_22_3	V_1_2	2.737952	Vietnam
234	V_22_4	V_1_2	1.912677	Vietnam
235	V_1_2	V_2_2	NA	Vietnam
236	V_2_2	V_2_2	NA	Vietnam
237	V_3_1	V_2_2	-0.84011	Vietnam
238	V_3_2	V_2_2	-0.41991	Vietnam
239	V_5_3	V_2_2	-2.01591	Vietnam
240	V_6_1	V_2_2	-1.88815	Vietnam
241	V_6_2	V_2_2	-1.92191	Vietnam
242	V_6_3	V_2_2	-0.66917	Vietnam
243	V_7_1	V_2_2	-1.08144	Vietnam
244	V_7_2	V_2_2	-1.05816	Vietnam
245	V_7_3	V_2_2	0.510332	Vietnam
246	V_8_2	V_2_2	-0.86033	Vietnam
247	V_9_1	V_2_2	-0.61412	Vietnam
248	V_9_2	V_2_2	-1.8466	Vietnam
249	V_9_4	V_2_2	-0.44786	Vietnam

250	V_10_1	V_2_2	0.004361	Vietnam
251	V_11_1	V_2_2	-2.42459	Vietnam
252	V_11_3	V_2_2	-1.65494	Vietnam
253	V_12_1	V_2_2	-1.26137	Vietnam
254	V_13_2	V_2_2	-0.09071	Vietnam
255	V_14_1	V_2_2	0.658697	Vietnam
256	V_15_1	V_2_2	-0.45705	Vietnam
257	V_15_2	V_2_2	-0.247	Vietnam
258	V_15_3	V_2_2	2.003859	Vietnam
259	V_16_1	V_2_2	1.558517	Vietnam
260	V_16_2	V_2_2	1.082721	Vietnam
261	V_17_1	V_2_2	-0.96832	Vietnam
262	V_17_2	V_2_2	4.024651	Vietnam
263	V_18_1	V_2_2	0.912259	Vietnam
264	V_18_2	V_2_2	0.315467	Vietnam
265	V_18_4	V_2_2	0.181236	Vietnam
266	V_19_1	V_2_2	4.466169	Vietnam
267	V_19_3	V_2_2	-0.72476	Vietnam
268	V_20_1	V_2_2	-2.82869	Vietnam
269	V_21_1	V_2_2	-1.85995	Vietnam
270	V_22_1	V_2_2	-0.58121	Vietnam
271	V_22_3	V_2_2	-1.28617	Vietnam
272	V_22_4	V_2_2	-0.80285	Vietnam
273	V_1_2	V_3_1	NA	Vietnam
274	V_2_2	V_3_1	NA	Vietnam
275	V_3_1	V_3_1	NA	Vietnam
276	V_3_2	V_3_1	-2.30881	Vietnam
277	V_5_3	V_3_1	0.332981	Vietnam
278	V_6_1	V_3_1	0.675017	Vietnam
279	V_6_2	V_3_1	3.133822	Vietnam
280	V_6_3	V_3_1	-0.05112	Vietnam
281	V_7_1	V_3_1	6.162878	Vietnam
282	V_7_2	V_3_1	2.019022	Vietnam
283	V_7_3	V_3_1	4.27158	Vietnam
284	V_8_2	V_3_1	0.606392	Vietnam
285	V_9_1	V_3_1	6.129861	Vietnam
286	V_9_2	V_3_1	0.079093	Vietnam
287	V_9_4	V_3_1	2.256627	Vietnam
288	V_10_1	V_3_1	7.667776	Vietnam
289	V_11_1	V_3_1	-0.94474	Vietnam
290	V_11_3	V_3_1	-0.74436	Vietnam
291	V_12_1	V_3_1	2.414925	Vietnam
292	V_13_2	V_3_1	5.326273	Vietnam

293	V_14_1	V_3_1	8.153672	Vietnam
294	V_15_1	V_3_1	3.511873	Vietnam
295	V_15_2	V_3_1	1.775169	Vietnam
296	V_15_3	V_3_1	4.254848	Vietnam
297	V_16_1	V_3_1	7.947256	Vietnam
298	V_16_2	V_3_1	6.924358	Vietnam
299	V_17_1	V_3_1	5.175528	Vietnam
300	V_17_2	V_3_1	6.071753	Vietnam
301	V_18_1	V_3_1	4.830369	Vietnam
302	V_18_2	V_3_1	1.437653	Vietnam
303	V_18_4	V_3_1	1.13987	Vietnam
304	V_19_1	V_3_1	6.710413	Vietnam
305	V_19_3	V_3_1	1.530914	Vietnam
306	V_20_1	V_3_1	4.039704	Vietnam
307	V_21_1	V_3_1	-0.35921	Vietnam
308	V_22_1	V_3_1	-0.91933	Vietnam
309	V_22_3	V_3_1	-1.02934	Vietnam
310	V_22_4	V_3_1	-1.15887	Vietnam
311	V_1_2	V_3_2	NA	Vietnam
312	V_2_2	V_3_2	NA	Vietnam
313	V_3_1	V_3_2	NA	Vietnam
314	V_3_2	V_3_2	NA	Vietnam
315	V_5_3	V_3_2	1.082826	Vietnam
316	V_6_1	V_3_2	0.141219	Vietnam
317	V_6_2	V_3_2	1.507845	Vietnam
318	V_6_3	V_3_2	-1.35708	Vietnam
319	V_7_1	V_3_2	4.44556	Vietnam
320	V_7_2	V_3_2	1.334352	Vietnam
321	V_7_3	V_3_2	1.857112	Vietnam
322	V_8_2	V_3_2	0.894688	Vietnam
323	V_9_1	V_3_2	5.350882	Vietnam
324	V_9_2	V_3_2	-1.14204	Vietnam
325	V_9_4	V_3_2	1.340938	Vietnam
326	V_10_1	V_3_2	5.851808	Vietnam
327	V_11_1	V_3_2	-2.19321	Vietnam
328	V_11_3	V_3_2	-1.18688	Vietnam
329	V_12_1	V_3_2	0.663698	Vietnam
330	V_13_2	V_3_2	2.815853	Vietnam
331	V_14_1	V_3_2	4.483638	Vietnam
332	V_15_1	V_3_2	1.171166	Vietnam
333	V_15_2	V_3_2	0.017427	Vietnam
334	V_15_3	V_3_2	2.920204	Vietnam
335	V_16_1	V_3_2	6.062932	Vietnam

336	V_16_2	V_3_2	7.896041	Vietnam
337	V_17_1	V_3_2	4.80467	Vietnam
338	V_17_2	V_3_2	4.370243	Vietnam
339	V_18_1	V_3_2	3.88068	Vietnam
340	V_18_2	V_3_2	1.83099	Vietnam
341	V_18_4	V_3_2	0.794068	Vietnam
342	V_19_1	V_3_2	3.578489	Vietnam
343	V_19_3	V_3_2	0.975583	Vietnam
344	V_20_1	V_3_2	1.264724	Vietnam
345	V_21_1	V_3_2	-1.71282	Vietnam
346	V_22_1	V_3_2	-0.81696	Vietnam
347	V_22_3	V_3_2	-0.87432	Vietnam
348	V_22_4	V_3_2	-2.42139	Vietnam
349	V_1_2	V_5_3	NA	Vietnam
350	V_2_2	V_5_3	NA	Vietnam
351	V_3_1	V_5_3	NA	Vietnam
352	V_3_2	V_5_3	NA	Vietnam
353	V_5_3	V_5_3	NA	Vietnam
354	V_6_1	V_5_3	-1.65433	Vietnam
355	V_6_2	V_5_3	-1.7462	Vietnam
356	V_6_3	V_5_3	-0.84778	Vietnam
357	V_7_1	V_5_3	-1.01439	Vietnam
358	V_7_2	V_5_3	0.763923	Vietnam
359	V_7_3	V_5_3	5.044385	Vietnam
360	V_8_2	V_5_3	-0.99838	Vietnam
361	V_9_1	V_5_3	1.994779	Vietnam
362	V_9_2	V_5_3	-1.04473	Vietnam
363	V_9_4	V_5_3	0.525203	Vietnam
364	V_10_1	V_5_3	3.197461	Vietnam
365	V_11_1	V_5_3	-1.04979	Vietnam
366	V_11_3	V_5_3	-0.62499	Vietnam
367	V_12_1	V_5_3	-0.01228	Vietnam
368	V_13_2	V_5_3	1.800995	Vietnam
369	V_14_1	V_5_3	3.466561	Vietnam
370	V_15_1	V_5_3	-0.49053	Vietnam
371	V_15_2	V_5_3	-0.92286	Vietnam
372	V_15_3	V_5_3	1.10785	Vietnam
373	V_16_1	V_5_3	6.021236	Vietnam
374	V_16_2	V_5_3	5.524094	Vietnam
375	V_17_1	V_5_3	1.640111	Vietnam
376	V_17_2	V_5_3	2.605358	Vietnam
377	V_18_1	V_5_3	3.047233	Vietnam
378	V_18_2	V_5_3	0.15832	Vietnam

379	V_18_4	V_5_3	1.037231	Vietnam
380	V_19_1	V_5_3	2.754563	Vietnam
381	V_19_3	V_5_3	-1.05504	Vietnam
382	V_20_1	V_5_3	-1.15163	Vietnam
383	V_21_1	V_5_3	-1.01034	Vietnam
384	V_22_1	V_5_3	1.483216	Vietnam
385	V_22_3	V_5_3	-0.83898	Vietnam
386	V_22_4	V_5_3	-0.77135	Vietnam
387	V_1_2	V_6_1	NA	Vietnam
388	V_2_2	V_6_1	NA	Vietnam
389	V_3_1	V_6_1	NA	Vietnam
390	V_3_2	V_6_1	NA	Vietnam
391	V_5_3	V_6_1	NA	Vietnam
392	V_6_1	V_6_1	NA	Vietnam
393	V_6_2	V_6_1	-1.02311	Vietnam
394	V_6_3	V_6_1	0.45457	Vietnam
395	V_7_1	V_6_1	-1.28057	Vietnam
396	V_7_2	V_6_1	-2.09115	Vietnam
397	V_7_3	V_6_1	1.482387	Vietnam
398	V_8_2	V_6_1	-1.572	Vietnam
399	V_9_1	V_6_1	0.424852	Vietnam
400	V_9_2	V_6_1	-0.53237	Vietnam
401	V_9_4	V_6_1	0.35997	Vietnam
402	V_10_1	V_6_1	1.686468	Vietnam
403	V_11_1	V_6_1	-1.39838	Vietnam
404	V_11_3	V_6_1	-0.48803	Vietnam
405	V_12_1	V_6_1	0.081741	Vietnam
406	V_13_2	V_6_1	1.092187	Vietnam
407	V_14_1	V_6_1	3.077653	Vietnam
408	V_15_1	V_6_1	0.960467	Vietnam
409	V_15_2	V_6_1	-1.81502	Vietnam
410	V_15_3	V_6_1	0.480662	Vietnam
411	V_16_1	V_6_1	2.911663	Vietnam
412	V_16_2	V_6_1	4.167717	Vietnam
413	V_17_1	V_6_1	0.156045	Vietnam
414	V_17_2	V_6_1	1.201464	Vietnam
415	V_18_1	V_6_1	3.476943	Vietnam
416	V_18_2	V_6_1	0.699481	Vietnam
417	V_18_4	V_6_1	-0.95671	Vietnam
418	V_19_1	V_6_1	0.92724	Vietnam
419	V_19_3	V_6_1	-1.49385	Vietnam
420	V_20_1	V_6_1	-1.73245	Vietnam
421	V_21_1	V_6_1	-2.18732	Vietnam

422	V_22_1	V_6_1	-0.4451	Vietnam
423	V_22_3	V_6_1	0.863187	Vietnam
424	V_22_4	V_6_1	-0.70045	Vietnam
425	V_1_2	V_6_2	NA	Vietnam
426	V_2_2	V_6_2	NA	Vietnam
427	V_3_1	V_6_2	NA	Vietnam
428	V_3_2	V_6_2	NA	Vietnam
429	V_5_3	V_6_2	NA	Vietnam
430	V_6_1	V_6_2	NA	Vietnam
431	V_6_2	V_6_2	NA	Vietnam
432	V_6_3	V_6_2	3.769491	Vietnam
433	V_7_1	V_6_2	-1.38426	Vietnam
434	V_7_2	V_6_2	0.411401	Vietnam
435	V_7_3	V_6_2	5.960723	Vietnam
436	V_8_2	V_6_2	0.490399	Vietnam
437	V_9_1	V_6_2	-1.9755	Vietnam
438	V_9_2	V_6_2	1.0935	Vietnam
439	V_9_4	V_6_2	0.778303	Vietnam
440	V_10_1	V_6_2	-0.71431	Vietnam
441	V_11_1	V_6_2	0.622488	Vietnam
442	V_11_3	V_6_2	0.871057	Vietnam
443	V_12_1	V_6_2	-2.31249	Vietnam
444	V_13_2	V_6_2	0.578622	Vietnam
445	V_14_1	V_6_2	-0.69414	Vietnam
446	V_15_1	V_6_2	0.939827	Vietnam
447	V_15_2	V_6_2	1.150346	Vietnam
448	V_15_3	V_6_2	0.862008	Vietnam
449	V_16_1	V_6_2	-0.95998	Vietnam
450	V_16_2	V_6_2	0.23026	Vietnam
451	V_17_1	V_6_2	-1.71081	Vietnam
452	V_17_2	V_6_2	-1.93966	Vietnam
453	V_18_1	V_6_2	0.365558	Vietnam
454	V_18_2	V_6_2	-2.29687	Vietnam
455	V_18_4	V_6_2	3.113196	Vietnam
456	V_19_1	V_6_2	1.186393	Vietnam
457	V_19_3	V_6_2	0.352445	Vietnam
458	V_20_1	V_6_2	-1.76361	Vietnam
459	V_21_1	V_6_2	-2.42631	Vietnam
460	V_22_1	V_6_2	3.336689	Vietnam
461	V_22_3	V_6_2	1.987933	Vietnam
462	V_22_4	V_6_2	1.650308	Vietnam
463	V_1_2	V_6_3	NA	Vietnam
464	V_2_2	V_6_3	NA	Vietnam

465	V_3_1	V_6_3	NA	Vietnam
466	V_3_2	V_6_3	NA	Vietnam
467	V_5_3	V_6_3	NA	Vietnam
468	V_6_1	V_6_3	NA	Vietnam
469	V_6_2	V_6_3	NA	Vietnam
470	V_6_3	V_6_3	NA	Vietnam
471	V_7_1	V_6_3	-0.70328	Vietnam
472	V_7_2	V_6_3	-2.39139	Vietnam
473	V_7_3	V_6_3	0.494384	Vietnam
474	V_8_2	V_6_3	-0.07271	Vietnam
475	V_9_1	V_6_3	-0.08883	Vietnam
476	V_9_2	V_6_3	0.882968	Vietnam
477	V_9_4	V_6_3	0.036606	Vietnam
478	V_10_1	V_6_3	5.493392	Vietnam
479	V_11_1	V_6_3	-0.34669	Vietnam
480	V_11_3	V_6_3	-0.17348	Vietnam
481	V_12_1	V_6_3	0.291285	Vietnam
482	V_13_2	V_6_3	4.383303	Vietnam
483	V_14_1	V_6_3	3.491583	Vietnam
484	V_15_1	V_6_3	4.370259	Vietnam
485	V_15_2	V_6_3	0.815986	Vietnam
486	V_15_3	V_6_3	1.973082	Vietnam
487	V_16_1	V_6_3	3.144496	Vietnam
488	V_16_2	V_6_3	3.253759	Vietnam
489	V_17_1	V_6_3	2.556365	Vietnam
490	V_17_2	V_6_3	2.343509	Vietnam
491	V_18_1	V_6_3	2.88248	Vietnam
492	V_18_2	V_6_3	0.905171	Vietnam
493	V_18_4	V_6_3	-1.27968	Vietnam
494	V_19_1	V_6_3	1.320374	Vietnam
495	V_19_3	V_6_3	-0.43657	Vietnam
496	V_20_1	V_6_3	-0.77253	Vietnam
497	V_21_1	V_6_3	-0.86577	Vietnam
498	V_22_1	V_6_3	-0.28878	Vietnam
499	V_22_3	V_6_3	1.116882	Vietnam
500	V_22_4	V_6_3	-0.3196	Vietnam
501	V_1_2	V_7_1	NA	Vietnam
502	V_2_2	V_7_1	NA	Vietnam
503	V_3_1	V_7_1	NA	Vietnam
504	V_3_2	V_7_1	NA	Vietnam
505	V_5_3	V_7_1	NA	Vietnam
506	V_6_1	V_7_1	NA	Vietnam
507	V_6_2	V_7_1	NA	Vietnam

508	V_6_3	V_7_1	NA	Vietnam
509	V_7_1	V_7_1	NA	Vietnam
510	V_7_2	V_7_1	2.857915	Vietnam
511	V_7_3	V_7_1	5.131299	Vietnam
512	V_8_2	V_7_1	1.271836	Vietnam
513	V_9_1	V_7_1	-1.37723	Vietnam
514	V_9_2	V_7_1	1.429088	Vietnam
515	V_9_4	V_7_1	0.965346	Vietnam
516	V_10_1	V_7_1	-0.40308	Vietnam
517	V_11_1	V_7_1	-1.07036	Vietnam
518	V_11_3	V_7_1	0.958139	Vietnam
519	V_12_1	V_7_1	-1.06402	Vietnam
520	V_13_2	V_7_1	0.120975	Vietnam
521	V_14_1	V_7_1	-0.39882	Vietnam
522	V_15_1	V_7_1	-0.00635	Vietnam
523	V_15_2	V_7_1	0.302729	Vietnam
524	V_15_3	V_7_1	1.0965	Vietnam
525	V_16_1	V_7_1	0.670089	Vietnam
526	V_16_2	V_7_1	1.693781	Vietnam
527	V_17_1	V_7_1	-2.50708	Vietnam
528	V_17_2	V_7_1	-0.82342	Vietnam
529	V_18_1	V_7_1	-1.14679	Vietnam
530	V_18_2	V_7_1	-2.04961	Vietnam
531	V_18_4	V_7_1	1.481354	Vietnam
532	V_19_1	V_7_1	2.481586	Vietnam
533	V_19_3	V_7_1	1.477739	Vietnam
534	V_20_1	V_7_1	-0.59452	Vietnam
535	V_21_1	V_7_1	-1.41944	Vietnam
536	V_22_1	V_7_1	9.533653	Vietnam
537	V_22_3	V_7_1	3.619858	Vietnam
538	V_22_4	V_7_1	4.845845	Vietnam
539	V_1_2	V_7_2	NA	Vietnam
540	V_2_2	V_7_2	NA	Vietnam
541	V_3_1	V_7_2	NA	Vietnam
542	V_3_2	V_7_2	NA	Vietnam
543	V_5_3	V_7_2	NA	Vietnam
544	V_6_1	V_7_2	NA	Vietnam
545	V_6_2	V_7_2	NA	Vietnam
546	V_6_3	V_7_2	NA	Vietnam
547	V_7_1	V_7_2	NA	Vietnam
548	V_7_2	V_7_2	NA	Vietnam
549	V_7_3	V_7_2	1.35858	Vietnam
550	V_8_2	V_7_2	-1.79664	Vietnam

551	V_9_1	V_7_2	3.884713	Vietnam
552	V_9_2	V_7_2	-0.47536	Vietnam
553	V_9_4	V_7_2	1.268772	Vietnam
554	V_10_1	V_7_2	7.408879	Vietnam
555	V_11_1	V_7_2	0.248842	Vietnam
556	V_11_3	V_7_2	-1.86942	Vietnam
557	V_12_1	V_7_2	1.055218	Vietnam
558	V_13_2	V_7_2	6.256798	Vietnam
559	V_14_1	V_7_2	7.65548	Vietnam
560	V_15_1	V_7_2	2.911144	Vietnam
561	V_15_2	V_7_2	-1.41102	Vietnam
562	V_15_3	V_7_2	0.619117	Vietnam
563	V_16_1	V_7_2	9.532935	Vietnam
564	V_16_2	V_7_2	10.61363	Vietnam
565	V_17_1	V_7_2	2.585495	Vietnam
566	V_17_2	V_7_2	5.880927	Vietnam
567	V_18_1	V_7_2	3.470091	Vietnam
568	V_18_2	V_7_2	-0.20732	Vietnam
569	V_18_4	V_7_2	-1.44818	Vietnam
570	V_19_1	V_7_2	3.408047	Vietnam
571	V_19_3	V_7_2	-0.28571	Vietnam
572	V_20_1	V_7_2	2.097965	Vietnam
573	V_21_1	V_7_2	0.008922	Vietnam
574	V_22_1	V_7_2	-0.34933	Vietnam
575	V_22_3	V_7_2	-1.1815	Vietnam
576	V_22_4	V_7_2	-0.06866	Vietnam
577	V_1_2	V_7_3	NA	Vietnam
578	V_2_2	V_7_3	NA	Vietnam
579	V_3_1	V_7_3	NA	Vietnam
580	V_3_2	V_7_3	NA	Vietnam
581	V_5_3	V_7_3	NA	Vietnam
582	V_6_1	V_7_3	NA	Vietnam
583	V_6_2	V_7_3	NA	Vietnam
584	V_6_3	V_7_3	NA	Vietnam
585	V_7_1	V_7_3	NA	Vietnam
586	V_7_2	V_7_3	NA	Vietnam
587	V_7_3	V_7_3	NA	Vietnam
588	V_8_2	V_7_3	2.441823	Vietnam
589	V_9_1	V_7_3	4.259304	Vietnam
590	V_9_2	V_7_3	1.902619	Vietnam
591	V_9_4	V_7_3	2.127444	Vietnam
592	V_10_1	V_7_3	6.673456	Vietnam
593	V_11_1	V_7_3	3.82115	Vietnam

594	V_11_3	V_7_3	1.004114	Vietnam
595	V_12_1	V_7_3	2.69641	Vietnam
596	V_13_2	V_7_3	6.562025	Vietnam
597	V_14_1	V_7_3	7.642351	Vietnam
598	V_15_1	V_7_3	6.911599	Vietnam
599	V_15_2	V_7_3	4.051467	Vietnam
600	V_15_3	V_7_3	4.606331	Vietnam
601	V_16_1	V_7_3	8.663628	Vietnam
602	V_16_2	V_7_3	8.456317	Vietnam
603	V_17_1	V_7_3	3.834982	Vietnam
604	V_17_2	V_7_3	7.149961	Vietnam
605	V_18_1	V_7_3	4.680706	Vietnam
606	V_18_2	V_7_3	3.702273	Vietnam
607	V_18_4	V_7_3	1.966189	Vietnam
608	V_19_1	V_7_3	4.989203	Vietnam
609	V_19_3	V_7_3	0.570324	Vietnam
610	V_20_1	V_7_3	4.956633	Vietnam
611	V_21_1	V_7_3	3.836734	Vietnam
612	V_22_1	V_7_3	1.457386	Vietnam
613	V_22_3	V_7_3	1.738602	Vietnam
614	V_22_4	V_7_3	0.528583	Vietnam
615	V_1_2	V_8_2	NA	Vietnam
616	V_2_2	V_8_2	NA	Vietnam
617	V_3_1	V_8_2	NA	Vietnam
618	V_3_2	V_8_2	NA	Vietnam
619	V_5_3	V_8_2	NA	Vietnam
620	V_6_1	V_8_2	NA	Vietnam
621	V_6_2	V_8_2	NA	Vietnam
622	V_6_3	V_8_2	NA	Vietnam
623	V_7_1	V_8_2	NA	Vietnam
624	V_7_2	V_8_2	NA	Vietnam
625	V_7_3	V_8_2	NA	Vietnam
626	V_8_2	V_8_2	NA	Vietnam
627	V_9_1	V_8_2	2.141762	Vietnam
628	V_9_2	V_8_2	1.253094	Vietnam
629	V_9_4	V_8_2	0.328254	Vietnam
630	V_10_1	V_8_2	2.786792	Vietnam
631	V_11_1	V_8_2	-0.14477	Vietnam
632	V_11_3	V_8_2	-2.76863	Vietnam
633	V_12_1	V_8_2	1.251819	Vietnam
634	V_13_2	V_8_2	2.647809	Vietnam
635	V_14_1	V_8_2	3.184755	Vietnam
636	V_15_1	V_8_2	2.567143	Vietnam

637	V_15_2	V_8_2	-0.65095	Vietnam
638	V_15_3	V_8_2	1.245923	Vietnam
639	V_16_1	V_8_2	3.148245	Vietnam
640	V_16_2	V_8_2	5.783759	Vietnam
641	V_17_1	V_8_2	1.331023	Vietnam
642	V_17_2	V_8_2	3.16992	Vietnam
643	V_18_1	V_8_2	4.018924	Vietnam
644	V_18_2	V_8_2	1.666849	Vietnam
645	V_18_4	V_8_2	-0.52603	Vietnam
646	V_19_1	V_8_2	2.395946	Vietnam
647	V_19_3	V_8_2	-0.53297	Vietnam
648	V_20_1	V_8_2	-0.4749	Vietnam
649	V_21_1	V_8_2	1.113153	Vietnam
650	V_22_1	V_8_2	-0.18663	Vietnam
651	V_22_3	V_8_2	-0.74072	Vietnam
652	V_22_4	V_8_2	-0.00794	Vietnam
653	V_1_2	V_9_1	NA	Vietnam
654	V_2_2	V_9_1	NA	Vietnam
655	V_3_1	V_9_1	NA	Vietnam
656	V_3_2	V_9_1	NA	Vietnam
657	V_5_3	V_9_1	NA	Vietnam
658	V_6_1	V_9_1	NA	Vietnam
659	V_6_2	V_9_1	NA	Vietnam
660	V_6_3	V_9_1	NA	Vietnam
661	V_7_1	V_9_1	NA	Vietnam
662	V_7_2	V_9_1	NA	Vietnam
663	V_7_3	V_9_1	NA	Vietnam
664	V_8_2	V_9_1	NA	Vietnam
665	V_9_1	V_9_1	NA	Vietnam
666	V_9_2	V_9_1	1.985955	Vietnam
667	V_9_4	V_9_1	0.783745	Vietnam
668	V_10_1	V_9_1	-1.48395	Vietnam
669	V_11_1	V_9_1	-0.63361	Vietnam
670	V_11_3	V_9_1	2.716951	Vietnam
671	V_12_1	V_9_1	-1.3628	Vietnam
672	V_13_2	V_9_1	-0.26018	Vietnam
673	V_14_1	V_9_1	-2.90787	Vietnam
674	V_15_1	V_9_1	-0.30337	Vietnam
675	V_15_2	V_9_1	0.346509	Vietnam
676	V_15_3	V_9_1	1.341661	Vietnam
677	V_16_1	V_9_1	-1.22073	Vietnam
678	V_16_2	V_9_1	1.007119	Vietnam
679	V_17_1	V_9_1	-2.54254	Vietnam

680	V_17_2	V_9_1	-1.89449	Vietnam
681	V_18_1	V_9_1	-2.0222	Vietnam
682	V_18_2	V_9_1	-1.46733	Vietnam
683	V_18_4	V_9_1	1.798329	Vietnam
684	V_19_1	V_9_1	-1.93758	Vietnam
685	V_19_3	V_9_1	1.158348	Vietnam
686	V_20_1	V_9_1	-2.70605	Vietnam
687	V_21_1	V_9_1	-1.54316	Vietnam
688	V_22_1	V_9_1	7.670917	Vietnam
689	V_22_3	V_9_1	1.059675	Vietnam
690	V_22_4	V_9_1	5.17294	Vietnam
691	V_1_2	V_9_2	NA	Vietnam
692	V_2_2	V_9_2	NA	Vietnam
693	V_3_1	V_9_2	NA	Vietnam
694	V_3_2	V_9_2	NA	Vietnam
695	V_5_3	V_9_2	NA	Vietnam
696	V_6_1	V_9_2	NA	Vietnam
697	V_6_2	V_9_2	NA	Vietnam
698	V_6_3	V_9_2	NA	Vietnam
699	V_7_1	V_9_2	NA	Vietnam
700	V_7_2	V_9_2	NA	Vietnam
701	V_7_3	V_9_2	NA	Vietnam
702	V_8_2	V_9_2	NA	Vietnam
703	V_9_1	V_9_2	NA	Vietnam
704	V_9_2	V_9_2	NA	Vietnam
705	V_9_4	V_9_2	-1.18368	Vietnam
706	V_10_1	V_9_2	3.606211	Vietnam
707	V_11_1	V_9_2	-1.49816	Vietnam
708	V_11_3	V_9_2	-1.14142	Vietnam
709	V_12_1	V_9_2	-0.15295	Vietnam
710	V_13_2	V_9_2	3.80434	Vietnam
711	V_14_1	V_9_2	1.724048	Vietnam
712	V_15_1	V_9_2	4.734227	Vietnam
713	V_15_2	V_9_2	2.617964	Vietnam
714	V_15_3	V_9_2	4.204042	Vietnam
715	V_16_1	V_9_2	4.772058	Vietnam
716	V_16_2	V_9_2	6.55008	Vietnam
717	V_17_1	V_9_2	2.47305	Vietnam
718	V_17_2	V_9_2	4.135014	Vietnam
719	V_18_1	V_9_2	3.529319	Vietnam
720	V_18_2	V_9_2	3.281681	Vietnam
721	V_18_4	V_9_2	1.687799	Vietnam
722	V_19_1	V_9_2	1.369673	Vietnam

723	V_19_3	V_9_2	0.048076	Vietnam
724	V_20_1	V_9_2	2.059965	Vietnam
725	V_21_1	V_9_2	-0.55101	Vietnam
726	V_22_1	V_9_2	0.004575	Vietnam
727	V_22_3	V_9_2	-3.16031	Vietnam
728	V_22_4	V_9_2	-2.49432	Vietnam
729	V_1_2	V_9_4	NA	Vietnam
730	V_2_2	V_9_4	NA	Vietnam
731	V_3_1	V_9_4	NA	Vietnam
732	V_3_2	V_9_4	NA	Vietnam
733	V_5_3	V_9_4	NA	Vietnam
734	V_6_1	V_9_4	NA	Vietnam
735	V_6_2	V_9_4	NA	Vietnam
736	V_6_3	V_9_4	NA	Vietnam
737	V_7_1	V_9_4	NA	Vietnam
738	V_7_2	V_9_4	NA	Vietnam
739	V_7_3	V_9_4	NA	Vietnam
740	V_8_2	V_9_4	NA	Vietnam
741	V_9_1	V_9_4	NA	Vietnam
742	V_9_2	V_9_4	NA	Vietnam
743	V_9_4	V_9_4	NA	Vietnam
744	V_10_1	V_9_4	1.580623	Vietnam
745	V_11_1	V_9_4	1.892694	Vietnam
746	V_11_3	V_9_4	0.478071	Vietnam
747	V_12_1	V_9_4	0.770498	Vietnam
748	V_13_2	V_9_4	2.195978	Vietnam
749	V_14_1	V_9_4	2.045281	Vietnam
750	V_15_1	V_9_4	2.624187	Vietnam
751	V_15_2	V_9_4	2.738222	Vietnam
752	V_15_3	V_9_4	1.488515	Vietnam
753	V_16_1	V_9_4	2.542493	Vietnam
754	V_16_2	V_9_4	3.662802	Vietnam
755	V_17_1	V_9_4	1.400588	Vietnam
756	V_17_2	V_9_4	2.258406	Vietnam
757	V_18_1	V_9_4	2.000233	Vietnam
758	V_18_2	V_9_4	1.083503	Vietnam
759	V_18_4	V_9_4	1.30957	Vietnam
760	V_19_1	V_9_4	0.8046	Vietnam
761	V_19_3	V_9_4	0.194585	Vietnam
762	V_20_1	V_9_4	0.369627	Vietnam
763	V_21_1	V_9_4	0.195423	Vietnam
764	V_22_1	V_9_4	-0.0588	Vietnam
765	V_22_3	V_9_4	-0.47978	Vietnam

766	V_22_4	V_9_4	-0.94056	Vietnam
767	V_1_2	V_10_1	NA	Vietnam
768	V_2_2	V_10_1	NA	Vietnam
769	V_3_1	V_10_1	NA	Vietnam
770	V_3_2	V_10_1	NA	Vietnam
771	V_5_3	V_10_1	NA	Vietnam
772	V_6_1	V_10_1	NA	Vietnam
773	V_6_2	V_10_1	NA	Vietnam
774	V_6_3	V_10_1	NA	Vietnam
775	V_7_1	V_10_1	NA	Vietnam
776	V_7_2	V_10_1	NA	Vietnam
777	V_7_3	V_10_1	NA	Vietnam
778	V_8_2	V_10_1	NA	Vietnam
779	V_9_1	V_10_1	NA	Vietnam
780	V_9_2	V_10_1	NA	Vietnam
781	V_9_4	V_10_1	NA	Vietnam
782	V_10_1	V_10_1	NA	Vietnam
783	V_11_1	V_10_1	0.643846	Vietnam
784	V_11_3	V_10_1	3.868193	Vietnam
785	V_12_1	V_10_1	-0.73854	Vietnam
786	V_13_2	V_10_1	-1.17953	Vietnam
787	V_14_1	V_10_1	-1.74227	Vietnam
788	V_15_1	V_10_1	-1.22221	Vietnam
789	V_15_2	V_10_1	2.392592	Vietnam
790	V_15_3	V_10_1	3.120163	Vietnam
791	V_16_1	V_10_1	-2.3531	Vietnam
792	V_16_2	V_10_1	-1.39676	Vietnam
793	V_17_1	V_10_1	-3.01664	Vietnam
794	V_17_2	V_10_1	-2.20548	Vietnam
795	V_18_1	V_10_1	-1.2024	Vietnam
796	V_18_2	V_10_1	-1.61124	Vietnam
797	V_18_4	V_10_1	5.205317	Vietnam
798	V_19_1	V_10_1	1.597157	Vietnam
799	V_19_3	V_10_1	2.661168	Vietnam
800	V_20_1	V_10_1	-1.00861	Vietnam
801	V_21_1	V_10_1	-1.91849	Vietnam
802	V_22_1	V_10_1	11.88826	Vietnam
803	V_22_3	V_10_1	5.093311	Vietnam
804	V_22_4	V_10_1	6.91119	Vietnam
805	V_1_2	V_11_1	NA	Vietnam
806	V_2_2	V_11_1	NA	Vietnam
807	V_3_1	V_11_1	NA	Vietnam
808	V_3_2	V_11_1	NA	Vietnam

809	V_5_3	V_11_1	NA	Vietnam
810	V_6_1	V_11_1	NA	Vietnam
811	V_6_2	V_11_1	NA	Vietnam
812	V_6_3	V_11_1	NA	Vietnam
813	V_7_1	V_11_1	NA	Vietnam
814	V_7_2	V_11_1	NA	Vietnam
815	V_7_3	V_11_1	NA	Vietnam
816	V_8_2	V_11_1	NA	Vietnam
817	V_9_1	V_11_1	NA	Vietnam
818	V_9_2	V_11_1	NA	Vietnam
819	V_9_4	V_11_1	NA	Vietnam
820	V_10_1	V_11_1	NA	Vietnam
821	V_11_1	V_11_1	NA	Vietnam
822	V_11_3	V_11_1	-0.26529	Vietnam
823	V_12_1	V_11_1	-1.05231	Vietnam
824	V_13_2	V_11_1	2.203111	Vietnam
825	V_14_1	V_11_1	4.282757	Vietnam
826	V_15_1	V_11_1	1.97904	Vietnam
827	V_15_2	V_11_1	2.042231	Vietnam
828	V_15_3	V_11_1	1.567764	Vietnam
829	V_16_1	V_11_1	3.475201	Vietnam
830	V_16_2	V_11_1	4.224636	Vietnam
831	V_17_1	V_11_1	-2.19203	Vietnam
832	V_17_2	V_11_1	1.419901	Vietnam
833	V_18_1	V_11_1	-0.56419	Vietnam
834	V_18_2	V_11_1	-1.88418	Vietnam
835	V_18_4	V_11_1	0.506275	Vietnam
836	V_19_1	V_11_1	5.968284	Vietnam
837	V_19_3	V_11_1	1.228127	Vietnam
838	V_20_1	V_11_1	2.633783	Vietnam
839	V_21_1	V_11_1	-1.55834	Vietnam
840	V_22_1	V_11_1	-0.41991	Vietnam
841	V_22_3	V_11_1	0.199103	Vietnam
842	V_22_4	V_11_1	-0.4953	Vietnam
843	V_1_2	V_11_3	NA	Vietnam
844	V_2_2	V_11_3	NA	Vietnam
845	V_3_1	V_11_3	NA	Vietnam
846	V_3_2	V_11_3	NA	Vietnam
847	V_5_3	V_11_3	NA	Vietnam
848	V_6_1	V_11_3	NA	Vietnam
849	V_6_2	V_11_3	NA	Vietnam
850	V_6_3	V_11_3	NA	Vietnam
851	V_7_1	V_11_3	NA	Vietnam

852	V_7_2	V_11_3	NA	Vietnam
853	V_7_3	V_11_3	NA	Vietnam
854	V_8_2	V_11_3	NA	Vietnam
855	V_9_1	V_11_3	NA	Vietnam
856	V_9_2	V_11_3	NA	Vietnam
857	V_9_4	V_11_3	NA	Vietnam
858	V_10_1	V_11_3	NA	Vietnam
859	V_11_1	V_11_3	NA	Vietnam
860	V_11_3	V_11_3	NA	Vietnam
861	V_12_1	V_11_3	1.422668	Vietnam
862	V_13_2	V_11_3	5.331461	Vietnam
863	V_14_1	V_11_3	4.643097	Vietnam
864	V_15_1	V_11_3	3.978355	Vietnam
865	V_15_2	V_11_3	-0.17536	Vietnam
866	V_15_3	V_11_3	3.520263	Vietnam
867	V_16_1	V_11_3	5.401053	Vietnam
868	V_16_2	V_11_3	8.585383	Vietnam
869	V_17_1	V_11_3	1.734157	Vietnam
870	V_17_2	V_11_3	4.212561	Vietnam
871	V_18_1	V_11_3	3.135467	Vietnam
872	V_18_2	V_11_3	0.2504	Vietnam
873	V_18_4	V_11_3	-0.18712	Vietnam
874	V_19_1	V_11_3	3.122062	Vietnam
875	V_19_3	V_11_3	-1.56585	Vietnam
876	V_20_1	V_11_3	0.253584	Vietnam
877	V_21_1	V_11_3	-0.1531	Vietnam
878	V_22_1	V_11_3	-1.61493	Vietnam
879	V_22_3	V_11_3	-1.90694	Vietnam
880	V_22_4	V_11_3	-1.74275	Vietnam
881	V_1_2	V_12_1	NA	Vietnam
882	V_2_2	V_12_1	NA	Vietnam
883	V_3_1	V_12_1	NA	Vietnam
884	V_3_2	V_12_1	NA	Vietnam
885	V_5_3	V_12_1	NA	Vietnam
886	V_6_1	V_12_1	NA	Vietnam
887	V_6_2	V_12_1	NA	Vietnam
888	V_6_3	V_12_1	NA	Vietnam
889	V_7_1	V_12_1	NA	Vietnam
890	V_7_2	V_12_1	NA	Vietnam
891	V_7_3	V_12_1	NA	Vietnam
892	V_8_2	V_12_1	NA	Vietnam
893	V_9_1	V_12_1	NA	Vietnam
894	V_9_2	V_12_1	NA	Vietnam

895	V_9_4	V_12_1	NA	Vietnam
896	V_10_1	V_12_1	NA	Vietnam
897	V_11_1	V_12_1	NA	Vietnam
898	V_11_3	V_12_1	NA	Vietnam
899	V_12_1	V_12_1	NA	Vietnam
900	V_13_2	V_12_1	-0.15251	Vietnam
901	V_14_1	V_12_1	0.358886	Vietnam
902	V_15_1	V_12_1	-0.7659	Vietnam
903	V_15_2	V_12_1	0.01031	Vietnam
904	V_15_3	V_12_1	0.630901	Vietnam
905	V_16_1	V_12_1	1.392891	Vietnam
906	V_16_2	V_12_1	2.15645	Vietnam
907	V_17_1	V_12_1	-0.55751	Vietnam
908	V_17_2	V_12_1	-0.66522	Vietnam
909	V_18_1	V_12_1	-0.89389	Vietnam
910	V_18_2	V_12_1	-0.07208	Vietnam
911	V_18_4	V_12_1	0.760379	Vietnam
912	V_19_1	V_12_1	-0.01183	Vietnam
913	V_19_3	V_12_1	0.42544	Vietnam
914	V_20_1	V_12_1	-1.4267	Vietnam
915	V_21_1	V_12_1	-1.4775	Vietnam
916	V_22_1	V_12_1	3.979258	Vietnam
917	V_22_3	V_12_1	0.120631	Vietnam
918	V_22_4	V_12_1	-0.04149	Vietnam
919	V_1_2	V_13_2	NA	Vietnam
920	V_2_2	V_13_2	NA	Vietnam
921	V_3_1	V_13_2	NA	Vietnam
922	V_3_2	V_13_2	NA	Vietnam
923	V_5_3	V_13_2	NA	Vietnam
924	V_6_1	V_13_2	NA	Vietnam
925	V_6_2	V_13_2	NA	Vietnam
926	V_6_3	V_13_2	NA	Vietnam
927	V_7_1	V_13_2	NA	Vietnam
928	V_7_2	V_13_2	NA	Vietnam
929	V_7_3	V_13_2	NA	Vietnam
930	V_8_2	V_13_2	NA	Vietnam
931	V_9_1	V_13_2	NA	Vietnam
932	V_9_2	V_13_2	NA	Vietnam
933	V_9_4	V_13_2	NA	Vietnam
934	V_10_1	V_13_2	NA	Vietnam
935	V_11_1	V_13_2	NA	Vietnam
936	V_11_3	V_13_2	NA	Vietnam
937	V_12_1	V_13_2	NA	Vietnam

938	V_13_2	V_13_2	NA	Vietnam
939	V_14_1	V_13_2	1.598089	Vietnam
940	V_15_1	V_13_2	-1.36402	Vietnam
941	V_15_2	V_13_2	2.477192	Vietnam
942	V_15_3	V_13_2	4.074779	Vietnam
943	V_16_1	V_13_2	-1.31058	Vietnam
944	V_16_2	V_13_2	0.828815	Vietnam
945	V_17_1	V_13_2	-0.79797	Vietnam
946	V_17_2	V_13_2	-2.24081	Vietnam
947	V_18_1	V_13_2	-0.32516	Vietnam
948	V_18_2	V_13_2	-2.15627	Vietnam
949	V_18_4	V_13_2	1.724363	Vietnam
950	V_19_1	V_13_2	5.058386	Vietnam
951	V_19_3	V_13_2	2.067769	Vietnam
952	V_20_1	V_13_2	-0.33251	Vietnam
953	V_21_1	V_13_2	-0.73489	Vietnam
954	V_22_1	V_13_2	9.08923	Vietnam
955	V_22_3	V_13_2	2.035563	Vietnam
956	V_22_4	V_13_2	1.788749	Vietnam
957	V_1_2	V_14_1	NA	Vietnam
958	V_2_2	V_14_1	NA	Vietnam
959	V_3_1	V_14_1	NA	Vietnam
960	V_3_2	V_14_1	NA	Vietnam
961	V_5_3	V_14_1	NA	Vietnam
962	V_6_1	V_14_1	NA	Vietnam
963	V_6_2	V_14_1	NA	Vietnam
964	V_6_3	V_14_1	NA	Vietnam
965	V_7_1	V_14_1	NA	Vietnam
966	V_7_2	V_14_1	NA	Vietnam
967	V_7_3	V_14_1	NA	Vietnam
968	V_8_2	V_14_1	NA	Vietnam
969	V_9_1	V_14_1	NA	Vietnam
970	V_9_2	V_14_1	NA	Vietnam
971	V_9_4	V_14_1	NA	Vietnam
972	V_10_1	V_14_1	NA	Vietnam
973	V_11_1	V_14_1	NA	Vietnam
974	V_11_3	V_14_1	NA	Vietnam
975	V_12_1	V_14_1	NA	Vietnam
976	V_13_2	V_14_1	NA	Vietnam
977	V_14_1	V_14_1	NA	Vietnam
978	V_15_1	V_14_1	0.906155	Vietnam
979	V_15_2	V_14_1	5.726508	Vietnam
980	V_15_3	V_14_1	5.716365	Vietnam

981	V_16_1	V_14_1	-2.20562	Vietnam
982	V_16_2	V_14_1	-1.18245	Vietnam
983	V_17_1	V_14_1	-2.00274	Vietnam
984	V_17_2	V_14_1	-2.81979	Vietnam
985	V_18_1	V_14_1	-1.20053	Vietnam
986	V_18_2	V_14_1	-1.5962	Vietnam
987	V_18_4	V_14_1	5.22448	Vietnam
988	V_19_1	V_14_1	-0.40519	Vietnam
989	V_19_3	V_14_1	3.261785	Vietnam
990	V_20_1	V_14_1	0.404186	Vietnam
991	V_21_1	V_14_1	-0.38222	Vietnam
992	V_22_1	V_14_1	11.082	Vietnam
993	V_22_3	V_14_1	2.871014	Vietnam
994	V_22_4	V_14_1	3.947305	Vietnam
995	V_1_2	V_15_1	NA	Vietnam
996	V_2_2	V_15_1	NA	Vietnam
997	V_3_1	V_15_1	NA	Vietnam
998	V_3_2	V_15_1	NA	Vietnam
999	V_5_3	V_15_1	NA	Vietnam
1000	V_6_1	V_15_1	NA	Vietnam
1001	V_6_2	V_15_1	NA	Vietnam
1002	V_6_3	V_15_1	NA	Vietnam
1003	V_7_1	V_15_1	NA	Vietnam
1004	V_7_2	V_15_1	NA	Vietnam
1005	V_7_3	V_15_1	NA	Vietnam
1006	V_8_2	V_15_1	NA	Vietnam
1007	V_9_1	V_15_1	NA	Vietnam
1008	V_9_2	V_15_1	NA	Vietnam
1009	V_9_4	V_15_1	NA	Vietnam
1010	V_10_1	V_15_1	NA	Vietnam
1011	V_11_1	V_15_1	NA	Vietnam
1012	V_11_3	V_15_1	NA	Vietnam
1013	V_12_1	V_15_1	NA	Vietnam
1014	V_13_2	V_15_1	NA	Vietnam
1015	V_14_1	V_15_1	NA	Vietnam
1016	V_15_1	V_15_1	NA	Vietnam
1017	V_15_2	V_15_1	1.863544	Vietnam
1018	V_15_3	V_15_1	3.733856	Vietnam
1019	V_16_1	V_15_1	-1.03454	Vietnam
1020	V_16_2	V_15_1	-0.634	Vietnam
1021	V_17_1	V_15_1	-0.16517	Vietnam
1022	V_17_2	V_15_1	-1.47489	Vietnam
1023	V_18_1	V_15_1	-1.06663	Vietnam

1024	V_18_2	V_15_1	-1.5905	Vietnam
1025	V_18_4	V_15_1	3.71076	Vietnam
1026	V_19_1	V_15_1	3.583915	Vietnam
1027	V_19_3	V_15_1	1.461212	Vietnam
1028	V_20_1	V_15_1	-0.19498	Vietnam
1029	V_21_1	V_15_1	-1.12879	Vietnam
1030	V_22_1	V_15_1	8.671091	Vietnam
1031	V_22_3	V_15_1	4.511318	Vietnam
1032	V_22_4	V_15_1	3.904118	Vietnam
1033	V_1_2	V_15_2	NA	Vietnam
1034	V_2_2	V_15_2	NA	Vietnam
1035	V_3_1	V_15_2	NA	Vietnam
1036	V_3_2	V_15_2	NA	Vietnam
1037	V_5_3	V_15_2	NA	Vietnam
1038	V_6_1	V_15_2	NA	Vietnam
1039	V_6_2	V_15_2	NA	Vietnam
1040	V_6_3	V_15_2	NA	Vietnam
1041	V_7_1	V_15_2	NA	Vietnam
1042	V_7_2	V_15_2	NA	Vietnam
1043	V_7_3	V_15_2	NA	Vietnam
1044	V_8_2	V_15_2	NA	Vietnam
1045	V_9_1	V_15_2	NA	Vietnam
1046	V_9_2	V_15_2	NA	Vietnam
1047	V_9_4	V_15_2	NA	Vietnam
1048	V_10_1	V_15_2	NA	Vietnam
1049	V_11_1	V_15_2	NA	Vietnam
1050	V_11_3	V_15_2	NA	Vietnam
1051	V_12_1	V_15_2	NA	Vietnam
1052	V_13_2	V_15_2	NA	Vietnam
1053	V_14_1	V_15_2	NA	Vietnam
1054	V_15_1	V_15_2	NA	Vietnam
1055	V_15_2	V_15_2	NA	Vietnam
1056	V_15_3	V_15_2	0.273551	Vietnam
1057	V_16_1	V_15_2	4.249682	Vietnam
1058	V_16_2	V_15_2	4.646486	Vietnam
1059	V_17_1	V_15_2	1.619809	Vietnam
1060	V_17_2	V_15_2	2.479889	Vietnam
1061	V_18_1	V_15_2	1.614261	Vietnam
1062	V_18_2	V_15_2	-0.29388	Vietnam
1063	V_18_4	V_15_2	-0.90327	Vietnam
1064	V_19_1	V_15_2	3.347227	Vietnam
1065	V_19_3	V_15_2	0.580942	Vietnam
1066	V_20_1	V_15_2	0.87096	Vietnam

1067	V_21_1	V_15_2	-0.11688	Vietnam
1068	V_22_1	V_15_2	3.950733	Vietnam
1069	V_22_3	V_15_2	2.236524	Vietnam
1070	V_22_4	V_15_2	2.670976	Vietnam
1071	V_1_2	V_15_3	NA	Vietnam
1072	V_2_2	V_15_3	NA	Vietnam
1073	V_3_1	V_15_3	NA	Vietnam
1074	V_3_2	V_15_3	NA	Vietnam
1075	V_5_3	V_15_3	NA	Vietnam
1076	V_6_1	V_15_3	NA	Vietnam
1077	V_6_2	V_15_3	NA	Vietnam
1078	V_6_3	V_15_3	NA	Vietnam
1079	V_7_1	V_15_3	NA	Vietnam
1080	V_7_2	V_15_3	NA	Vietnam
1081	V_7_3	V_15_3	NA	Vietnam
1082	V_8_2	V_15_3	NA	Vietnam
1083	V_9_1	V_15_3	NA	Vietnam
1084	V_9_2	V_15_3	NA	Vietnam
1085	V_9_4	V_15_3	NA	Vietnam
1086	V_10_1	V_15_3	NA	Vietnam
1087	V_11_1	V_15_3	NA	Vietnam
1088	V_11_3	V_15_3	NA	Vietnam
1089	V_12_1	V_15_3	NA	Vietnam
1090	V_13_2	V_15_3	NA	Vietnam
1091	V_14_1	V_15_3	NA	Vietnam
1092	V_15_1	V_15_3	NA	Vietnam
1093	V_15_2	V_15_3	NA	Vietnam
1094	V_15_3	V_15_3	NA	Vietnam
1095	V_16_1	V_15_3	4.836514	Vietnam
1096	V_16_2	V_15_3	4.796382	Vietnam
1097	V_17_1	V_15_3	2.980296	Vietnam
1098	V_17_2	V_15_3	3.546816	Vietnam
1099	V_18_1	V_15_3	1.990973	Vietnam
1100	V_18_2	V_15_3	0.345893	Vietnam
1101	V_18_4	V_15_3	2.265624	Vietnam
1102	V_19_1	V_15_3	3.873963	Vietnam
1103	V_19_3	V_15_3	2.104932	Vietnam
1104	V_20_1	V_15_3	1.018684	Vietnam
1105	V_21_1	V_15_3	1.144845	Vietnam
1106	V_22_1	V_15_3	5.662733	Vietnam
1107	V_22_3	V_15_3	2.533242	Vietnam
1108	V_22_4	V_15_3	3.227812	Vietnam
1109	V_1_2	V_16_1	NA	Vietnam

1110	V_2_2	V_16_1	NA	Vietnam
1111	V_3_1	V_16_1	NA	Vietnam
1112	V_3_2	V_16_1	NA	Vietnam
1113	V_5_3	V_16_1	NA	Vietnam
1114	V_6_1	V_16_1	NA	Vietnam
1115	V_6_2	V_16_1	NA	Vietnam
1116	V_6_3	V_16_1	NA	Vietnam
1117	V_7_1	V_16_1	NA	Vietnam
1118	V_7_2	V_16_1	NA	Vietnam
1119	V_7_3	V_16_1	NA	Vietnam
1120	V_8_2	V_16_1	NA	Vietnam
1121	V_9_1	V_16_1	NA	Vietnam
1122	V_9_2	V_16_1	NA	Vietnam
1123	V_9_4	V_16_1	NA	Vietnam
1124	V_10_1	V_16_1	NA	Vietnam
1125	V_11_1	V_16_1	NA	Vietnam
1126	V_11_3	V_16_1	NA	Vietnam
1127	V_12_1	V_16_1	NA	Vietnam
1128	V_13_2	V_16_1	NA	Vietnam
1129	V_14_1	V_16_1	NA	Vietnam
1130	V_15_1	V_16_1	NA	Vietnam
1131	V_15_2	V_16_1	NA	Vietnam
1132	V_15_3	V_16_1	NA	Vietnam
1133	V_16_1	V_16_1	NA	Vietnam
1134	V_16_2	V_16_1	0.523779	Vietnam
1135	V_17_1	V_16_1	-2.51781	Vietnam
1136	V_17_2	V_16_1	-2.06064	Vietnam
1137	V_18_1	V_16_1	-1.63794	Vietnam
1138	V_18_2	V_16_1	-1.42562	Vietnam
1139	V_18_4	V_16_1	3.562665	Vietnam
1140	V_19_1	V_16_1	-0.90215	Vietnam
1141	V_19_3	V_16_1	2.464613	Vietnam
1142	V_20_1	V_16_1	-0.65187	Vietnam
1143	V_21_1	V_16_1	-1.35326	Vietnam
1144	V_22_1	V_16_1	13.0731	Vietnam
1145	V_22_3	V_16_1	4.795129	Vietnam
1146	V_22_4	V_16_1	7.15591	Vietnam
1147	V_1_2	V_16_2	NA	Vietnam
1148	V_2_2	V_16_2	NA	Vietnam
1149	V_3_1	V_16_2	NA	Vietnam
1150	V_3_2	V_16_2	NA	Vietnam
1151	V_5_3	V_16_2	NA	Vietnam
1152	V_6_1	V_16_2	NA	Vietnam

1153	V_6_2	V_16_2	NA	Vietnam
1154	V_6_3	V_16_2	NA	Vietnam
1155	V_7_1	V_16_2	NA	Vietnam
1156	V_7_2	V_16_2	NA	Vietnam
1157	V_7_3	V_16_2	NA	Vietnam
1158	V_8_2	V_16_2	NA	Vietnam
1159	V_9_1	V_16_2	NA	Vietnam
1160	V_9_2	V_16_2	NA	Vietnam
1161	V_9_4	V_16_2	NA	Vietnam
1162	V_10_1	V_16_2	NA	Vietnam
1163	V_11_1	V_16_2	NA	Vietnam
1164	V_11_3	V_16_2	NA	Vietnam
1165	V_12_1	V_16_2	NA	Vietnam
1166	V_13_2	V_16_2	NA	Vietnam
1167	V_14_1	V_16_2	NA	Vietnam
1168	V_15_1	V_16_2	NA	Vietnam
1169	V_15_2	V_16_2	NA	Vietnam
1170	V_15_3	V_16_2	NA	Vietnam
1171	V_16_1	V_16_2	NA	Vietnam
1172	V_16_2	V_16_2	NA	Vietnam
1173	V_17_1	V_16_2	-1.06843	Vietnam
1174	V_17_2	V_16_2	-2.25038	Vietnam
1175	V_18_1	V_16_2	-1.17734	Vietnam
1176	V_18_2	V_16_2	0.351009	Vietnam
1177	V_18_4	V_16_2	3.709525	Vietnam
1178	V_19_1	V_16_2	3.455972	Vietnam
1179	V_19_3	V_16_2	3.596637	Vietnam
1180	V_20_1	V_16_2	1.847086	Vietnam
1181	V_21_1	V_16_2	2.045006	Vietnam
1182	V_22_1	V_16_2	13.64006	Vietnam
1183	V_22_3	V_16_2	6.953363	Vietnam
1184	V_22_4	V_16_2	8.006244	Vietnam
1185	V_1_2	V_17_1	NA	Vietnam
1186	V_2_2	V_17_1	NA	Vietnam
1187	V_3_1	V_17_1	NA	Vietnam
1188	V_3_2	V_17_1	NA	Vietnam
1189	V_5_3	V_17_1	NA	Vietnam
1190	V_6_1	V_17_1	NA	Vietnam
1191	V_6_2	V_17_1	NA	Vietnam
1192	V_6_3	V_17_1	NA	Vietnam
1193	V_7_1	V_17_1	NA	Vietnam
1194	V_7_2	V_17_1	NA	Vietnam
1195	V_7_3	V_17_1	NA	Vietnam

1196	V_8_2	V_17_1	NA	Vietnam
1197	V_9_1	V_17_1	NA	Vietnam
1198	V_9_2	V_17_1	NA	Vietnam
1199	V_9_4	V_17_1	NA	Vietnam
1200	V_10_1	V_17_1	NA	Vietnam
1201	V_11_1	V_17_1	NA	Vietnam
1202	V_11_3	V_17_1	NA	Vietnam
1203	V_12_1	V_17_1	NA	Vietnam
1204	V_13_2	V_17_1	NA	Vietnam
1205	V_14_1	V_17_1	NA	Vietnam
1206	V_15_1	V_17_1	NA	Vietnam
1207	V_15_2	V_17_1	NA	Vietnam
1208	V_15_3	V_17_1	NA	Vietnam
1209	V_16_1	V_17_1	NA	Vietnam
1210	V_16_2	V_17_1	NA	Vietnam
1211	V_17_1	V_17_1	NA	Vietnam
1212	V_17_2	V_17_1	-2.71743	Vietnam
1213	V_18_1	V_17_1	-1.82033	Vietnam
1214	V_18_2	V_17_1	-0.80474	Vietnam
1215	V_18_4	V_17_1	2.298695	Vietnam
1216	V_19_1	V_17_1	1.491764	Vietnam
1217	V_19_3	V_17_1	0.954514	Vietnam
1218	V_20_1	V_17_1	-1.89987	Vietnam
1219	V_21_1	V_17_1	-1.62928	Vietnam
1220	V_22_1	V_17_1	7.07108	Vietnam
1221	V_22_3	V_17_1	1.51159	Vietnam
1222	V_22_4	V_17_1	4.671122	Vietnam
1223	V_1_2	V_17_2	NA	Vietnam
1224	V_2_2	V_17_2	NA	Vietnam
1225	V_3_1	V_17_2	NA	Vietnam
1226	V_3_2	V_17_2	NA	Vietnam
1227	V_5_3	V_17_2	NA	Vietnam
1228	V_6_1	V_17_2	NA	Vietnam
1229	V_6_2	V_17_2	NA	Vietnam
1230	V_6_3	V_17_2	NA	Vietnam
1231	V_7_1	V_17_2	NA	Vietnam
1232	V_7_2	V_17_2	NA	Vietnam
1233	V_7_3	V_17_2	NA	Vietnam
1234	V_8_2	V_17_2	NA	Vietnam
1235	V_9_1	V_17_2	NA	Vietnam
1236	V_9_2	V_17_2	NA	Vietnam
1237	V_9_4	V_17_2	NA	Vietnam
1238	V_10_1	V_17_2	NA	Vietnam

1239	V_11_1	V_17_2	NA	Vietnam
1240	V_11_3	V_17_2	NA	Vietnam
1241	V_12_1	V_17_2	NA	Vietnam
1242	V_13_2	V_17_2	NA	Vietnam
1243	V_14_1	V_17_2	NA	Vietnam
1244	V_15_1	V_17_2	NA	Vietnam
1245	V_15_2	V_17_2	NA	Vietnam
1246	V_15_3	V_17_2	NA	Vietnam
1247	V_16_1	V_17_2	NA	Vietnam
1248	V_16_2	V_17_2	NA	Vietnam
1249	V_17_1	V_17_2	NA	Vietnam
1250	V_17_2	V_17_2	NA	Vietnam
1251	V_18_1	V_17_2	-2.17508	Vietnam
1252	V_18_2	V_17_2	-1.58484	Vietnam
1253	V_18_4	V_17_2	2.94562	Vietnam
1254	V_19_1	V_17_2	0.530268	Vietnam
1255	V_19_3	V_17_2	2.363313	Vietnam
1256	V_20_1	V_17_2	-0.58323	Vietnam
1257	V_21_1	V_17_2	-1.86958	Vietnam
1258	V_22_1	V_17_2	11.62461	Vietnam
1259	V_22_3	V_17_2	5.207269	Vietnam
1260	V_22_4	V_17_2	6.216235	Vietnam
1261	V_1_2	V_18_1	NA	Vietnam
1262	V_2_2	V_18_1	NA	Vietnam
1263	V_3_1	V_18_1	NA	Vietnam
1264	V_3_2	V_18_1	NA	Vietnam
1265	V_5_3	V_18_1	NA	Vietnam
1266	V_6_1	V_18_1	NA	Vietnam
1267	V_6_2	V_18_1	NA	Vietnam
1268	V_6_3	V_18_1	NA	Vietnam
1269	V_7_1	V_18_1	NA	Vietnam
1270	V_7_2	V_18_1	NA	Vietnam
1271	V_7_3	V_18_1	NA	Vietnam
1272	V_8_2	V_18_1	NA	Vietnam
1273	V_9_1	V_18_1	NA	Vietnam
1274	V_9_2	V_18_1	NA	Vietnam
1275	V_9_4	V_18_1	NA	Vietnam
1276	V_10_1	V_18_1	NA	Vietnam
1277	V_11_1	V_18_1	NA	Vietnam
1278	V_11_3	V_18_1	NA	Vietnam
1279	V_12_1	V_18_1	NA	Vietnam
1280	V_13_2	V_18_1	NA	Vietnam
1281	V_14_1	V_18_1	NA	Vietnam

1282	V_15_1	V_18_1	NA	Vietnam
1283	V_15_2	V_18_1	NA	Vietnam
1284	V_15_3	V_18_1	NA	Vietnam
1285	V_16_1	V_18_1	NA	Vietnam
1286	V_16_2	V_18_1	NA	Vietnam
1287	V_17_1	V_18_1	NA	Vietnam
1288	V_17_2	V_18_1	NA	Vietnam
1289	V_18_1	V_18_1	NA	Vietnam
1290	V_18_2	V_18_1	-1.06518	Vietnam
1291	V_18_4	V_18_1	5.520067	Vietnam
1292	V_19_1	V_18_1	1.623724	Vietnam
1293	V_19_3	V_18_1	1.498623	Vietnam
1294	V_20_1	V_18_1	-0.02019	Vietnam
1295	V_21_1	V_18_1	-0.19414	Vietnam
1296	V_22_1	V_18_1	8.048116	Vietnam
1297	V_22_3	V_18_1	4.714812	Vietnam
1298	V_22_4	V_18_1	4.891438	Vietnam
1299	V_1_2	V_18_2	NA	Vietnam
1300	V_2_2	V_18_2	NA	Vietnam
1301	V_3_1	V_18_2	NA	Vietnam
1302	V_3_2	V_18_2	NA	Vietnam
1303	V_5_3	V_18_2	NA	Vietnam
1304	V_6_1	V_18_2	NA	Vietnam
1305	V_6_2	V_18_2	NA	Vietnam
1306	V_6_3	V_18_2	NA	Vietnam
1307	V_7_1	V_18_2	NA	Vietnam
1308	V_7_2	V_18_2	NA	Vietnam
1309	V_7_3	V_18_2	NA	Vietnam
1310	V_8_2	V_18_2	NA	Vietnam
1311	V_9_1	V_18_2	NA	Vietnam
1312	V_9_2	V_18_2	NA	Vietnam
1313	V_9_4	V_18_2	NA	Vietnam
1314	V_10_1	V_18_2	NA	Vietnam
1315	V_11_1	V_18_2	NA	Vietnam
1316	V_11_3	V_18_2	NA	Vietnam
1317	V_12_1	V_18_2	NA	Vietnam
1318	V_13_2	V_18_2	NA	Vietnam
1319	V_14_1	V_18_2	NA	Vietnam
1320	V_15_1	V_18_2	NA	Vietnam
1321	V_15_2	V_18_2	NA	Vietnam
1322	V_15_3	V_18_2	NA	Vietnam
1323	V_16_1	V_18_2	NA	Vietnam
1324	V_16_2	V_18_2	NA	Vietnam

1325	V_17_1	V_18_2	NA	Vietnam
1326	V_17_2	V_18_2	NA	Vietnam
1327	V_18_1	V_18_2	NA	Vietnam
1328	V_18_2	V_18_2	NA	Vietnam
1329	V_18_4	V_18_2	3.042625	Vietnam
1330	V_19_1	V_18_2	0.474086	Vietnam
1331	V_19_3	V_18_2	0.986335	Vietnam
1332	V_20_1	V_18_2	-2.11763	Vietnam
1333	V_21_1	V_18_2	-2.02207	Vietnam
1334	V_22_1	V_18_2	4.076311	Vietnam
1335	V_22_3	V_18_2	1.788263	Vietnam
1336	V_22_4	V_18_2	3.682468	Vietnam
1337	V_1_2	V_18_4	NA	Vietnam
1338	V_2_2	V_18_4	NA	Vietnam
1339	V_3_1	V_18_4	NA	Vietnam
1340	V_3_2	V_18_4	NA	Vietnam
1341	V_5_3	V_18_4	NA	Vietnam
1342	V_6_1	V_18_4	NA	Vietnam
1343	V_6_2	V_18_4	NA	Vietnam
1344	V_6_3	V_18_4	NA	Vietnam
1345	V_7_1	V_18_4	NA	Vietnam
1346	V_7_2	V_18_4	NA	Vietnam
1347	V_7_3	V_18_4	NA	Vietnam
1348	V_8_2	V_18_4	NA	Vietnam
1349	V_9_1	V_18_4	NA	Vietnam
1350	V_9_2	V_18_4	NA	Vietnam
1351	V_9_4	V_18_4	NA	Vietnam
1352	V_10_1	V_18_4	NA	Vietnam
1353	V_11_1	V_18_4	NA	Vietnam
1354	V_11_3	V_18_4	NA	Vietnam
1355	V_12_1	V_18_4	NA	Vietnam
1356	V_13_2	V_18_4	NA	Vietnam
1357	V_14_1	V_18_4	NA	Vietnam
1358	V_15_1	V_18_4	NA	Vietnam
1359	V_15_2	V_18_4	NA	Vietnam
1360	V_15_3	V_18_4	NA	Vietnam
1361	V_16_1	V_18_4	NA	Vietnam
1362	V_16_2	V_18_4	NA	Vietnam
1363	V_17_1	V_18_4	NA	Vietnam
1364	V_17_2	V_18_4	NA	Vietnam
1365	V_18_1	V_18_4	NA	Vietnam
1366	V_18_2	V_18_4	NA	Vietnam
1367	V_18_4	V_18_4	NA	Vietnam

1368	V_19_1	V_18_4	2.945609	Vietnam
1369	V_19_3	V_18_4	-0.84718	Vietnam
1370	V_20_1	V_18_4	1.584861	Vietnam
1371	V_21_1	V_18_4	0.774931	Vietnam
1372	V_22_1	V_18_4	0.03642	Vietnam
1373	V_22_3	V_18_4	1.359947	Vietnam
1374	V_22_4	V_18_4	0.744188	Vietnam
1375	V_1_2	V_19_1	NA	Vietnam
1376	V_2_2	V_19_1	NA	Vietnam
1377	V_3_1	V_19_1	NA	Vietnam
1378	V_3_2	V_19_1	NA	Vietnam
1379	V_5_3	V_19_1	NA	Vietnam
1380	V_6_1	V_19_1	NA	Vietnam
1381	V_6_2	V_19_1	NA	Vietnam
1382	V_6_3	V_19_1	NA	Vietnam
1383	V_7_1	V_19_1	NA	Vietnam
1384	V_7_2	V_19_1	NA	Vietnam
1385	V_7_3	V_19_1	NA	Vietnam
1386	V_8_2	V_19_1	NA	Vietnam
1387	V_9_1	V_19_1	NA	Vietnam
1388	V_9_2	V_19_1	NA	Vietnam
1389	V_9_4	V_19_1	NA	Vietnam
1390	V_10_1	V_19_1	NA	Vietnam
1391	V_11_1	V_19_1	NA	Vietnam
1392	V_11_3	V_19_1	NA	Vietnam
1393	V_12_1	V_19_1	NA	Vietnam
1394	V_13_2	V_19_1	NA	Vietnam
1395	V_14_1	V_19_1	NA	Vietnam
1396	V_15_1	V_19_1	NA	Vietnam
1397	V_15_2	V_19_1	NA	Vietnam
1398	V_15_3	V_19_1	NA	Vietnam
1399	V_16_1	V_19_1	NA	Vietnam
1400	V_16_2	V_19_1	NA	Vietnam
1401	V_17_1	V_19_1	NA	Vietnam
1402	V_17_2	V_19_1	NA	Vietnam
1403	V_18_1	V_19_1	NA	Vietnam
1404	V_18_2	V_19_1	NA	Vietnam
1405	V_18_4	V_19_1	NA	Vietnam
1406	V_19_1	V_19_1	NA	Vietnam
1407	V_19_3	V_19_1	2.17686	Vietnam
1408	V_20_1	V_19_1	1.216426	Vietnam
1409	V_21_1	V_19_1	0.462206	Vietnam
1410	V_22_1	V_19_1	7.126444	Vietnam

1411	V_22_3	V_19_1	1.688695	Vietnam
1412	V_22_4	V_19_1	2.350042	Vietnam
1413	V_1_2	V_19_3	NA	Vietnam
1414	V_2_2	V_19_3	NA	Vietnam
1415	V_3_1	V_19_3	NA	Vietnam
1416	V_3_2	V_19_3	NA	Vietnam
1417	V_5_3	V_19_3	NA	Vietnam
1418	V_6_1	V_19_3	NA	Vietnam
1419	V_6_2	V_19_3	NA	Vietnam
1420	V_6_3	V_19_3	NA	Vietnam
1421	V_7_1	V_19_3	NA	Vietnam
1422	V_7_2	V_19_3	NA	Vietnam
1423	V_7_3	V_19_3	NA	Vietnam
1424	V_8_2	V_19_3	NA	Vietnam
1425	V_9_1	V_19_3	NA	Vietnam
1426	V_9_2	V_19_3	NA	Vietnam
1427	V_9_4	V_19_3	NA	Vietnam
1428	V_10_1	V_19_3	NA	Vietnam
1429	V_11_1	V_19_3	NA	Vietnam
1430	V_11_3	V_19_3	NA	Vietnam
1431	V_12_1	V_19_3	NA	Vietnam
1432	V_13_2	V_19_3	NA	Vietnam
1433	V_14_1	V_19_3	NA	Vietnam
1434	V_15_1	V_19_3	NA	Vietnam
1435	V_15_2	V_19_3	NA	Vietnam
1436	V_15_3	V_19_3	NA	Vietnam
1437	V_16_1	V_19_3	NA	Vietnam
1438	V_16_2	V_19_3	NA	Vietnam
1439	V_17_1	V_19_3	NA	Vietnam
1440	V_17_2	V_19_3	NA	Vietnam
1441	V_18_1	V_19_3	NA	Vietnam
1442	V_18_2	V_19_3	NA	Vietnam
1443	V_18_4	V_19_3	NA	Vietnam
1444	V_19_1	V_19_3	NA	Vietnam
1445	V_19_3	V_19_3	NA	Vietnam
1446	V_20_1	V_19_3	0.843879	Vietnam
1447	V_21_1	V_19_3	0.259908	Vietnam
1448	V_22_1	V_19_3	-1.6536	Vietnam
1449	V_22_3	V_19_3	-0.49562	Vietnam
1450	V_22_4	V_19_3	-0.53648	Vietnam
1451	V_1_2	V_20_1	NA	Vietnam
1452	V_2_2	V_20_1	NA	Vietnam
1453	V_3_1	V_20_1	NA	Vietnam

1454	V_3_2	V_20_1	NA	Vietnam
1455	V_5_3	V_20_1	NA	Vietnam
1456	V_6_1	V_20_1	NA	Vietnam
1457	V_6_2	V_20_1	NA	Vietnam
1458	V_6_3	V_20_1	NA	Vietnam
1459	V_7_1	V_20_1	NA	Vietnam
1460	V_7_2	V_20_1	NA	Vietnam
1461	V_7_3	V_20_1	NA	Vietnam
1462	V_8_2	V_20_1	NA	Vietnam
1463	V_9_1	V_20_1	NA	Vietnam
1464	V_9_2	V_20_1	NA	Vietnam
1465	V_9_4	V_20_1	NA	Vietnam
1466	V_10_1	V_20_1	NA	Vietnam
1467	V_11_1	V_20_1	NA	Vietnam
1468	V_11_3	V_20_1	NA	Vietnam
1469	V_12_1	V_20_1	NA	Vietnam
1470	V_13_2	V_20_1	NA	Vietnam
1471	V_14_1	V_20_1	NA	Vietnam
1472	V_15_1	V_20_1	NA	Vietnam
1473	V_15_2	V_20_1	NA	Vietnam
1474	V_15_3	V_20_1	NA	Vietnam
1475	V_16_1	V_20_1	NA	Vietnam
1476	V_16_2	V_20_1	NA	Vietnam
1477	V_17_1	V_20_1	NA	Vietnam
1478	V_17_2	V_20_1	NA	Vietnam
1479	V_18_1	V_20_1	NA	Vietnam
1480	V_18_2	V_20_1	NA	Vietnam
1481	V_18_4	V_20_1	NA	Vietnam
1482	V_19_1	V_20_1	NA	Vietnam
1483	V_19_3	V_20_1	NA	Vietnam
1484	V_20_1	V_20_1	NA	Vietnam
1485	V_21_1	V_20_1	-2.33157	Vietnam
1486	V_22_1	V_20_1	7.332752	Vietnam
1487	V_22_3	V_20_1	1.871069	Vietnam
1488	V_22_4	V_20_1	2.152567	Vietnam
1489	V_1_2	V_21_1	NA	Vietnam
1490	V_2_2	V_21_1	NA	Vietnam
1491	V_3_1	V_21_1	NA	Vietnam
1492	V_3_2	V_21_1	NA	Vietnam
1493	V_5_3	V_21_1	NA	Vietnam
1494	V_6_1	V_21_1	NA	Vietnam
1495	V_6_2	V_21_1	NA	Vietnam
1496	V_6_3	V_21_1	NA	Vietnam

1497	V_7_1	V_21_1	NA	Vietnam
1498	V_7_2	V_21_1	NA	Vietnam
1499	V_7_3	V_21_1	NA	Vietnam
1500	V_8_2	V_21_1	NA	Vietnam
1501	V_9_1	V_21_1	NA	Vietnam
1502	V_9_2	V_21_1	NA	Vietnam
1503	V_9_4	V_21_1	NA	Vietnam
1504	V_10_1	V_21_1	NA	Vietnam
1505	V_11_1	V_21_1	NA	Vietnam
1506	V_11_3	V_21_1	NA	Vietnam
1507	V_12_1	V_21_1	NA	Vietnam
1508	V_13_2	V_21_1	NA	Vietnam
1509	V_14_1	V_21_1	NA	Vietnam
1510	V_15_1	V_21_1	NA	Vietnam
1511	V_15_2	V_21_1	NA	Vietnam
1512	V_15_3	V_21_1	NA	Vietnam
1513	V_16_1	V_21_1	NA	Vietnam
1514	V_16_2	V_21_1	NA	Vietnam
1515	V_17_1	V_21_1	NA	Vietnam
1516	V_17_2	V_21_1	NA	Vietnam
1517	V_18_1	V_21_1	NA	Vietnam
1518	V_18_2	V_21_1	NA	Vietnam
1519	V_18_4	V_21_1	NA	Vietnam
1520	V_19_1	V_21_1	NA	Vietnam
1521	V_19_3	V_21_1	NA	Vietnam
1522	V_20_1	V_21_1	NA	Vietnam
1523	V_21_1	V_21_1	NA	Vietnam
1524	V_22_1	V_21_1	4.255296	Vietnam
1525	V_22_3	V_21_1	-0.08753	Vietnam
1526	V_22_4	V_21_1	-0.15268	Vietnam
1527	V_1_2	V_22_1	NA	Vietnam
1528	V_2_2	V_22_1	NA	Vietnam
1529	V_3_1	V_22_1	NA	Vietnam
1530	V_3_2	V_22_1	NA	Vietnam
1531	V_5_3	V_22_1	NA	Vietnam
1532	V_6_1	V_22_1	NA	Vietnam
1533	V_6_2	V_22_1	NA	Vietnam
1534	V_6_3	V_22_1	NA	Vietnam
1535	V_7_1	V_22_1	NA	Vietnam
1536	V_7_2	V_22_1	NA	Vietnam
1537	V_7_3	V_22_1	NA	Vietnam
1538	V_8_2	V_22_1	NA	Vietnam
1539	V_9_1	V_22_1	NA	Vietnam

1540	V_9_2	V_22_1	NA	Vietnam
1541	V_9_4	V_22_1	NA	Vietnam
1542	V_10_1	V_22_1	NA	Vietnam
1543	V_11_1	V_22_1	NA	Vietnam
1544	V_11_3	V_22_1	NA	Vietnam
1545	V_12_1	V_22_1	NA	Vietnam
1546	V_13_2	V_22_1	NA	Vietnam
1547	V_14_1	V_22_1	NA	Vietnam
1548	V_15_1	V_22_1	NA	Vietnam
1549	V_15_2	V_22_1	NA	Vietnam
1550	V_15_3	V_22_1	NA	Vietnam
1551	V_16_1	V_22_1	NA	Vietnam
1552	V_16_2	V_22_1	NA	Vietnam
1553	V_17_1	V_22_1	NA	Vietnam
1554	V_17_2	V_22_1	NA	Vietnam
1555	V_18_1	V_22_1	NA	Vietnam
1556	V_18_2	V_22_1	NA	Vietnam
1557	V_18_4	V_22_1	NA	Vietnam
1558	V_19_1	V_22_1	NA	Vietnam
1559	V_19_3	V_22_1	NA	Vietnam
1560	V_20_1	V_22_1	NA	Vietnam
1561	V_21_1	V_22_1	NA	Vietnam
1562	V_22_1	V_22_1	NA	Vietnam
1563	V_22_3	V_22_1	-0.49613	Vietnam
1564	V_22_4	V_22_1	0.418977	Vietnam
1565	V_1_2	V_22_3	NA	Vietnam
1566	V_2_2	V_22_3	NA	Vietnam
1567	V_3_1	V_22_3	NA	Vietnam
1568	V_3_2	V_22_3	NA	Vietnam
1569	V_5_3	V_22_3	NA	Vietnam
1570	V_6_1	V_22_3	NA	Vietnam
1571	V_6_2	V_22_3	NA	Vietnam
1572	V_6_3	V_22_3	NA	Vietnam
1573	V_7_1	V_22_3	NA	Vietnam
1574	V_7_2	V_22_3	NA	Vietnam
1575	V_7_3	V_22_3	NA	Vietnam
1576	V_8_2	V_22_3	NA	Vietnam
1577	V_9_1	V_22_3	NA	Vietnam
1578	V_9_2	V_22_3	NA	Vietnam
1579	V_9_4	V_22_3	NA	Vietnam
1580	V_10_1	V_22_3	NA	Vietnam
1581	V_11_1	V_22_3	NA	Vietnam
1582	V_11_3	V_22_3	NA	Vietnam

1583	V_12_1	V_22_3	NA	Vietnam
1584	V_13_2	V_22_3	NA	Vietnam
1585	V_14_1	V_22_3	NA	Vietnam
1586	V_15_1	V_22_3	NA	Vietnam
1587	V_15_2	V_22_3	NA	Vietnam
1588	V_15_3	V_22_3	NA	Vietnam
1589	V_16_1	V_22_3	NA	Vietnam
1590	V_16_2	V_22_3	NA	Vietnam
1591	V_17_1	V_22_3	NA	Vietnam
1592	V_17_2	V_22_3	NA	Vietnam
1593	V_18_1	V_22_3	NA	Vietnam
1594	V_18_2	V_22_3	NA	Vietnam
1595	V_18_4	V_22_3	NA	Vietnam
1596	V_19_1	V_22_3	NA	Vietnam
1597	V_19_3	V_22_3	NA	Vietnam
1598	V_20_1	V_22_3	NA	Vietnam
1599	V_21_1	V_22_3	NA	Vietnam
1600	V_22_1	V_22_3	NA	Vietnam
1601	V_22_3	V_22_3	NA	Vietnam
1602	V_22_4	V_22_3	-1.06849	Vietnam
1603	V_1_2	V_22_4	NA	Vietnam
1604	V_2_2	V_22_4	NA	Vietnam
1605	V_3_1	V_22_4	NA	Vietnam
1606	V_3_2	V_22_4	NA	Vietnam
1607	V_5_3	V_22_4	NA	Vietnam
1608	V_6_1	V_22_4	NA	Vietnam
1609	V_6_2	V_22_4	NA	Vietnam
1610	V_6_3	V_22_4	NA	Vietnam
1611	V_7_1	V_22_4	NA	Vietnam
1612	V_7_2	V_22_4	NA	Vietnam
1613	V_7_3	V_22_4	NA	Vietnam
1614	V_8_2	V_22_4	NA	Vietnam
1615	V_9_1	V_22_4	NA	Vietnam
1616	V_9_2	V_22_4	NA	Vietnam
1617	V_9_4	V_22_4	NA	Vietnam
1618	V_10_1	V_22_4	NA	Vietnam
1619	V_11_1	V_22_4	NA	Vietnam
1620	V_11_3	V_22_4	NA	Vietnam
1621	V_12_1	V_22_4	NA	Vietnam
1622	V_13_2	V_22_4	NA	Vietnam
1623	V_14_1	V_22_4	NA	Vietnam
1624	V_15_1	V_22_4	NA	Vietnam
1625	V_15_2	V_22_4	NA	Vietnam

1626	V_15_3	V_22_4	NA	Vietnam
1627	V_16_1	V_22_4	NA	Vietnam
1628	V_16_2	V_22_4	NA	Vietnam
1629	V_17_1	V_22_4	NA	Vietnam
1630	V_17_2	V_22_4	NA	Vietnam
1631	V_18_1	V_22_4	NA	Vietnam
1632	V_18_2	V_22_4	NA	Vietnam
1633	V_18_4	V_22_4	NA	Vietnam
1634	V_19_1	V_22_4	NA	Vietnam
1635	V_19_3	V_22_4	NA	Vietnam
1636	V_20_1	V_22_4	NA	Vietnam
1637	V_21_1	V_22_4	NA	Vietnam
1638	V_22_1	V_22_4	NA	Vietnam
1639	V_22_3	V_22_4	NA	Vietnam
1640	V_22_4	V_22_4	NA	Vietnam

Table 7： pairwise βNTI value of hypothesis 1.

	Var1	Var2	value	Groups
1	T_4_4	T_4_4	NA	4
2	T_9_4	T_4_4	0.729492	4
3	V_9_4	T_4_4	1.054236	4
4	V_18_4	T_4_4	2.494619	4
5	V_22_4	T_4_4	1.396131	4
6	T_4_4	T_9_4	NA	4
7	T_9_4	T_9_4	NA	4
8	V_9_4	T_9_4	7.2162	4
9	V_18_4	T_9_4	8.035921	4
10	V_22_4	T_9_4	9.094179	4
11	T_4_4	V_9_4	NA	4
12	T_9_4	V_9_4	NA	4
13	V_9_4	V_9_4	NA	4
14	V_18_4	V_9_4	1.988388	4
15	V_22_4	V_9_4	-1.33989	4
16	T_4_4	V_18_4	NA	4
17	T_9_4	V_18_4	NA	4
18	V_9_4	V_18_4	NA	4
19	V_18_4	V_18_4	NA	4
20	V_22_4	V_18_4	0.671733	4
21	T_4_4	V_22_4	NA	4
22	T_9_4	V_22_4	NA	4
23	V_9_4	V_22_4	NA	4
24	V_18_4	V_22_4	NA	4
25	V_22_4	V_22_4	NA	4

26	T_2_3	T_2_3	NA	3
27	T_4_3	T_2_3	-0.44566	3
28	T_5_3	T_2_3	0.367692	3
29	V_5_3	T_2_3	10.41882	3
30	V_6_3	T_2_3	6.463338	3
31	V_7_3	T_2_3	9.964291	3
32	V_11_3	T_2_3	11.1648	3
33	V_15_3	T_2_3	7.850084	3
34	V_19_3	T_2_3	6.879101	3
35	V_22_3	T_2_3	6.459021	3
36	T_2_3	T_4_3	NA	3
37	T_4_3	T_4_3	NA	3
38	T_5_3	T_4_3	2.49348	3
39	V_5_3	T_4_3	0.039155	3
40	V_6_3	T_4_3	-0.31823	3
41	V_7_3	T_4_3	-0.89168	3
42	V_11_3	T_4_3	1.174402	3
43	V_15_3	T_4_3	0.552414	3
44	V_19_3	T_4_3	-0.52681	3
45	V_22_3	T_4_3	0.277188	3
46	T_2_3	T_5_3	NA	3
47	T_4_3	T_5_3	NA	3
48	T_5_3	T_5_3	NA	3
49	V_5_3	T_5_3	11.44121	3
50	V_6_3	T_5_3	8.66145	3
51	V_7_3	T_5_3	10.83759	3
52	V_11_3	T_5_3	12.20188	3
53	V_15_3	T_5_3	8.021167	3
54	V_19_3	T_5_3	8.068306	3
55	V_22_3	T_5_3	9.250543	3
56	T_2_3	V_5_3	NA	3
57	T_4_3	V_5_3	NA	3
58	T_5_3	V_5_3	NA	3
59	V_5_3	V_5_3	NA	3
60	V_6_3	V_5_3	-0.51776	3
61	V_7_3	V_5_3	4.587258	3
62	V_11_3	V_5_3	-1.59131	3
63	V_15_3	V_5_3	-0.53526	3
64	V_19_3	V_5_3	-1.08866	3
65	V_22_3	V_5_3	-0.93829	3
66	T_2_3	V_6_3	NA	3
67	T_4_3	V_6_3	NA	3
68	T_5_3	V_6_3	NA	3

69	V_5_3	V_6_3	NA	3
70	V_6_3	V_6_3	NA	3
71	V_7_3	V_6_3	0.93361	3
72	V_11_3	V_6_3	-1.43315	3
73	V_15_3	V_6_3	1.567625	3
74	V_19_3	V_6_3	-1.14945	3
75	V_22_3	V_6_3	0.168412	3
76	T_2_3	V_7_3	NA	3
77	T_4_3	V_7_3	NA	3
78	T_5_3	V_7_3	NA	3
79	V_5_3	V_7_3	NA	3
80	V_6_3	V_7_3	NA	3
81	V_7_3	V_7_3	NA	3
82	V_11_3	V_7_3	0.778224	3
83	V_15_3	V_7_3	4.505787	3
84	V_19_3	V_7_3	1.331054	3
85	V_22_3	V_7_3	1.523021	3
86	T_2_3	V_11_3	NA	3
87	T_4_3	V_11_3	NA	3
88	T_5_3	V_11_3	NA	3
89	V_5_3	V_11_3	NA	3
90	V_6_3	V_11_3	NA	3
91	V_7_3	V_11_3	NA	3
92	V_11_3	V_11_3	NA	3
93	V_15_3	V_11_3	2.504709	3
94	V_19_3	V_11_3	-2.01685	3
95	V_22_3	V_11_3	-1.67393	3
96	T_2_3	V_15_3	NA	3
97	T_4_3	V_15_3	NA	3
98	T_5_3	V_15_3	NA	3
99	V_5_3	V_15_3	NA	3
100	V_6_3	V_15_3	NA	3
101	V_7_3	V_15_3	NA	3
102	V_11_3	V_15_3	NA	3
103	V_15_3	V_15_3	NA	3
104	V_19_3	V_15_3	0.518435	3
105	V_22_3	V_15_3	1.020047	3
106	T_2_3	V_19_3	NA	3
107	T_4_3	V_19_3	NA	3
108	T_5_3	V_19_3	NA	3
109	V_5_3	V_19_3	NA	3
110	V_6_3	V_19_3	NA	3
111	V_7_3	V_19_3	NA	3

112	V_11_3	V_19_3	NA	3
113	V_15_3	V_19_3	NA	3
114	V_19_3	V_19_3	NA	3
115	V_22_3	V_19_3	-0.71172	3
116	T_2_3	V_22_3	NA	3
117	T_4_3	V_22_3	NA	3
118	T_5_3	V_22_3	NA	3
119	V_5_3	V_22_3	NA	3
120	V_6_3	V_22_3	NA	3
121	V_7_3	V_22_3	NA	3
122	V_11_3	V_22_3	NA	3
123	V_15_3	V_22_3	NA	3
124	V_19_3	V_22_3	NA	3
125	V_22_3	V_22_3	NA	3
126	T_2_2	T_2_2	NA	2
127	T_5_2	T_2_2	0.289126	2
128	T_9_2	T_2_2	-1.85939	2
129	V_1_2	T_2_2	4.103924	2
130	V_2_2	T_2_2	5.114672	2
131	V_3_2	T_2_2	4.659967	2
132	V_6_2	T_2_2	3.507924	2
133	V_7_2	T_2_2	18.62847	2
134	V_8_2	T_2_2	8.267888	2
135	V_9_2	T_2_2	9.601187	2
136	V_13_2	T_2_2	5.012573	2
137	V_15_2	T_2_2	7.366052	2
138	V_16_2	T_2_2	1.161644	2
139	V_17_2	T_2_2	2.402495	2
140	V_18_2	T_2_2	2.974855	2
141	T_2_2	T_5_2	NA	2
142	T_5_2	T_5_2	NA	2
143	T_9_2	T_5_2	-2.51675	2
144	V_1_2	T_5_2	5.834718	2
145	V_2_2	T_5_2	12.09088	2
146	V_3_2	T_5_2	8.46487	2
147	V_6_2	T_5_2	5.168693	2
148	V_7_2	T_5_2	17.59136	2
149	V_8_2	T_5_2	12.17392	2
150	V_9_2	T_5_2	11.02514	2
151	V_13_2	T_5_2	6.215141	2
152	V_15_2	T_5_2	8.071044	2
153	V_16_2	T_5_2	3.643617	2
154	V_17_2	T_5_2	5.03285	2

155	V_18_2	T_5_2	5.241882	2
156	T_2_2	T_9_2	NA	2
157	T_5_2	T_9_2	NA	2
158	T_9_2	T_9_2	NA	2
159	V_1_2	T_9_2	4.684326	2
160	V_2_2	T_9_2	6.327813	2
161	V_3_2	T_9_2	7.504806	2
162	V_6_2	T_9_2	5.653916	2
163	V_7_2	T_9_2	8.391031	2
164	V_8_2	T_9_2	6.439403	2
165	V_9_2	T_9_2	5.966096	2
166	V_13_2	T_9_2	3.993682	2
167	V_15_2	T_9_2	5.420296	2
168	V_16_2	T_9_2	3.128465	2
169	V_17_2	T_9_2	4.266854	2
170	V_18_2	T_9_2	4.368272	2
171	T_2_2	V_1_2	NA	2
172	T_5_2	V_1_2	NA	2
173	T_9_2	V_1_2	NA	2
174	V_1_2	V_1_2	NA	2
175	V_2_2	V_1_2	-0.34311	2
176	V_3_2	V_1_2	0.174012	2
177	V_6_2	V_1_2	-1.10415	2
178	V_7_2	V_1_2	4.556272	2
179	V_8_2	V_1_2	1.908432	2
180	V_9_2	V_1_2	-0.15656	2
181	V_13_2	V_1_2	-0.47494	2
182	V_15_2	V_1_2	1.837934	2
183	V_16_2	V_1_2	3.267847	2
184	V_17_2	V_1_2	-0.19975	2
185	V_18_2	V_1_2	-2.73551	2
186	T_2_2	V_2_2	NA	2
187	T_5_2	V_2_2	NA	2
188	T_9_2	V_2_2	NA	2
189	V_1_2	V_2_2	NA	2
190	V_2_2	V_2_2	NA	2
191	V_3_2	V_2_2	-0.28817	2
192	V_6_2	V_2_2	-1.25809	2
193	V_7_2	V_2_2	-1.07119	2
194	V_8_2	V_2_2	-0.15784	2
195	V_9_2	V_2_2	-1.73859	2
196	V_13_2	V_2_2	-1.02251	2
197	V_15_2	V_2_2	0.307183	2

198	V_16_2	V_2_2	2.177121	2
199	V_17_2	V_2_2	4.654748	2
200	V_18_2	V_2_2	-0.87587	2
201	T_2_2	V_3_2	NA	2
202	T_5_2	V_3_2	NA	2
203	T_9_2	V_3_2	NA	2
204	V_1_2	V_3_2	NA	2
205	V_2_2	V_3_2	NA	2
206	V_3_2	V_3_2	NA	2
207	V_6_2	V_3_2	1.191736	2
208	V_7_2	V_3_2	1.009155	2
209	V_8_2	V_3_2	1.386218	2
210	V_9_2	V_3_2	-0.68699	2
211	V_13_2	V_3_2	0.969557	2
212	V_15_2	V_3_2	-0.81868	2
213	V_16_2	V_3_2	4.695665	2
214	V_17_2	V_3_2	2.391148	2
215	V_18_2	V_3_2	0.406394	2
216	T_2_2	V_6_2	NA	2
217	T_5_2	V_6_2	NA	2
218	T_9_2	V_6_2	NA	2
219	V_1_2	V_6_2	NA	2
220	V_2_2	V_6_2	NA	2
221	V_3_2	V_6_2	NA	2
222	V_6_2	V_6_2	NA	2
223	V_7_2	V_6_2	0.864567	2
224	V_8_2	V_6_2	1.859401	2
225	V_9_2	V_6_2	0.974473	2
226	V_13_2	V_6_2	0.574259	2
227	V_15_2	V_6_2	1.513088	2
228	V_16_2	V_6_2	1.203232	2
229	V_17_2	V_6_2	-1.60343	2
230	V_18_2	V_6_2	-1.15549	2
231	T_2_2	V_7_2	NA	2
232	T_5_2	V_7_2	NA	2
233	T_9_2	V_7_2	NA	2
234	V_1_2	V_7_2	NA	2
235	V_2_2	V_7_2	NA	2
236	V_3_2	V_7_2	NA	2
237	V_6_2	V_7_2	NA	2
238	V_7_2	V_7_2	NA	2
239	V_8_2	V_7_2	-2.18686	2
240	V_9_2	V_7_2	0.478111	2

241	V_13_2	V_7_2	4.557468	2
242	V_15_2	V_7_2	-0.54509	2
243	V_16_2	V_7_2	12.23582	2
244	V_17_2	V_7_2	7.077851	2
245	V_18_2	V_7_2	0.335535	2
246	T_2_2	V_8_2	NA	2
247	T_5_2	V_8_2	NA	2
248	T_9_2	V_8_2	NA	2
249	V_1_2	V_8_2	NA	2
250	V_2_2	V_8_2	NA	2
251	V_3_2	V_8_2	NA	2
252	V_6_2	V_8_2	NA	2
253	V_7_2	V_8_2	NA	2
254	V_8_2	V_8_2	NA	2
255	V_9_2	V_8_2	0.905829	2
256	V_13_2	V_8_2	2.910803	2
257	V_15_2	V_8_2	-0.75553	2
258	V_16_2	V_8_2	5.889113	2
259	V_17_2	V_8_2	2.554934	2
260	V_18_2	V_8_2	1.670815	2
261	T_2_2	V_9_2	NA	2
262	T_5_2	V_9_2	NA	2
263	T_9_2	V_9_2	NA	2
264	V_1_2	V_9_2	NA	2
265	V_2_2	V_9_2	NA	2
266	V_3_2	V_9_2	NA	2
267	V_6_2	V_9_2	NA	2
268	V_7_2	V_9_2	NA	2
269	V_8_2	V_9_2	NA	2
270	V_9_2	V_9_2	NA	2
271	V_13_2	V_9_2	2.860682	2
272	V_15_2	V_9_2	0.38116	2
273	V_16_2	V_9_2	6.018309	2
274	V_17_2	V_9_2	2.781798	2
275	V_18_2	V_9_2	1.156282	2
276	T_2_2	V_13_2	NA	2
277	T_5_2	V_13_2	NA	2
278	T_9_2	V_13_2	NA	2
279	V_1_2	V_13_2	NA	2
280	V_2_2	V_13_2	NA	2
281	V_3_2	V_13_2	NA	2
282	V_6_2	V_13_2	NA	2
283	V_7_2	V_13_2	NA	2

284	V_8_2	V_13_2	NA	2
285	V_9_2	V_13_2	NA	2
286	V_13_2	V_13_2	NA	2
287	V_15_2	V_13_2	0.411506	2
288	V_16_2	V_13_2	0.012896	2
289	V_17_2	V_13_2	-1.84005	2
290	V_18_2	V_13_2	-1.10401	2
291	T_2_2	V_15_2	NA	2
292	T_5_2	V_15_2	NA	2
293	T_9_2	V_15_2	NA	2
294	V_1_2	V_15_2	NA	2
295	V_2_2	V_15_2	NA	2
296	V_3_2	V_15_2	NA	2
297	V_6_2	V_15_2	NA	2
298	V_7_2	V_15_2	NA	2
299	V_8_2	V_15_2	NA	2
300	V_9_2	V_15_2	NA	2
301	V_13_2	V_15_2	NA	2
302	V_15_2	V_15_2	NA	2
303	V_16_2	V_15_2	3.828501	2
304	V_17_2	V_15_2	2.455398	2
305	V_18_2	V_15_2	-0.14369	2
306	T_2_2	V_16_2	NA	2
307	T_5_2	V_16_2	NA	2
308	T_9_2	V_16_2	NA	2
309	V_1_2	V_16_2	NA	2
310	V_2_2	V_16_2	NA	2
311	V_3_2	V_16_2	NA	2
312	V_6_2	V_16_2	NA	2
313	V_7_2	V_16_2	NA	2
314	V_8_2	V_16_2	NA	2
315	V_9_2	V_16_2	NA	2
316	V_13_2	V_16_2	NA	2
317	V_15_2	V_16_2	NA	2
318	V_16_2	V_16_2	NA	2
319	V_17_2	V_16_2	-2.5636	2
320	V_18_2	V_16_2	-0.14421	2
321	T_2_2	V_17_2	NA	2
322	T_5_2	V_17_2	NA	2
323	T_9_2	V_17_2	NA	2
324	V_1_2	V_17_2	NA	2
325	V_2_2	V_17_2	NA	2
326	V_3_2	V_17_2	NA	2

327	V_6_2	V_17_2	NA	2
328	V_7_2	V_17_2	NA	2
329	V_8_2	V_17_2	NA	2
330	V_9_2	V_17_2	NA	2
331	V_13_2	V_17_2	NA	2
332	V_15_2	V_17_2	NA	2
333	V_16_2	V_17_2	NA	2
334	V_17_2	V_17_2	NA	2
335	V_18_2	V_17_2	-1.9052	2
336	T_2_2	V_18_2	NA	2
337	T_5_2	V_18_2	NA	2
338	T_9_2	V_18_2	NA	2
339	V_1_2	V_18_2	NA	2
340	V_2_2	V_18_2	NA	2
341	V_3_2	V_18_2	NA	2
342	V_6_2	V_18_2	NA	2
343	V_7_2	V_18_2	NA	2
344	V_8_2	V_18_2	NA	2
345	V_9_2	V_18_2	NA	2
346	V_13_2	V_18_2	NA	2
347	V_15_2	V_18_2	NA	2
348	V_16_2	V_18_2	NA	2
349	V_17_2	V_18_2	NA	2
350	V_18_2	V_18_2	NA	2
351	T_2_1	T_2_1	NA	1
352	V_3_1	T_2_1	13.36708	1
353	V_6_1	T_2_1	9.248943	1
354	V_7_1	T_2_1	4.520806	1
355	V_9_1	T_2_1	4.254834	1
356	V_10_1	T_2_1	2.82096	1
357	V_11_1	T_2_1	9.16093	1
358	V_12_1	T_2_1	5.950075	1
359	V_14_1	T_2_1	2.048554	1
360	V_15_1	T_2_1	3.963853	1
361	V_16_1	T_2_1	2.695156	1
362	V_17_1	T_2_1	2.979218	1
363	V_18_1	T_2_1	1.662996	1
364	V_19_1	T_2_1	5.178533	1
365	V_20_1	T_2_1	4.971385	1
366	V_21_1	T_2_1	6.867535	1
367	V_22_1	T_2_1	21.18904	1
368	T_2_1	V_3_1	NA	1
369	V_3_1	V_3_1	NA	1

370	V_6_1	V_3_1	0.02574	1
371	V_7_1	V_3_1	2.114234	1
372	V_9_1	V_3_1	3.121164	1
373	V_10_1	V_3_1	5.341756	1
374	V_11_1	V_3_1	-0.38567	1
375	V_12_1	V_3_1	1.635935	1
376	V_14_1	V_3_1	6.283749	1
377	V_15_1	V_3_1	3.926545	1
378	V_16_1	V_3_1	4.351862	1
379	V_17_1	V_3_1	2.370215	1
380	V_18_1	V_3_1	2.915112	1
381	V_19_1	V_3_1	5.911511	1
382	V_20_1	V_3_1	3.155928	1
383	V_21_1	V_3_1	-0.06746	1
384	V_22_1	V_3_1	-0.95818	1
385	T_2_1	V_6_1	NA	1
386	V_3_1	V_6_1	NA	1
387	V_6_1	V_6_1	NA	1
388	V_7_1	V_6_1	-0.5881	1
389	V_9_1	V_6_1	-0.80205	1
390	V_10_1	V_6_1	0.702991	1
391	V_11_1	V_6_1	-0.97149	1
392	V_12_1	V_6_1	0.069236	1
393	V_14_1	V_6_1	2.18293	1
394	V_15_1	V_6_1	1.773459	1
395	V_16_1	V_6_1	2.216175	1
396	V_17_1	V_6_1	-0.83956	1
397	V_18_1	V_6_1	1.348266	1
398	V_19_1	V_6_1	1.145456	1
399	V_20_1	V_6_1	-1.08076	1
400	V_21_1	V_6_1	-1.9505	1
401	V_22_1	V_6_1	-0.68338	1
402	T_2_1	V_7_1	NA	1
403	V_3_1	V_7_1	NA	1
404	V_6_1	V_7_1	NA	1
405	V_7_1	V_7_1	NA	1
406	V_9_1	V_7_1	-0.82978	1
407	V_10_1	V_7_1	-0.44294	1
408	V_11_1	V_7_1	-0.41102	1
409	V_12_1	V_7_1	-0.98838	1
410	V_14_1	V_7_1	0.300087	1
411	V_15_1	V_7_1	0.38624	1
412	V_16_1	V_7_1	-0.46323	1

413	V_17_1	V_7_1	-2.22424	1
414	V_18_1	V_7_1	-1.31238	1
415	V_19_1	V_7_1	2.260601	1
416	V_20_1	V_7_1	-0.7481	1
417	V_21_1	V_7_1	-1.63955	1
418	V_22_1	V_7_1	10.48183	1
419	T_2_1	V_9_1	NA	1
420	V_3_1	V_9_1	NA	1
421	V_6_1	V_9_1	NA	1
422	V_7_1	V_9_1	NA	1
423	V_9_1	V_9_1	NA	1
424	V_10_1	V_9_1	-1.6573	1
425	V_11_1	V_9_1	0.731237	1
426	V_12_1	V_9_1	-1.34748	1
427	V_14_1	V_9_1	-2.66774	1
428	V_15_1	V_9_1	-0.96101	1
429	V_16_1	V_9_1	-1.24537	1
430	V_17_1	V_9_1	-2.08323	1
431	V_18_1	V_9_1	-2.15435	1
432	V_19_1	V_9_1	-1.19224	1
433	V_20_1	V_9_1	-2.53531	1
434	V_21_1	V_9_1	-0.91158	1
435	V_22_1	V_9_1	7.381878	1
436	T_2_1	V_10_1	NA	1
437	V_3_1	V_10_1	NA	1
438	V_6_1	V_10_1	NA	1
439	V_7_1	V_10_1	NA	1
440	V_9_1	V_10_1	NA	1
441	V_10_1	V_10_1	NA	1
442	V_11_1	V_10_1	0.964979	1
443	V_12_1	V_10_1	0.157352	1
444	V_14_1	V_10_1	-1.61249	1
445	V_15_1	V_10_1	-1.36189	1
446	V_16_1	V_10_1	-1.87271	1
447	V_17_1	V_10_1	-1.79054	1
448	V_18_1	V_10_1	-1.30131	1
449	V_19_1	V_10_1	1.85775	1
450	V_20_1	V_10_1	-1.08081	1
451	V_21_1	V_10_1	-1.08846	1
452	V_22_1	V_10_1	11.14892	1
453	T_2_1	V_11_1	NA	1
454	V_3_1	V_11_1	NA	1
455	V_6_1	V_11_1	NA	1

456	V_7_1	V_11_1	NA	1
457	V_9_1	V_11_1	NA	1
458	V_10_1	V_11_1	NA	1
459	V_11_1	V_11_1	NA	1
460	V_12_1	V_11_1	-1.39283	1
461	V_14_1	V_11_1	3.966998	1
462	V_15_1	V_11_1	0.816873	1
463	V_16_1	V_11_1	0.716058	1
464	V_17_1	V_11_1	-0.41747	1
465	V_18_1	V_11_1	-1.03839	1
466	V_19_1	V_11_1	3.987674	1
467	V_20_1	V_11_1	0.524793	1
468	V_21_1	V_11_1	-2.23862	1
469	V_22_1	V_11_1	3.158109	1
470	T_2_1	V_12_1	NA	1
471	V_3_1	V_12_1	NA	1
472	V_6_1	V_12_1	NA	1
473	V_7_1	V_12_1	NA	1
474	V_9_1	V_12_1	NA	1
475	V_10_1	V_12_1	NA	1
476	V_11_1	V_12_1	NA	1
477	V_12_1	V_12_1	NA	1
478	V_14_1	V_12_1	-0.64394	1
479	V_15_1	V_12_1	-0.51734	1
480	V_16_1	V_12_1	-0.76824	1
481	V_17_1	V_12_1	-0.30253	1
482	V_18_1	V_12_1	-0.43746	1
483	V_19_1	V_12_1	0.15674	1
484	V_20_1	V_12_1	-1.66727	1
485	V_21_1	V_12_1	-1.42529	1
486	V_22_1	V_12_1	6.392616	1
487	T_2_1	V_14_1	NA	1
488	V_3_1	V_14_1	NA	1
489	V_6_1	V_14_1	NA	1
490	V_7_1	V_14_1	NA	1
491	V_9_1	V_14_1	NA	1
492	V_10_1	V_14_1	NA	1
493	V_11_1	V_14_1	NA	1
494	V_12_1	V_14_1	NA	1
495	V_14_1	V_14_1	NA	1
496	V_15_1	V_14_1	-0.82347	1
497	V_16_1	V_14_1	-1.58269	1
498	V_17_1	V_14_1	-2.21329	1

499	V_18_1	V_14_1	-1.1595	1
500	V_19_1	V_14_1	-2.0422	1
501	V_20_1	V_14_1	-1.42569	1
502	V_21_1	V_14_1	-0.84637	1
503	V_22_1	V_14_1	11.14098	1
504	T_2_1	V_15_1	NA	1
505	V_3_1	V_15_1	NA	1
506	V_6_1	V_15_1	NA	1
507	V_7_1	V_15_1	NA	1
508	V_9_1	V_15_1	NA	1
509	V_10_1	V_15_1	NA	1
510	V_11_1	V_15_1	NA	1
511	V_12_1	V_15_1	NA	1
512	V_14_1	V_15_1	NA	1
513	V_15_1	V_15_1	NA	1
514	V_16_1	V_15_1	-1.86595	1
515	V_17_1	V_15_1	-0.89816	1
516	V_18_1	V_15_1	-1.61821	1
517	V_19_1	V_15_1	3.830378	1
518	V_20_1	V_15_1	-1.55665	1
519	V_21_1	V_15_1	-1.34616	1
520	V_22_1	V_15_1	10.03104	1
521	T_2_1	V_16_1	NA	1
522	V_3_1	V_16_1	NA	1
523	V_6_1	V_16_1	NA	1
524	V_7_1	V_16_1	NA	1
525	V_9_1	V_16_1	NA	1
526	V_10_1	V_16_1	NA	1
527	V_11_1	V_16_1	NA	1
528	V_12_1	V_16_1	NA	1
529	V_14_1	V_16_1	NA	1
530	V_15_1	V_16_1	NA	1
531	V_16_1	V_16_1	NA	1
532	V_17_1	V_16_1	-0.42569	1
533	V_18_1	V_16_1	-1.22869	1
534	V_19_1	V_16_1	0.128184	1
535	V_20_1	V_16_1	0.167753	1
536	V_21_1	V_16_1	-0.28109	1
537	V_22_1	V_16_1	11.00437	1
538	T_2_1	V_17_1	NA	1
539	V_3_1	V_17_1	NA	1
540	V_6_1	V_17_1	NA	1
541	V_7_1	V_17_1	NA	1

542	V_9_1	V_17_1	NA	1
543	V_10_1	V_17_1	NA	1
544	V_11_1	V_17_1	NA	1
545	V_12_1	V_17_1	NA	1
546	V_14_1	V_17_1	NA	1
547	V_15_1	V_17_1	NA	1
548	V_16_1	V_17_1	NA	1
549	V_17_1	V_17_1	NA	1
550	V_18_1	V_17_1	-1.74571	1
551	V_19_1	V_17_1	0.888688	1
552	V_20_1	V_17_1	-1.89257	1
553	V_21_1	V_17_1	-0.17905	1
554	V_22_1	V_17_1	7.090893	1
555	T_2_1	V_18_1	NA	1
556	V_3_1	V_18_1	NA	1
557	V_6_1	V_18_1	NA	1
558	V_7_1	V_18_1	NA	1
559	V_9_1	V_18_1	NA	1
560	V_10_1	V_18_1	NA	1
561	V_11_1	V_18_1	NA	1
562	V_12_1	V_18_1	NA	1
563	V_14_1	V_18_1	NA	1
564	V_15_1	V_18_1	NA	1
565	V_16_1	V_18_1	NA	1
566	V_17_1	V_18_1	NA	1
567	V_18_1	V_18_1	NA	1
568	V_19_1	V_18_1	1.094735	1
569	V_20_1	V_18_1	-0.35785	1
570	V_21_1	V_18_1	0.043329	1
571	V_22_1	V_18_1	6.354008	1
572	T_2_1	V_19_1	NA	1
573	V_3_1	V_19_1	NA	1
574	V_6_1	V_19_1	NA	1
575	V_7_1	V_19_1	NA	1
576	V_9_1	V_19_1	NA	1
577	V_10_1	V_19_1	NA	1
578	V_11_1	V_19_1	NA	1
579	V_12_1	V_19_1	NA	1
580	V_14_1	V_19_1	NA	1
581	V_15_1	V_19_1	NA	1
582	V_16_1	V_19_1	NA	1
583	V_17_1	V_19_1	NA	1
584	V_18_1	V_19_1	NA	1

585	V_19_1	V_19_1	NA	1
586	V_20_1	V_19_1	1.195949	1
587	V_21_1	V_19_1	0.172083	1
588	V_22_1	V_19_1	8.462687	1
589	T_2_1	V_20_1	NA	1
590	V_3_1	V_20_1	NA	1
591	V_6_1	V_20_1	NA	1
592	V_7_1	V_20_1	NA	1
593	V_9_1	V_20_1	NA	1
594	V_10_1	V_20_1	NA	1
595	V_11_1	V_20_1	NA	1
596	V_12_1	V_20_1	NA	1
597	V_14_1	V_20_1	NA	1
598	V_15_1	V_20_1	NA	1
599	V_16_1	V_20_1	NA	1
600	V_17_1	V_20_1	NA	1
601	V_18_1	V_20_1	NA	1
602	V_19_1	V_20_1	NA	1
603	V_20_1	V_20_1	NA	1
604	V_21_1	V_20_1	-2.66014	1
605	V_22_1	V_20_1	8.917409	1
606	T_2_1	V_21_1	NA	1
607	V_3_1	V_21_1	NA	1
608	V_6_1	V_21_1	NA	1
609	V_7_1	V_21_1	NA	1
610	V_9_1	V_21_1	NA	1
611	V_10_1	V_21_1	NA	1
612	V_11_1	V_21_1	NA	1
613	V_12_1	V_21_1	NA	1
614	V_14_1	V_21_1	NA	1
615	V_15_1	V_21_1	NA	1
616	V_16_1	V_21_1	NA	1
617	V_17_1	V_21_1	NA	1
618	V_18_1	V_21_1	NA	1
619	V_19_1	V_21_1	NA	1
620	V_20_1	V_21_1	NA	1
621	V_21_1	V_21_1	NA	1
622	V_22_1	V_21_1	4.828924	1
623	T_2_1	V_22_1	NA	1
624	V_3_1	V_22_1	NA	1
625	V_6_1	V_22_1	NA	1
626	V_7_1	V_22_1	NA	1
627	V_9_1	V_22_1	NA	1

628	V_10_1	V_22_1	NA	1
629	V_11_1	V_22_1	NA	1
630	V_12_1	V_22_1	NA	1
631	V_14_1	V_22_1	NA	1
632	V_15_1	V_22_1	NA	1
633	V_16_1	V_22_1	NA	1
634	V_17_1	V_22_1	NA	1
635	V_18_1	V_22_1	NA	1
636	V_19_1	V_22_1	NA	1
637	V_20_1	V_22_1	NA	1
638	V_21_1	V_22_1	NA	1
639	V_22_1	V_22_1	NA	1

Table 7： pairwise βNTI value of hypothesis 2.

	Var1	Var2	value	Groups
1	T_2_1	T_2_1	0	Tanzania
2	T_2_2	T_2_1	-0.32	Tanzania
3	T_2_3	T_2_1	0.46	Tanzania
4	T_2_6	T_2_1	0.99	Tanzania
5	T_2_9	T_2_1	1	Tanzania
6	T_4_3	T_2_1	1	Tanzania
7	T_4_4	T_2_1	1	Tanzania
8	T_4_5	T_2_1	1	Tanzania
9	T_5_2	T_2_1	0.97	Tanzania
10	T_5_3	T_2_1	0.98	Tanzania
11	T_6_7	T_2_1	1	Tanzania
12	T_6_8	T_2_1	1	Tanzania
13	T_9_2	T_2_1	1	Tanzania
14	T_9_4	T_2_1	1	Tanzania
15	T_2_1	T_2_2	-0.32	Tanzania
16	T_2_2	T_2_2	0	Tanzania
17	T_2_3	T_2_2	-0.97	Tanzania
18	T_2_6	T_2_2	0.85	Tanzania
19	T_2_9	T_2_2	0.95	Tanzania
20	T_4_3	T_2_2	1	Tanzania
21	T_4_4	T_2_2	0.91	Tanzania
22	T_4_5	T_2_2	1	Tanzania
23	T_5_2	T_2_2	0.97	Tanzania
24	T_5_3	T_2_2	0.97	Tanzania
25	T_6_7	T_2_2	0.86	Tanzania
26	T_6_8	T_2_2	0.99	Tanzania
27	T_9_2	T_2_2	1	Tanzania
28	T_9_4	T_2_2	1	Tanzania

29	T_2_1	T_2_3	0.46	Tanzania
30	T_2_2	T_2_3	-0.97	Tanzania
31	T_2_3	T_2_3	0	Tanzania
32	T_2_6	T_2_3	0.65	Tanzania
33	T_2_9	T_2_3	0.88	Tanzania
34	T_4_3	T_2_3	0.95	Tanzania
35	T_4_4	T_2_3	0.79	Tanzania
36	T_4_5	T_2_3	1	Tanzania
37	T_5_2	T_2_3	0.94	Tanzania
38	T_5_3	T_2_3	0.96	Tanzania
39	T_6_7	T_2_3	0.77	Tanzania
40	T_6_8	T_2_3	0.99	Tanzania
41	T_9_2	T_2_3	1	Tanzania
42	T_9_4	T_2_3	1	Tanzania
43	T_2_1	T_2_6	0.99	Tanzania
44	T_2_2	T_2_6	0.85	Tanzania
45	T_2_3	T_2_6	0.65	Tanzania
46	T_2_6	T_2_6	0	Tanzania
47	T_2_9	T_2_6	-0.94	Tanzania
48	T_4_3	T_2_6	0.97	Tanzania
49	T_4_4	T_2_6	-0.91	Tanzania
50	T_4_5	T_2_6	0.87	Tanzania
51	T_5_2	T_2_6	1	Tanzania
52	T_5_3	T_2_6	1	Tanzania
53	T_6_7	T_2_6	-0.46	Tanzania
54	T_6_8	T_2_6	0.93	Tanzania
55	T_9_2	T_2_6	1	Tanzania
56	T_9_4	T_2_6	1	Tanzania
57	T_2_1	T_2_9	1	Tanzania
58	T_2_2	T_2_9	0.95	Tanzania
59	T_2_3	T_2_9	0.88	Tanzania
60	T_2_6	T_2_9	-0.94	Tanzania
61	T_2_9	T_2_9	0	Tanzania
62	T_4_3	T_2_9	1	Tanzania
63	T_4_4	T_2_9	0.44	Tanzania
64	T_4_5	T_2_9	0.99	Tanzania
65	T_5_2	T_2_9	1	Tanzania
66	T_5_3	T_2_9	1	Tanzania
67	T_6_7	T_2_9	-0.11	Tanzania
68	T_6_8	T_2_9	0.95	Tanzania
69	T_9_2	T_2_9	1	Tanzania
70	T_9_4	T_2_9	1	Tanzania
71	T_2_1	T_4_3	1	Tanzania

72	T_2_2	T_4_3	1	Tanzania
73	T_2_3	T_4_3	0.95	Tanzania
74	T_2_6	T_4_3	0.97	Tanzania
75	T_2_9	T_4_3	1	Tanzania
76	T_4_3	T_4_3	0	Tanzania
77	T_4_4	T_4_3	-0.44	Tanzania
78	T_4_5	T_4_3	-0.54	Tanzania
79	T_5_2	T_4_3	-0.47	Tanzania
80	T_5_3	T_4_3	-0.34	Tanzania
81	T_6_7	T_4_3	-0.02	Tanzania
82	T_6_8	T_4_3	-1	Tanzania
83	T_9_2	T_4_3	0.87	Tanzania
84	T_9_4	T_4_3	1	Tanzania
85	T_2_1	T_4_4	1	Tanzania
86	T_2_2	T_4_4	0.91	Tanzania
87	T_2_3	T_4_4	0.79	Tanzania
88	T_2_6	T_4_4	-0.91	Tanzania
89	T_2_9	T_4_4	0.44	Tanzania
90	T_4_3	T_4_4	-0.44	Tanzania
91	T_4_4	T_4_4	0	Tanzania
92	T_4_5	T_4_4	0.38	Tanzania
93	T_5_2	T_4_4	0.99	Tanzania
94	T_5_3	T_4_4	1	Tanzania
95	T_6_7	T_4_4	-0.83	Tanzania
96	T_6_8	T_4_4	0.89	Tanzania
97	T_9_2	T_4_4	1	Tanzania
98	T_9_4	T_4_4	1	Tanzania
99	T_2_1	T_4_5	1	Tanzania
100	T_2_2	T_4_5	1	Tanzania
101	T_2_3	T_4_5	1	Tanzania
102	T_2_6	T_4_5	0.87	Tanzania
103	T_2_9	T_4_5	0.99	Tanzania
104	T_4_3	T_4_5	-0.54	Tanzania
105	T_4_4	T_4_5	0.38	Tanzania
106	T_4_5	T_4_5	0	Tanzania
107	T_5_2	T_4_5	0.99	Tanzania
108	T_5_3	T_4_5	1	Tanzania
109	T_6_7	T_4_5	0.81	Tanzania
110	T_6_8	T_4_5	0.91	Tanzania
111	T_9_2	T_4_5	1	Tanzania
112	T_9_4	T_4_5	1	Tanzania
113	T_2_1	T_5_2	0.97	Tanzania
114	T_2_2	T_5_2	0.97	Tanzania

115	T_2_3	T_5_2	0.94	Tanzania
116	T_2_6	T_5_2	1	Tanzania
117	T_2_9	T_5_2	1	Tanzania
118	T_4_3	T_5_2	-0.47	Tanzania
119	T_4_4	T_5_2	0.99	Tanzania
120	T_4_5	T_5_2	0.99	Tanzania
121	T_5_2	T_5_2	0	Tanzania
122	T_5_3	T_5_2	-1	Tanzania
123	T_6_7	T_5_2	0.98	Tanzania
124	T_6_8	T_5_2	1	Tanzania
125	T_9_2	T_5_2	0.88	Tanzania
126	T_9_4	T_5_2	1	Tanzania
127	T_2_1	T_5_3	0.98	Tanzania
128	T_2_2	T_5_3	0.97	Tanzania
129	T_2_3	T_5_3	0.96	Tanzania
130	T_2_6	T_5_3	1	Tanzania
131	T_2_9	T_5_3	1	Tanzania
132	T_4_3	T_5_3	-0.34	Tanzania
133	T_4_4	T_5_3	1	Tanzania
134	T_4_5	T_5_3	1	Tanzania
135	T_5_2	T_5_3	-1	Tanzania
136	T_5_3	T_5_3	0	Tanzania
137	T_6_7	T_5_3	0.98	Tanzania
138	T_6_8	T_5_3	1	Tanzania
139	T_9_2	T_5_3	0.83	Tanzania
140	T_9_4	T_5_3	1	Tanzania
141	T_2_1	T_6_7	1	Tanzania
142	T_2_2	T_6_7	0.86	Tanzania
143	T_2_3	T_6_7	0.77	Tanzania
144	T_2_6	T_6_7	-0.46	Tanzania
145	T_2_9	T_6_7	-0.11	Tanzania
146	T_4_3	T_6_7	-0.02	Tanzania
147	T_4_4	T_6_7	-0.83	Tanzania
148	T_4_5	T_6_7	0.81	Tanzania
149	T_5_2	T_6_7	0.98	Tanzania
150	T_5_3	T_6_7	0.98	Tanzania
151	T_6_7	T_6_7	0	Tanzania
152	T_6_8	T_6_7	0.61	Tanzania
153	T_9_2	T_6_7	1	Tanzania
154	T_9_4	T_6_7	1	Tanzania
155	T_2_1	T_6_8	1	Tanzania
156	T_2_2	T_6_8	0.99	Tanzania
157	T_2_3	T_6_8	0.99	Tanzania

158	T_2_6	T_6_8	0.93	Tanzania
159	T_2_9	T_6_8	0.95	Tanzania
160	T_4_3	T_6_8	-1	Tanzania
161	T_4_4	T_6_8	0.89	Tanzania
162	T_4_5	T_6_8	0.91	Tanzania
163	T_5_2	T_6_8	1	Tanzania
164	T_5_3	T_6_8	1	Tanzania
165	T_6_7	T_6_8	0.61	Tanzania
166	T_6_8	T_6_8	0	Tanzania
167	T_9_2	T_6_8	1	Tanzania
168	T_9_4	T_6_8	1	Tanzania
169	T_2_1	T_9_2	1	Tanzania
170	T_2_2	T_9_2	1	Tanzania
171	T_2_3	T_9_2	1	Tanzania
172	T_2_6	T_9_2	1	Tanzania
173	T_2_9	T_9_2	1	Tanzania
174	T_4_3	T_9_2	0.87	Tanzania
175	T_4_4	T_9_2	1	Tanzania
176	T_4_5	T_9_2	1	Tanzania
177	T_5_2	T_9_2	0.88	Tanzania
178	T_5_3	T_9_2	0.83	Tanzania
179	T_6_7	T_9_2	1	Tanzania
180	T_6_8	T_9_2	1	Tanzania
181	T_9_2	T_9_2	0	Tanzania
182	T_9_4	T_9_2	-0.91	Tanzania
183	T_2_1	T_9_4	1	Tanzania
184	T_2_2	T_9_4	1	Tanzania
185	T_2_3	T_9_4	1	Tanzania
186	T_2_6	T_9_4	1	Tanzania
187	T_2_9	T_9_4	1	Tanzania
188	T_4_3	T_9_4	1	Tanzania
189	T_4_4	T_9_4	1	Tanzania
190	T_4_5	T_9_4	1	Tanzania
191	T_5_2	T_9_4	1	Tanzania
192	T_5_3	T_9_4	1	Tanzania
193	T_6_7	T_9_4	1	Tanzania
194	T_6_8	T_9_4	1	Tanzania
195	T_9_2	T_9_4	-0.91	Tanzania
196	T_9_4	T_9_4	0	Tanzania
197	V_1_2	V_1_2	0	Vietnam
198	V_2_2	V_1_2	1	Vietnam
199	V_3_1	V_1_2	1	Vietnam
200	V_3_2	V_1_2	1	Vietnam

201	V_5_3	V_1_2	1	Vietnam
202	V_6_1	V_1_2	1	Vietnam
203	V_6_2	V_1_2	0.69	Vietnam
204	V_6_3	V_1_2	1	Vietnam
205	V_7_1	V_1_2	1	Vietnam
206	V_7_2	V_1_2	1	Vietnam
207	V_7_3	V_1_2	1	Vietnam
208	V_8_2	V_1_2	1	Vietnam
209	V_9_1	V_1_2	0.98	Vietnam
210	V_9_2	V_1_2	1	Vietnam
211	V_9_4	V_1_2	0.98	Vietnam
212	V_10_1	V_1_2	1	Vietnam
213	V_11_1	V_1_2	1	Vietnam
214	V_11_3	V_1_2	1	Vietnam
215	V_12_1	V_1_2	0.93	Vietnam
216	V_13_2	V_1_2	0.75	Vietnam
217	V_14_1	V_1_2	-0.29	Vietnam
218	V_15_1	V_1_2	0.64	Vietnam
219	V_15_2	V_1_2	0.36	Vietnam
220	V_15_3	V_1_2	0.55	Vietnam
221	V_16_1	V_1_2	0.98	Vietnam
222	V_16_2	V_1_2	0.92	Vietnam
223	V_17_1	V_1_2	1	Vietnam
224	V_17_2	V_1_2	0.89	Vietnam
225	V_18_1	V_1_2	0.47	Vietnam
226	V_18_2	V_1_2	0.81	Vietnam
227	V_18_4	V_1_2	0.99	Vietnam
228	V_19_1	V_1_2	0.99	Vietnam
229	V_19_3	V_1_2	0.99	Vietnam
230	V_20_1	V_1_2	0.98	Vietnam
231	V_21_1	V_1_2	0.74	Vietnam
232	V_22_1	V_1_2	1	Vietnam
233	V_22_3	V_1_2	1	Vietnam
234	V_22_4	V_1_2	1	Vietnam
235	V_1_2	V_2_2	1	Vietnam
236	V_2_2	V_2_2	0	Vietnam
237	V_3_1	V_2_2	1	Vietnam
238	V_3_2	V_2_2	1	Vietnam
239	V_5_3	V_2_2	1	Vietnam
240	V_6_1	V_2_2	1	Vietnam
241	V_6_2	V_2_2	1	Vietnam
242	V_6_3	V_2_2	1	Vietnam
243	V_7_1	V_2_2	1	Vietnam

244	V_7_2	V_2_2	1	Vietnam
245	V_7_3	V_2_2	1	Vietnam
246	V_8_2	V_2_2	1	Vietnam
247	V_9_1	V_2_2	1	Vietnam
248	V_9_2	V_2_2	1	Vietnam
249	V_9_4	V_2_2	1	Vietnam
250	V_10_1	V_2_2	1	Vietnam
251	V_11_1	V_2_2	1	Vietnam
252	V_11_3	V_2_2	1	Vietnam
253	V_12_1	V_2_2	1	Vietnam
254	V_13_2	V_2_2	1	Vietnam
255	V_14_1	V_2_2	1	Vietnam
256	V_15_1	V_2_2	1	Vietnam
257	V_15_2	V_2_2	1	Vietnam
258	V_15_3	V_2_2	1	Vietnam
259	V_16_1	V_2_2	1	Vietnam
260	V_16_2	V_2_2	1	Vietnam
261	V_17_1	V_2_2	1	Vietnam
262	V_17_2	V_2_2	1	Vietnam
263	V_18_1	V_2_2	1	Vietnam
264	V_18_2	V_2_2	1	Vietnam
265	V_18_4	V_2_2	1	Vietnam
266	V_19_1	V_2_2	1	Vietnam
267	V_19_3	V_2_2	1	Vietnam
268	V_20_1	V_2_2	1	Vietnam
269	V_21_1	V_2_2	1	Vietnam
270	V_22_1	V_2_2	1	Vietnam
271	V_22_3	V_2_2	1	Vietnam
272	V_22_4	V_2_2	1	Vietnam
273	V_1_2	V_3_1	1	Vietnam
274	V_2_2	V_3_1	1	Vietnam
275	V_3_1	V_3_1	0	Vietnam
276	V_3_2	V_3_1	-0.95	Vietnam
277	V_5_3	V_3_1	1	Vietnam
278	V_6_1	V_3_1	1	Vietnam
279	V_6_2	V_3_1	1	Vietnam
280	V_6_3	V_3_1	1	Vietnam
281	V_7_1	V_3_1	1	Vietnam
282	V_7_2	V_3_1	1	Vietnam
283	V_7_3	V_3_1	1	Vietnam
284	V_8_2	V_3_1	1	Vietnam
285	V_9_1	V_3_1	1	Vietnam
286	V_9_2	V_3_1	1	Vietnam

287	V_9_4	V_3_1	1	Vietnam
288	V_10_1	V_3_1	1	Vietnam
289	V_11_1	V_3_1	0.96	Vietnam
290	V_11_3	V_3_1	1	Vietnam
291	V_12_1	V_3_1	1	Vietnam
292	V_13_2	V_3_1	1	Vietnam
293	V_14_1	V_3_1	1	Vietnam
294	V_15_1	V_3_1	1	Vietnam
295	V_15_2	V_3_1	1	Vietnam
296	V_15_3	V_3_1	1	Vietnam
297	V_16_1	V_3_1	1	Vietnam
298	V_16_2	V_3_1	1	Vietnam
299	V_17_1	V_3_1	1	Vietnam
300	V_17_2	V_3_1	1	Vietnam
301	V_18_1	V_3_1	1	Vietnam
302	V_18_2	V_3_1	1	Vietnam
303	V_18_4	V_3_1	1	Vietnam
304	V_19_1	V_3_1	1	Vietnam
305	V_19_3	V_3_1	1	Vietnam
306	V_20_1	V_3_1	1	Vietnam
307	V_21_1	V_3_1	1	Vietnam
308	V_22_1	V_3_1	1	Vietnam
309	V_22_3	V_3_1	1	Vietnam
310	V_22_4	V_3_1	1	Vietnam
311	V_1_2	V_3_2	1	Vietnam
312	V_2_2	V_3_2	1	Vietnam
313	V_3_1	V_3_2	-0.95	Vietnam
314	V_3_2	V_3_2	0	Vietnam
315	V_5_3	V_3_2	1	Vietnam
316	V_6_1	V_3_2	1	Vietnam
317	V_6_2	V_3_2	1	Vietnam
318	V_6_3	V_3_2	1	Vietnam
319	V_7_1	V_3_2	1	Vietnam
320	V_7_2	V_3_2	1	Vietnam
321	V_7_3	V_3_2	1	Vietnam
322	V_8_2	V_3_2	1	Vietnam
323	V_9_1	V_3_2	1	Vietnam
324	V_9_2	V_3_2	1	Vietnam
325	V_9_4	V_3_2	1	Vietnam
326	V_10_1	V_3_2	1	Vietnam
327	V_11_1	V_3_2	0.94	Vietnam
328	V_11_3	V_3_2	1	Vietnam
329	V_12_1	V_3_2	1	Vietnam

330	V_13_2	V_3_2	1	Vietnam
331	V_14_1	V_3_2	1	Vietnam
332	V_15_1	V_3_2	1	Vietnam
333	V_15_2	V_3_2	1	Vietnam
334	V_15_3	V_3_2	1	Vietnam
335	V_16_1	V_3_2	1	Vietnam
336	V_16_2	V_3_2	1	Vietnam
337	V_17_1	V_3_2	1	Vietnam
338	V_17_2	V_3_2	1	Vietnam
339	V_18_1	V_3_2	1	Vietnam
340	V_18_2	V_3_2	1	Vietnam
341	V_18_4	V_3_2	1	Vietnam
342	V_19_1	V_3_2	1	Vietnam
343	V_19_3	V_3_2	1	Vietnam
344	V_20_1	V_3_2	1	Vietnam
345	V_21_1	V_3_2	1	Vietnam
346	V_22_1	V_3_2	1	Vietnam
347	V_22_3	V_3_2	1	Vietnam
348	V_22_4	V_3_2	1	Vietnam
349	V_1_2	V_5_3	1	Vietnam
350	V_2_2	V_5_3	1	Vietnam
351	V_3_1	V_5_3	1	Vietnam
352	V_3_2	V_5_3	1	Vietnam
353	V_5_3	V_5_3	0	Vietnam
354	V_6_1	V_5_3	0.86	Vietnam
355	V_6_2	V_5_3	1	Vietnam
356	V_6_3	V_5_3	1	Vietnam
357	V_7_1	V_5_3	1	Vietnam
358	V_7_2	V_5_3	1	Vietnam
359	V_7_3	V_5_3	1	Vietnam
360	V_8_2	V_5_3	1	Vietnam
361	V_9_1	V_5_3	1	Vietnam
362	V_9_2	V_5_3	1	Vietnam
363	V_9_4	V_5_3	1	Vietnam
364	V_10_1	V_5_3	1	Vietnam
365	V_11_1	V_5_3	1	Vietnam
366	V_11_3	V_5_3	1	Vietnam
367	V_12_1	V_5_3	0.86	Vietnam
368	V_13_2	V_5_3	1	Vietnam
369	V_14_1	V_5_3	1	Vietnam
370	V_15_1	V_5_3	1	Vietnam
371	V_15_2	V_5_3	1	Vietnam
372	V_15_3	V_5_3	1	Vietnam

373	V_16_1	V_5_3	1	Vietnam
374	V_16_2	V_5_3	1	Vietnam
375	V_17_1	V_5_3	1	Vietnam
376	V_17_2	V_5_3	1	Vietnam
377	V_18_1	V_5_3	0.98	Vietnam
378	V_18_2	V_5_3	1	Vietnam
379	V_18_4	V_5_3	1	Vietnam
380	V_19_1	V_5_3	1	Vietnam
381	V_19_3	V_5_3	0.99	Vietnam
382	V_20_1	V_5_3	1	Vietnam
383	V_21_1	V_5_3	0.35	Vietnam
384	V_22_1	V_5_3	1	Vietnam
385	V_22_3	V_5_3	1	Vietnam
386	V_22_4	V_5_3	1	Vietnam
387	V_1_2	V_6_1	1	Vietnam
388	V_2_2	V_6_1	1	Vietnam
389	V_3_1	V_6_1	1	Vietnam
390	V_3_2	V_6_1	1	Vietnam
391	V_5_3	V_6_1	0.86	Vietnam
392	V_6_1	V_6_1	0	Vietnam
393	V_6_2	V_6_1	1	Vietnam
394	V_6_3	V_6_1	0.95	Vietnam
395	V_7_1	V_6_1	1	Vietnam
396	V_7_2	V_6_1	1	Vietnam
397	V_7_3	V_6_1	1	Vietnam
398	V_8_2	V_6_1	1	Vietnam
399	V_9_1	V_6_1	1	Vietnam
400	V_9_2	V_6_1	0.99	Vietnam
401	V_9_4	V_6_1	1	Vietnam
402	V_10_1	V_6_1	1	Vietnam
403	V_11_1	V_6_1	1	Vietnam
404	V_11_3	V_6_1	0.46	Vietnam
405	V_12_1	V_6_1	0.91	Vietnam
406	V_13_2	V_6_1	1	Vietnam
407	V_14_1	V_6_1	1	Vietnam
408	V_15_1	V_6_1	1	Vietnam
409	V_15_2	V_6_1	1	Vietnam
410	V_15_3	V_6_1	1	Vietnam
411	V_16_1	V_6_1	1	Vietnam
412	V_16_2	V_6_1	1	Vietnam
413	V_17_1	V_6_1	1	Vietnam
414	V_17_2	V_6_1	1	Vietnam
415	V_18_1	V_6_1	1	Vietnam

416	V_18_2	V_6_1	1	Vietnam
417	V_18_4	V_6_1	1	Vietnam
418	V_19_1	V_6_1	1	Vietnam
419	V_19_3	V_6_1	1	Vietnam
420	V_20_1	V_6_1	1	Vietnam
421	V_21_1	V_6_1	0.97	Vietnam
422	V_22_1	V_6_1	1	Vietnam
423	V_22_3	V_6_1	1	Vietnam
424	V_22_4	V_6_1	1	Vietnam
425	V_1_2	V_6_2	0.69	Vietnam
426	V_2_2	V_6_2	1	Vietnam
427	V_3_1	V_6_2	1	Vietnam
428	V_3_2	V_6_2	1	Vietnam
429	V_5_3	V_6_2	1	Vietnam
430	V_6_1	V_6_2	1	Vietnam
431	V_6_2	V_6_2	0	Vietnam
432	V_6_3	V_6_2	1	Vietnam
433	V_7_1	V_6_2	1	Vietnam
434	V_7_2	V_6_2	1	Vietnam
435	V_7_3	V_6_2	1	Vietnam
436	V_8_2	V_6_2	1	Vietnam
437	V_9_1	V_6_2	0.67	Vietnam
438	V_9_2	V_6_2	1	Vietnam
439	V_9_4	V_6_2	1	Vietnam
440	V_10_1	V_6_2	0.95	Vietnam
441	V_11_1	V_6_2	1	Vietnam
442	V_11_3	V_6_2	1	Vietnam
443	V_12_1	V_6_2	0.94	Vietnam
444	V_13_2	V_6_2	0.83	Vietnam
445	V_14_1	V_6_2	0.23	Vietnam
446	V_15_1	V_6_2	0.6	Vietnam
447	V_15_2	V_6_2	0.79	Vietnam
448	V_15_3	V_6_2	0.91	Vietnam
449	V_16_1	V_6_2	0.96	Vietnam
450	V_16_2	V_6_2	0.91	Vietnam
451	V_17_1	V_6_2	0.94	Vietnam
452	V_17_2	V_6_2	0.93	Vietnam
453	V_18_1	V_6_2	-0.52	Vietnam
454	V_18_2	V_6_2	-0.65	Vietnam
455	V_18_4	V_6_2	1	Vietnam
456	V_19_1	V_6_2	1	Vietnam
457	V_19_3	V_6_2	1	Vietnam
458	V_20_1	V_6_2	1	Vietnam

459	V_21_1	V_6_2	0.26	Vietnam
460	V_22_1	V_6_2	1	Vietnam
461	V_22_3	V_6_2	1	Vietnam
462	V_22_4	V_6_2	1	Vietnam
463	V_1_2	V_6_3	1	Vietnam
464	V_2_2	V_6_3	1	Vietnam
465	V_3_1	V_6_3	1	Vietnam
466	V_3_2	V_6_3	1	Vietnam
467	V_5_3	V_6_3	1	Vietnam
468	V_6_1	V_6_3	0.95	Vietnam
469	V_6_2	V_6_3	1	Vietnam
470	V_6_3	V_6_3	0	Vietnam
471	V_7_1	V_6_3	1	Vietnam
472	V_7_2	V_6_3	1	Vietnam
473	V_7_3	V_6_3	1	Vietnam
474	V_8_2	V_6_3	1	Vietnam
475	V_9_1	V_6_3	1	Vietnam
476	V_9_2	V_6_3	1	Vietnam
477	V_9_4	V_6_3	1	Vietnam
478	V_10_1	V_6_3	1	Vietnam
479	V_11_1	V_6_3	1	Vietnam
480	V_11_3	V_6_3	1	Vietnam
481	V_12_1	V_6_3	1	Vietnam
482	V_13_2	V_6_3	1	Vietnam
483	V_14_1	V_6_3	1	Vietnam
484	V_15_1	V_6_3	1	Vietnam
485	V_15_2	V_6_3	1	Vietnam
486	V_15_3	V_6_3	1	Vietnam
487	V_16_1	V_6_3	1	Vietnam
488	V_16_2	V_6_3	1	Vietnam
489	V_17_1	V_6_3	1	Vietnam
490	V_17_2	V_6_3	1	Vietnam
491	V_18_1	V_6_3	1	Vietnam
492	V_18_2	V_6_3	1	Vietnam
493	V_18_4	V_6_3	1	Vietnam
494	V_19_1	V_6_3	1	Vietnam
495	V_19_3	V_6_3	1	Vietnam
496	V_20_1	V_6_3	1	Vietnam
497	V_21_1	V_6_3	0.98	Vietnam
498	V_22_1	V_6_3	1	Vietnam
499	V_22_3	V_6_3	1	Vietnam
500	V_22_4	V_6_3	1	Vietnam
501	V_1_2	V_7_1	1	Vietnam

502	V_2_2	V_7_1	1	Vietnam
503	V_3_1	V_7_1	1	Vietnam
504	V_3_2	V_7_1	1	Vietnam
505	V_5_3	V_7_1	1	Vietnam
506	V_6_1	V_7_1	1	Vietnam
507	V_6_2	V_7_1	1	Vietnam
508	V_6_3	V_7_1	1	Vietnam
509	V_7_1	V_7_1	0	Vietnam
510	V_7_2	V_7_1	1	Vietnam
511	V_7_3	V_7_1	1	Vietnam
512	V_8_2	V_7_1	1	Vietnam
513	V_9_1	V_7_1	0.4	Vietnam
514	V_9_2	V_7_1	1	Vietnam
515	V_9_4	V_7_1	1	Vietnam
516	V_10_1	V_7_1	-0.45	Vietnam
517	V_11_1	V_7_1	1	Vietnam
518	V_11_3	V_7_1	1	Vietnam
519	V_12_1	V_7_1	1	Vietnam
520	V_13_2	V_7_1	1	Vietnam
521	V_14_1	V_7_1	1	Vietnam
522	V_15_1	V_7_1	1	Vietnam
523	V_15_2	V_7_1	1	Vietnam
524	V_15_3	V_7_1	1	Vietnam
525	V_16_1	V_7_1	0.82	Vietnam
526	V_16_2	V_7_1	0.87	Vietnam
527	V_17_1	V_7_1	0.36	Vietnam
528	V_17_2	V_7_1	0.7	Vietnam
529	V_18_1	V_7_1	0.4	Vietnam
530	V_18_2	V_7_1	0.91	Vietnam
531	V_18_4	V_7_1	1	Vietnam
532	V_19_1	V_7_1	1	Vietnam
533	V_19_3	V_7_1	1	Vietnam
534	V_20_1	V_7_1	1	Vietnam
535	V_21_1	V_7_1	1	Vietnam
536	V_22_1	V_7_1	1	Vietnam
537	V_22_3	V_7_1	1	Vietnam
538	V_22_4	V_7_1	1	Vietnam
539	V_1_2	V_7_2	1	Vietnam
540	V_2_2	V_7_2	1	Vietnam
541	V_3_1	V_7_2	1	Vietnam
542	V_3_2	V_7_2	1	Vietnam
543	V_5_3	V_7_2	1	Vietnam
544	V_6_1	V_7_2	1	Vietnam

545	V_6_2	V_7_2	1	Vietnam
546	V_6_3	V_7_2	1	Vietnam
547	V_7_1	V_7_2	1	Vietnam
548	V_7_2	V_7_2	0	Vietnam
549	V_7_3	V_7_2	1	Vietnam
550	V_8_2	V_7_2	1	Vietnam
551	V_9_1	V_7_2	1	Vietnam
552	V_9_2	V_7_2	1	Vietnam
553	V_9_4	V_7_2	1	Vietnam
554	V_10_1	V_7_2	1	Vietnam
555	V_11_1	V_7_2	1	Vietnam
556	V_11_3	V_7_2	1	Vietnam
557	V_12_1	V_7_2	1	Vietnam
558	V_13_2	V_7_2	1	Vietnam
559	V_14_1	V_7_2	1	Vietnam
560	V_15_1	V_7_2	1	Vietnam
561	V_15_2	V_7_2	1	Vietnam
562	V_15_3	V_7_2	1	Vietnam
563	V_16_1	V_7_2	1	Vietnam
564	V_16_2	V_7_2	1	Vietnam
565	V_17_1	V_7_2	1	Vietnam
566	V_17_2	V_7_2	1	Vietnam
567	V_18_1	V_7_2	1	Vietnam
568	V_18_2	V_7_2	1	Vietnam
569	V_18_4	V_7_2	1	Vietnam
570	V_19_1	V_7_2	1	Vietnam
571	V_19_3	V_7_2	1	Vietnam
572	V_20_1	V_7_2	1	Vietnam
573	V_21_1	V_7_2	1	Vietnam
574	V_22_1	V_7_2	1	Vietnam
575	V_22_3	V_7_2	1	Vietnam
576	V_22_4	V_7_2	1	Vietnam
577	V_1_2	V_7_3	1	Vietnam
578	V_2_2	V_7_3	1	Vietnam
579	V_3_1	V_7_3	1	Vietnam
580	V_3_2	V_7_3	1	Vietnam
581	V_5_3	V_7_3	1	Vietnam
582	V_6_1	V_7_3	1	Vietnam
583	V_6_2	V_7_3	1	Vietnam
584	V_6_3	V_7_3	1	Vietnam
585	V_7_1	V_7_3	1	Vietnam
586	V_7_2	V_7_3	1	Vietnam
587	V_7_3	V_7_3	0	Vietnam

588	V_8_2	V_7_3	1	Vietnam
589	V_9_1	V_7_3	1	Vietnam
590	V_9_2	V_7_3	1	Vietnam
591	V_9_4	V_7_3	1	Vietnam
592	V_10_1	V_7_3	1	Vietnam
593	V_11_1	V_7_3	1	Vietnam
594	V_11_3	V_7_3	1	Vietnam
595	V_12_1	V_7_3	1	Vietnam
596	V_13_2	V_7_3	1	Vietnam
597	V_14_1	V_7_3	1	Vietnam
598	V_15_1	V_7_3	1	Vietnam
599	V_15_2	V_7_3	1	Vietnam
600	V_15_3	V_7_3	1	Vietnam
601	V_16_1	V_7_3	1	Vietnam
602	V_16_2	V_7_3	1	Vietnam
603	V_17_1	V_7_3	1	Vietnam
604	V_17_2	V_7_3	1	Vietnam
605	V_18_1	V_7_3	1	Vietnam
606	V_18_2	V_7_3	1	Vietnam
607	V_18_4	V_7_3	1	Vietnam
608	V_19_1	V_7_3	1	Vietnam
609	V_19_3	V_7_3	1	Vietnam
610	V_20_1	V_7_3	1	Vietnam
611	V_21_1	V_7_3	1	Vietnam
612	V_22_1	V_7_3	1	Vietnam
613	V_22_3	V_7_3	1	Vietnam
614	V_22_4	V_7_3	1	Vietnam
615	V_1_2	V_8_2	1	Vietnam
616	V_2_2	V_8_2	1	Vietnam
617	V_3_1	V_8_2	1	Vietnam
618	V_3_2	V_8_2	1	Vietnam
619	V_5_3	V_8_2	1	Vietnam
620	V_6_1	V_8_2	1	Vietnam
621	V_6_2	V_8_2	1	Vietnam
622	V_6_3	V_8_2	1	Vietnam
623	V_7_1	V_8_2	1	Vietnam
624	V_7_2	V_8_2	1	Vietnam
625	V_7_3	V_8_2	1	Vietnam
626	V_8_2	V_8_2	0	Vietnam
627	V_9_1	V_8_2	1	Vietnam
628	V_9_2	V_8_2	1	Vietnam
629	V_9_4	V_8_2	1	Vietnam
630	V_10_1	V_8_2	1	Vietnam

631	V_11_1	V_8_2	1	Vietnam
632	V_11_3	V_8_2	1	Vietnam
633	V_12_1	V_8_2	1	Vietnam
634	V_13_2	V_8_2	1	Vietnam
635	V_14_1	V_8_2	1	Vietnam
636	V_15_1	V_8_2	1	Vietnam
637	V_15_2	V_8_2	1	Vietnam
638	V_15_3	V_8_2	1	Vietnam
639	V_16_1	V_8_2	1	Vietnam
640	V_16_2	V_8_2	1	Vietnam
641	V_17_1	V_8_2	1	Vietnam
642	V_17_2	V_8_2	1	Vietnam
643	V_18_1	V_8_2	1	Vietnam
644	V_18_2	V_8_2	1	Vietnam
645	V_18_4	V_8_2	0.99	Vietnam
646	V_19_1	V_8_2	1	Vietnam
647	V_19_3	V_8_2	0.53	Vietnam
648	V_20_1	V_8_2	1	Vietnam
649	V_21_1	V_8_2	0.91	Vietnam
650	V_22_1	V_8_2	1	Vietnam
651	V_22_3	V_8_2	0.98	Vietnam
652	V_22_4	V_8_2	1	Vietnam
653	V_1_2	V_9_1	0.98	Vietnam
654	V_2_2	V_9_1	1	Vietnam
655	V_3_1	V_9_1	1	Vietnam
656	V_3_2	V_9_1	1	Vietnam
657	V_5_3	V_9_1	1	Vietnam
658	V_6_1	V_9_1	1	Vietnam
659	V_6_2	V_9_1	0.67	Vietnam
660	V_6_3	V_9_1	1	Vietnam
661	V_7_1	V_9_1	0.4	Vietnam
662	V_7_2	V_9_1	1	Vietnam
663	V_7_3	V_9_1	1	Vietnam
664	V_8_2	V_9_1	1	Vietnam
665	V_9_1	V_9_1	0	Vietnam
666	V_9_2	V_9_1	1	Vietnam
667	V_9_4	V_9_1	1	Vietnam
668	V_10_1	V_9_1	-0.92	Vietnam
669	V_11_1	V_9_1	1	Vietnam
670	V_11_3	V_9_1	1	Vietnam
671	V_12_1	V_9_1	1	Vietnam
672	V_13_2	V_9_1	0.78	Vietnam
673	V_14_1	V_9_1	0.82	Vietnam

674	V_15_1	V_9_1	0.62	Vietnam
675	V_15_2	V_9_1	0.79	Vietnam
676	V_15_3	V_9_1	0.78	Vietnam
677	V_16_1	V_9_1	-1	Vietnam
678	V_16_2	V_9_1	-0.54	Vietnam
679	V_17_1	V_9_1	-1	Vietnam
680	V_17_2	V_9_1	-0.41	Vietnam
681	V_18_1	V_9_1	-0.6	Vietnam
682	V_18_2	V_9_1	-0.15	Vietnam
683	V_18_4	V_9_1	1	Vietnam
684	V_19_1	V_9_1	1	Vietnam
685	V_19_3	V_9_1	1	Vietnam
686	V_20_1	V_9_1	0.99	Vietnam
687	V_21_1	V_9_1	0.98	Vietnam
688	V_22_1	V_9_1	1	Vietnam
689	V_22_3	V_9_1	1	Vietnam
690	V_22_4	V_9_1	1	Vietnam
691	V_1_2	V_9_2	1	Vietnam
692	V_2_2	V_9_2	1	Vietnam
693	V_3_1	V_9_2	1	Vietnam
694	V_3_2	V_9_2	1	Vietnam
695	V_5_3	V_9_2	1	Vietnam
696	V_6_1	V_9_2	0.99	Vietnam
697	V_6_2	V_9_2	1	Vietnam
698	V_6_3	V_9_2	1	Vietnam
699	V_7_1	V_9_2	1	Vietnam
700	V_7_2	V_9_2	1	Vietnam
701	V_7_3	V_9_2	1	Vietnam
702	V_8_2	V_9_2	1	Vietnam
703	V_9_1	V_9_2	1	Vietnam
704	V_9_2	V_9_2	0	Vietnam
705	V_9_4	V_9_2	1	Vietnam
706	V_10_1	V_9_2	1	Vietnam
707	V_11_1	V_9_2	1	Vietnam
708	V_11_3	V_9_2	0.99	Vietnam
709	V_12_1	V_9_2	1	Vietnam
710	V_13_2	V_9_2	1	Vietnam
711	V_14_1	V_9_2	1	Vietnam
712	V_15_1	V_9_2	1	Vietnam
713	V_15_2	V_9_2	1	Vietnam
714	V_15_3	V_9_2	1	Vietnam
715	V_16_1	V_9_2	1	Vietnam
716	V_16_2	V_9_2	1	Vietnam

717	V_17_1	V_9_2	1	Vietnam
718	V_17_2	V_9_2	1	Vietnam
719	V_18_1	V_9_2	1	Vietnam
720	V_18_2	V_9_2	1	Vietnam
721	V_18_4	V_9_2	1	Vietnam
722	V_19_1	V_9_2	1	Vietnam
723	V_19_3	V_9_2	1	Vietnam
724	V_20_1	V_9_2	1	Vietnam
725	V_21_1	V_9_2	1	Vietnam
726	V_22_1	V_9_2	1	Vietnam
727	V_22_3	V_9_2	1	Vietnam
728	V_22_4	V_9_2	0.99	Vietnam
729	V_1_2	V_9_4	0.98	Vietnam
730	V_2_2	V_9_4	1	Vietnam
731	V_3_1	V_9_4	1	Vietnam
732	V_3_2	V_9_4	1	Vietnam
733	V_5_3	V_9_4	1	Vietnam
734	V_6_1	V_9_4	1	Vietnam
735	V_6_2	V_9_4	1	Vietnam
736	V_6_3	V_9_4	1	Vietnam
737	V_7_1	V_9_4	1	Vietnam
738	V_7_2	V_9_4	1	Vietnam
739	V_7_3	V_9_4	1	Vietnam
740	V_8_2	V_9_4	1	Vietnam
741	V_9_1	V_9_4	1	Vietnam
742	V_9_2	V_9_4	1	Vietnam
743	V_9_4	V_9_4	0	Vietnam
744	V_10_1	V_9_4	1	Vietnam
745	V_11_1	V_9_4	1	Vietnam
746	V_11_3	V_9_4	1	Vietnam
747	V_12_1	V_9_4	1	Vietnam
748	V_13_2	V_9_4	0.99	Vietnam
749	V_14_1	V_9_4	0.95	Vietnam
750	V_15_1	V_9_4	1	Vietnam
751	V_15_2	V_9_4	1	Vietnam
752	V_15_3	V_9_4	1	Vietnam
753	V_16_1	V_9_4	1	Vietnam
754	V_16_2	V_9_4	1	Vietnam
755	V_17_1	V_9_4	1	Vietnam
756	V_17_2	V_9_4	1	Vietnam
757	V_18_1	V_9_4	1	Vietnam
758	V_18_2	V_9_4	1	Vietnam
759	V_18_4	V_9_4	1	Vietnam

760	V_19_1	V_9_4	1	Vietnam
761	V_19_3	V_9_4	1	Vietnam
762	V_20_1	V_9_4	1	Vietnam
763	V_21_1	V_9_4	1	Vietnam
764	V_22_1	V_9_4	1	Vietnam
765	V_22_3	V_9_4	1	Vietnam
766	V_22_4	V_9_4	1	Vietnam
767	V_1_2	V_10_1	1	Vietnam
768	V_2_2	V_10_1	1	Vietnam
769	V_3_1	V_10_1	1	Vietnam
770	V_3_2	V_10_1	1	Vietnam
771	V_5_3	V_10_1	1	Vietnam
772	V_6_1	V_10_1	1	Vietnam
773	V_6_2	V_10_1	0.95	Vietnam
774	V_6_3	V_10_1	1	Vietnam
775	V_7_1	V_10_1	-0.45	Vietnam
776	V_7_2	V_10_1	1	Vietnam
777	V_7_3	V_10_1	1	Vietnam
778	V_8_2	V_10_1	1	Vietnam
779	V_9_1	V_10_1	-0.92	Vietnam
780	V_9_2	V_10_1	1	Vietnam
781	V_9_4	V_10_1	1	Vietnam
782	V_10_1	V_10_1	0	Vietnam
783	V_11_1	V_10_1	1	Vietnam
784	V_11_3	V_10_1	1	Vietnam
785	V_12_1	V_10_1	1	Vietnam
786	V_13_2	V_10_1	0.92	Vietnam
787	V_14_1	V_10_1	0.92	Vietnam
788	V_15_1	V_10_1	0.48	Vietnam
789	V_15_2	V_10_1	0.92	Vietnam
790	V_15_3	V_10_1	0.93	Vietnam
791	V_16_1	V_10_1	-1	Vietnam
792	V_16_2	V_10_1	-0.7	Vietnam
793	V_17_1	V_10_1	-0.93	Vietnam
794	V_17_2	V_10_1	-0.77	Vietnam
795	V_18_1	V_10_1	-0.72	Vietnam
796	V_18_2	V_10_1	0.18	Vietnam
797	V_18_4	V_10_1	1	Vietnam
798	V_19_1	V_10_1	1	Vietnam
799	V_19_3	V_10_1	1	Vietnam
800	V_20_1	V_10_1	0.94	Vietnam
801	V_21_1	V_10_1	1	Vietnam
802	V_22_1	V_10_1	1	Vietnam

803	V_22_3	V_10_1	1	Vietnam
804	V_22_4	V_10_1	1	Vietnam
805	V_1_2	V_11_1	1	Vietnam
806	V_2_2	V_11_1	1	Vietnam
807	V_3_1	V_11_1	0.96	Vietnam
808	V_3_2	V_11_1	0.94	Vietnam
809	V_5_3	V_11_1	1	Vietnam
810	V_6_1	V_11_1	1	Vietnam
811	V_6_2	V_11_1	1	Vietnam
812	V_6_3	V_11_1	1	Vietnam
813	V_7_1	V_11_1	1	Vietnam
814	V_7_2	V_11_1	1	Vietnam
815	V_7_3	V_11_1	1	Vietnam
816	V_8_2	V_11_1	1	Vietnam
817	V_9_1	V_11_1	1	Vietnam
818	V_9_2	V_11_1	1	Vietnam
819	V_9_4	V_11_1	1	Vietnam
820	V_10_1	V_11_1	1	Vietnam
821	V_11_1	V_11_1	0	Vietnam
822	V_11_3	V_11_1	1	Vietnam
823	V_12_1	V_11_1	0.99	Vietnam
824	V_13_2	V_11_1	1	Vietnam
825	V_14_1	V_11_1	1	Vietnam
826	V_15_1	V_11_1	1	Vietnam
827	V_15_2	V_11_1	1	Vietnam
828	V_15_3	V_11_1	1	Vietnam
829	V_16_1	V_11_1	1	Vietnam
830	V_16_2	V_11_1	1	Vietnam
831	V_17_1	V_11_1	1	Vietnam
832	V_17_2	V_11_1	1	Vietnam
833	V_18_1	V_11_1	1	Vietnam
834	V_18_2	V_11_1	1	Vietnam
835	V_18_4	V_11_1	1	Vietnam
836	V_19_1	V_11_1	1	Vietnam
837	V_19_3	V_11_1	1	Vietnam
838	V_20_1	V_11_1	1	Vietnam
839	V_21_1	V_11_1	0.99	Vietnam
840	V_22_1	V_11_1	1	Vietnam
841	V_22_3	V_11_1	1	Vietnam
842	V_22_4	V_11_1	1	Vietnam
843	V_1_2	V_11_3	1	Vietnam
844	V_2_2	V_11_3	1	Vietnam
845	V_3_1	V_11_3	1	Vietnam

846	V_3_2	V_11_3	1	Vietnam
847	V_5_3	V_11_3	1	Vietnam
848	V_6_1	V_11_3	0.46	Vietnam
849	V_6_2	V_11_3	1	Vietnam
850	V_6_3	V_11_3	1	Vietnam
851	V_7_1	V_11_3	1	Vietnam
852	V_7_2	V_11_3	1	Vietnam
853	V_7_3	V_11_3	1	Vietnam
854	V_8_2	V_11_3	1	Vietnam
855	V_9_1	V_11_3	1	Vietnam
856	V_9_2	V_11_3	0.99	Vietnam
857	V_9_4	V_11_3	1	Vietnam
858	V_10_1	V_11_3	1	Vietnam
859	V_11_1	V_11_3	1	Vietnam
860	V_11_3	V_11_3	0	Vietnam
861	V_12_1	V_11_3	0.88	Vietnam
862	V_13_2	V_11_3	1	Vietnam
863	V_14_1	V_11_3	1	Vietnam
864	V_15_1	V_11_3	1	Vietnam
865	V_15_2	V_11_3	1	Vietnam
866	V_15_3	V_11_3	1	Vietnam
867	V_16_1	V_11_3	1	Vietnam
868	V_16_2	V_11_3	1	Vietnam
869	V_17_1	V_11_3	1	Vietnam
870	V_17_2	V_11_3	1	Vietnam
871	V_18_1	V_11_3	1	Vietnam
872	V_18_2	V_11_3	1	Vietnam
873	V_18_4	V_11_3	1	Vietnam
874	V_19_1	V_11_3	1	Vietnam
875	V_19_3	V_11_3	1	Vietnam
876	V_20_1	V_11_3	1	Vietnam
877	V_21_1	V_11_3	0.77	Vietnam
878	V_22_1	V_11_3	1	Vietnam
879	V_22_3	V_11_3	1	Vietnam
880	V_22_4	V_11_3	1	Vietnam
881	V_1_2	V_12_1	0.93	Vietnam
882	V_2_2	V_12_1	1	Vietnam
883	V_3_1	V_12_1	1	Vietnam
884	V_3_2	V_12_1	1	Vietnam
885	V_5_3	V_12_1	0.86	Vietnam
886	V_6_1	V_12_1	0.91	Vietnam
887	V_6_2	V_12_1	0.94	Vietnam
888	V_6_3	V_12_1	1	Vietnam

889	V_7_1	V_12_1	1	Vietnam
890	V_7_2	V_12_1	1	Vietnam
891	V_7_3	V_12_1	1	Vietnam
892	V_8_2	V_12_1	1	Vietnam
893	V_9_1	V_12_1	1	Vietnam
894	V_9_2	V_12_1	1	Vietnam
895	V_9_4	V_12_1	1	Vietnam
896	V_10_1	V_12_1	1	Vietnam
897	V_11_1	V_12_1	0.99	Vietnam
898	V_11_3	V_12_1	0.88	Vietnam
899	V_12_1	V_12_1	0	Vietnam
900	V_13_2	V_12_1	1	Vietnam
901	V_14_1	V_12_1	1	Vietnam
902	V_15_1	V_12_1	0.99	Vietnam
903	V_15_2	V_12_1	0.99	Vietnam
904	V_15_3	V_12_1	0.99	Vietnam
905	V_16_1	V_12_1	1	Vietnam
906	V_16_2	V_12_1	1	Vietnam
907	V_17_1	V_12_1	1	Vietnam
908	V_17_2	V_12_1	1	Vietnam
909	V_18_1	V_12_1	0.88	Vietnam
910	V_18_2	V_12_1	0.96	Vietnam
911	V_18_4	V_12_1	1	Vietnam
912	V_19_1	V_12_1	1	Vietnam
913	V_19_3	V_12_1	1	Vietnam
914	V_20_1	V_12_1	1	Vietnam
915	V_21_1	V_12_1	0.55	Vietnam
916	V_22_1	V_12_1	1	Vietnam
917	V_22_3	V_12_1	1	Vietnam
918	V_22_4	V_12_1	1	Vietnam
919	V_1_2	V_13_2	0.75	Vietnam
920	V_2_2	V_13_2	1	Vietnam
921	V_3_1	V_13_2	1	Vietnam
922	V_3_2	V_13_2	1	Vietnam
923	V_5_3	V_13_2	1	Vietnam
924	V_6_1	V_13_2	1	Vietnam
925	V_6_2	V_13_2	0.83	Vietnam
926	V_6_3	V_13_2	1	Vietnam
927	V_7_1	V_13_2	1	Vietnam
928	V_7_2	V_13_2	1	Vietnam
929	V_7_3	V_13_2	1	Vietnam
930	V_8_2	V_13_2	1	Vietnam
931	V_9_1	V_13_2	0.78	Vietnam

932	V_9_2	V_13_2	1	Vietnam
933	V_9_4	V_13_2	0.99	Vietnam
934	V_10_1	V_13_2	0.92	Vietnam
935	V_11_1	V_13_2	1	Vietnam
936	V_11_3	V_13_2	1	Vietnam
937	V_12_1	V_13_2	1	Vietnam
938	V_13_2	V_13_2	0	Vietnam
939	V_14_1	V_13_2	-0.76	Vietnam
940	V_15_1	V_13_2	0.59	Vietnam
941	V_15_2	V_13_2	0.84	Vietnam
942	V_15_3	V_13_2	0.98	Vietnam
943	V_16_1	V_13_2	0.98	Vietnam
944	V_16_2	V_13_2	0.84	Vietnam
945	V_17_1	V_13_2	0.95	Vietnam
946	V_17_2	V_13_2	0.9	Vietnam
947	V_18_1	V_13_2	0.23	Vietnam
948	V_18_2	V_13_2	0.69	Vietnam
949	V_18_4	V_13_2	1	Vietnam
950	V_19_1	V_13_2	0.98	Vietnam
951	V_19_3	V_13_2	1	Vietnam
952	V_20_1	V_13_2	0.98	Vietnam
953	V_21_1	V_13_2	0.13	Vietnam
954	V_22_1	V_13_2	1	Vietnam
955	V_22_3	V_13_2	1	Vietnam
956	V_22_4	V_13_2	1	Vietnam
957	V_1_2	V_14_1	-0.29	Vietnam
958	V_2_2	V_14_1	1	Vietnam
959	V_3_1	V_14_1	1	Vietnam
960	V_3_2	V_14_1	1	Vietnam
961	V_5_3	V_14_1	1	Vietnam
962	V_6_1	V_14_1	1	Vietnam
963	V_6_2	V_14_1	0.23	Vietnam
964	V_6_3	V_14_1	1	Vietnam
965	V_7_1	V_14_1	1	Vietnam
966	V_7_2	V_14_1	1	Vietnam
967	V_7_3	V_14_1	1	Vietnam
968	V_8_2	V_14_1	1	Vietnam
969	V_9_1	V_14_1	0.82	Vietnam
970	V_9_2	V_14_1	1	Vietnam
971	V_9_4	V_14_1	0.95	Vietnam
972	V_10_1	V_14_1	0.92	Vietnam
973	V_11_1	V_14_1	1	Vietnam
974	V_11_3	V_14_1	1	Vietnam

975	V_12_1	V_14_1	1	Vietnam
976	V_13_2	V_14_1	-0.76	Vietnam
977	V_14_1	V_14_1	0	Vietnam
978	V_15_1	V_14_1	0.59	Vietnam
979	V_15_2	V_14_1	0.04	Vietnam
980	V_15_3	V_14_1	0.52	Vietnam
981	V_16_1	V_14_1	0.82	Vietnam
982	V_16_2	V_14_1	0.66	Vietnam
983	V_17_1	V_14_1	0.96	Vietnam
984	V_17_2	V_14_1	0.35	Vietnam
985	V_18_1	V_14_1	0.04	Vietnam
986	V_18_2	V_14_1	0.71	Vietnam
987	V_18_4	V_14_1	1	Vietnam
988	V_19_1	V_14_1	0.92	Vietnam
989	V_19_3	V_14_1	1	Vietnam
990	V_20_1	V_14_1	0.8	Vietnam
991	V_21_1	V_14_1	0.46	Vietnam
992	V_22_1	V_14_1	1	Vietnam
993	V_22_3	V_14_1	1	Vietnam
994	V_22_4	V_14_1	1	Vietnam
995	V_1_2	V_15_1	0.64	Vietnam
996	V_2_2	V_15_1	1	Vietnam
997	V_3_1	V_15_1	1	Vietnam
998	V_3_2	V_15_1	1	Vietnam
999	V_5_3	V_15_1	1	Vietnam
1000	V_6_1	V_15_1	1	Vietnam
1001	V_6_2	V_15_1	0.6	Vietnam
1002	V_6_3	V_15_1	1	Vietnam
1003	V_7_1	V_15_1	1	Vietnam
1004	V_7_2	V_15_1	1	Vietnam
1005	V_7_3	V_15_1	1	Vietnam
1006	V_8_2	V_15_1	1	Vietnam
1007	V_9_1	V_15_1	0.62	Vietnam
1008	V_9_2	V_15_1	1	Vietnam
1009	V_9_4	V_15_1	1	Vietnam
1010	V_10_1	V_15_1	0.48	Vietnam
1011	V_11_1	V_15_1	1	Vietnam
1012	V_11_3	V_15_1	1	Vietnam
1013	V_12_1	V_15_1	0.99	Vietnam
1014	V_13_2	V_15_1	0.59	Vietnam
1015	V_14_1	V_15_1	0.59	Vietnam
1016	V_15_1	V_15_1	0	Vietnam
1017	V_15_2	V_15_1	-0.42	Vietnam

1018	V_15_3	V_15_1	0.42	Vietnam
1019	V_16_1	V_15_1	0.94	Vietnam
1020	V_16_2	V_15_1	0.42	Vietnam
1021	V_17_1	V_15_1	0.59	Vietnam
1022	V_17_2	V_15_1	0.57	Vietnam
1023	V_18_1	V_15_1	-0.7	Vietnam
1024	V_18_2	V_15_1	-0.11	Vietnam
1025	V_18_4	V_15_1	1	Vietnam
1026	V_19_1	V_15_1	1	Vietnam
1027	V_19_3	V_15_1	1	Vietnam
1028	V_20_1	V_15_1	0.98	Vietnam
1029	V_21_1	V_15_1	0.85	Vietnam
1030	V_22_1	V_15_1	1	Vietnam
1031	V_22_3	V_15_1	1	Vietnam
1032	V_22_4	V_15_1	1	Vietnam
1033	V_1_2	V_15_2	0.36	Vietnam
1034	V_2_2	V_15_2	1	Vietnam
1035	V_3_1	V_15_2	1	Vietnam
1036	V_3_2	V_15_2	1	Vietnam
1037	V_5_3	V_15_2	1	Vietnam
1038	V_6_1	V_15_2	1	Vietnam
1039	V_6_2	V_15_2	0.79	Vietnam
1040	V_6_3	V_15_2	1	Vietnam
1041	V_7_1	V_15_2	1	Vietnam
1042	V_7_2	V_15_2	1	Vietnam
1043	V_7_3	V_15_2	1	Vietnam
1044	V_8_2	V_15_2	1	Vietnam
1045	V_9_1	V_15_2	0.79	Vietnam
1046	V_9_2	V_15_2	1	Vietnam
1047	V_9_4	V_15_2	1	Vietnam
1048	V_10_1	V_15_2	0.92	Vietnam
1049	V_11_1	V_15_2	1	Vietnam
1050	V_11_3	V_15_2	1	Vietnam
1051	V_12_1	V_15_2	0.99	Vietnam
1052	V_13_2	V_15_2	0.84	Vietnam
1053	V_14_1	V_15_2	0.04	Vietnam
1054	V_15_1	V_15_2	-0.42	Vietnam
1055	V_15_2	V_15_2	0	Vietnam
1056	V_15_3	V_15_2	-1	Vietnam
1057	V_16_1	V_15_2	0.99	Vietnam
1058	V_16_2	V_15_2	0.52	Vietnam
1059	V_17_1	V_15_2	0.88	Vietnam
1060	V_17_2	V_15_2	0.73	Vietnam

1061	V_18_1	V_15_2	-0.72	Vietnam
1062	V_18_2	V_15_2	0.04	Vietnam
1063	V_18_4	V_15_2	1	Vietnam
1064	V_19_1	V_15_2	1	Vietnam
1065	V_19_3	V_15_2	0.93	Vietnam
1066	V_20_1	V_15_2	0.99	Vietnam
1067	V_21_1	V_15_2	0.08	Vietnam
1068	V_22_1	V_15_2	1	Vietnam
1069	V_22_3	V_15_2	1	Vietnam
1070	V_22_4	V_15_2	1	Vietnam
1071	V_1_2	V_15_3	0.55	Vietnam
1072	V_2_2	V_15_3	1	Vietnam
1073	V_3_1	V_15_3	1	Vietnam
1074	V_3_2	V_15_3	1	Vietnam
1075	V_5_3	V_15_3	1	Vietnam
1076	V_6_1	V_15_3	1	Vietnam
1077	V_6_2	V_15_3	0.91	Vietnam
1078	V_6_3	V_15_3	1	Vietnam
1079	V_7_1	V_15_3	1	Vietnam
1080	V_7_2	V_15_3	1	Vietnam
1081	V_7_3	V_15_3	1	Vietnam
1082	V_8_2	V_15_3	1	Vietnam
1083	V_9_1	V_15_3	0.78	Vietnam
1084	V_9_2	V_15_3	1	Vietnam
1085	V_9_4	V_15_3	1	Vietnam
1086	V_10_1	V_15_3	0.93	Vietnam
1087	V_11_1	V_15_3	1	Vietnam
1088	V_11_3	V_15_3	1	Vietnam
1089	V_12_1	V_15_3	0.99	Vietnam
1090	V_13_2	V_15_3	0.98	Vietnam
1091	V_14_1	V_15_3	0.52	Vietnam
1092	V_15_1	V_15_3	0.42	Vietnam
1093	V_15_2	V_15_3	-1	Vietnam
1094	V_15_3	V_15_3	0	Vietnam
1095	V_16_1	V_15_3	0.96	Vietnam
1096	V_16_2	V_15_3	0.64	Vietnam
1097	V_17_1	V_15_3	0.92	Vietnam
1098	V_17_2	V_15_3	0.67	Vietnam
1099	V_18_1	V_15_3	-0.66	Vietnam
1100	V_18_2	V_15_3	0.14	Vietnam
1101	V_18_4	V_15_3	1	Vietnam
1102	V_19_1	V_15_3	1	Vietnam
1103	V_19_3	V_15_3	0.96	Vietnam

1104	V_20_1	V_15_3	0.99	Vietnam
1105	V_21_1	V_15_3	0.33	Vietnam
1106	V_22_1	V_15_3	1	Vietnam
1107	V_22_3	V_15_3	1	Vietnam
1108	V_22_4	V_15_3	1	Vietnam
1109	V_1_2	V_16_1	0.98	Vietnam
1110	V_2_2	V_16_1	1	Vietnam
1111	V_3_1	V_16_1	1	Vietnam
1112	V_3_2	V_16_1	1	Vietnam
1113	V_5_3	V_16_1	1	Vietnam
1114	V_6_1	V_16_1	1	Vietnam
1115	V_6_2	V_16_1	0.96	Vietnam
1116	V_6_3	V_16_1	1	Vietnam
1117	V_7_1	V_16_1	0.82	Vietnam
1118	V_7_2	V_16_1	1	Vietnam
1119	V_7_3	V_16_1	1	Vietnam
1120	V_8_2	V_16_1	1	Vietnam
1121	V_9_1	V_16_1	-1	Vietnam
1122	V_9_2	V_16_1	1	Vietnam
1123	V_9_4	V_16_1	1	Vietnam
1124	V_10_1	V_16_1	-1	Vietnam
1125	V_11_1	V_16_1	1	Vietnam
1126	V_11_3	V_16_1	1	Vietnam
1127	V_12_1	V_16_1	1	Vietnam
1128	V_13_2	V_16_1	0.98	Vietnam
1129	V_14_1	V_16_1	0.82	Vietnam
1130	V_15_1	V_16_1	0.94	Vietnam
1131	V_15_2	V_16_1	0.99	Vietnam
1132	V_15_3	V_16_1	0.96	Vietnam
1133	V_16_1	V_16_1	0	Vietnam
1134	V_16_2	V_16_1	-0.99	Vietnam
1135	V_17_1	V_16_1	-0.99	Vietnam
1136	V_17_2	V_16_1	-0.85	Vietnam
1137	V_18_1	V_16_1	-0.97	Vietnam
1138	V_18_2	V_16_1	-0.48	Vietnam
1139	V_18_4	V_16_1	1	Vietnam
1140	V_19_1	V_16_1	1	Vietnam
1141	V_19_3	V_16_1	1	Vietnam
1142	V_20_1	V_16_1	1	Vietnam
1143	V_21_1	V_16_1	0.99	Vietnam
1144	V_22_1	V_16_1	1	Vietnam
1145	V_22_3	V_16_1	1	Vietnam
1146	V_22_4	V_16_1	1	Vietnam

1147	V_1_2	V_16_2	0.92	Vietnam
1148	V_2_2	V_16_2	1	Vietnam
1149	V_3_1	V_16_2	1	Vietnam
1150	V_3_2	V_16_2	1	Vietnam
1151	V_5_3	V_16_2	1	Vietnam
1152	V_6_1	V_16_2	1	Vietnam
1153	V_6_2	V_16_2	0.91	Vietnam
1154	V_6_3	V_16_2	1	Vietnam
1155	V_7_1	V_16_2	0.87	Vietnam
1156	V_7_2	V_16_2	1	Vietnam
1157	V_7_3	V_16_2	1	Vietnam
1158	V_8_2	V_16_2	1	Vietnam
1159	V_9_1	V_16_2	-0.54	Vietnam
1160	V_9_2	V_16_2	1	Vietnam
1161	V_9_4	V_16_2	1	Vietnam
1162	V_10_1	V_16_2	-0.7	Vietnam
1163	V_11_1	V_16_2	1	Vietnam
1164	V_11_3	V_16_2	1	Vietnam
1165	V_12_1	V_16_2	1	Vietnam
1166	V_13_2	V_16_2	0.84	Vietnam
1167	V_14_1	V_16_2	0.66	Vietnam
1168	V_15_1	V_16_2	0.42	Vietnam
1169	V_15_2	V_16_2	0.52	Vietnam
1170	V_15_3	V_16_2	0.64	Vietnam
1171	V_16_1	V_16_2	-0.99	Vietnam
1172	V_16_2	V_16_2	0	Vietnam
1173	V_17_1	V_16_2	-0.37	Vietnam
1174	V_17_2	V_16_2	-0.98	Vietnam
1175	V_18_1	V_16_2	-0.97	Vietnam
1176	V_18_2	V_16_2	-0.33	Vietnam
1177	V_18_4	V_16_2	1	Vietnam
1178	V_19_1	V_16_2	1	Vietnam
1179	V_19_3	V_16_2	1	Vietnam
1180	V_20_1	V_16_2	1	Vietnam
1181	V_21_1	V_16_2	0.98	Vietnam
1182	V_22_1	V_16_2	1	Vietnam
1183	V_22_3	V_16_2	1	Vietnam
1184	V_22_4	V_16_2	1	Vietnam
1185	V_1_2	V_17_1	1	Vietnam
1186	V_2_2	V_17_1	1	Vietnam
1187	V_3_1	V_17_1	1	Vietnam
1188	V_3_2	V_17_1	1	Vietnam
1189	V_5_3	V_17_1	1	Vietnam

1190	V_6_1	V_17_1	1	Vietnam
1191	V_6_2	V_17_1	0.94	Vietnam
1192	V_6_3	V_17_1	1	Vietnam
1193	V_7_1	V_17_1	0.36	Vietnam
1194	V_7_2	V_17_1	1	Vietnam
1195	V_7_3	V_17_1	1	Vietnam
1196	V_8_2	V_17_1	1	Vietnam
1197	V_9_1	V_17_1	-1	Vietnam
1198	V_9_2	V_17_1	1	Vietnam
1199	V_9_4	V_17_1	1	Vietnam
1200	V_10_1	V_17_1	-0.93	Vietnam
1201	V_11_1	V_17_1	1	Vietnam
1202	V_11_3	V_17_1	1	Vietnam
1203	V_12_1	V_17_1	1	Vietnam
1204	V_13_2	V_17_1	0.95	Vietnam
1205	V_14_1	V_17_1	0.96	Vietnam
1206	V_15_1	V_17_1	0.59	Vietnam
1207	V_15_2	V_17_1	0.88	Vietnam
1208	V_15_3	V_17_1	0.92	Vietnam
1209	V_16_1	V_17_1	-0.99	Vietnam
1210	V_16_2	V_17_1	-0.37	Vietnam
1211	V_17_1	V_17_1	0	Vietnam
1212	V_17_2	V_17_1	-0.47	Vietnam
1213	V_18_1	V_17_1	-0.61	Vietnam
1214	V_18_2	V_17_1	0.03	Vietnam
1215	V_18_4	V_17_1	1	Vietnam
1216	V_19_1	V_17_1	1	Vietnam
1217	V_19_3	V_17_1	1	Vietnam
1218	V_20_1	V_17_1	0.9	Vietnam
1219	V_21_1	V_17_1	1	Vietnam
1220	V_22_1	V_17_1	1	Vietnam
1221	V_22_3	V_17_1	1	Vietnam
1222	V_22_4	V_17_1	1	Vietnam
1223	V_1_2	V_17_2	0.89	Vietnam
1224	V_2_2	V_17_2	1	Vietnam
1225	V_3_1	V_17_2	1	Vietnam
1226	V_3_2	V_17_2	1	Vietnam
1227	V_5_3	V_17_2	1	Vietnam
1228	V_6_1	V_17_2	1	Vietnam
1229	V_6_2	V_17_2	0.93	Vietnam
1230	V_6_3	V_17_2	1	Vietnam
1231	V_7_1	V_17_2	0.7	Vietnam
1232	V_7_2	V_17_2	1	Vietnam

1233	V_7_3	V_17_2	1	Vietnam
1234	V_8_2	V_17_2	1	Vietnam
1235	V_9_1	V_17_2	-0.41	Vietnam
1236	V_9_2	V_17_2	1	Vietnam
1237	V_9_4	V_17_2	1	Vietnam
1238	V_10_1	V_17_2	-0.77	Vietnam
1239	V_11_1	V_17_2	1	Vietnam
1240	V_11_3	V_17_2	1	Vietnam
1241	V_12_1	V_17_2	1	Vietnam
1242	V_13_2	V_17_2	0.9	Vietnam
1243	V_14_1	V_17_2	0.35	Vietnam
1244	V_15_1	V_17_2	0.57	Vietnam
1245	V_15_2	V_17_2	0.73	Vietnam
1246	V_15_3	V_17_2	0.67	Vietnam
1247	V_16_1	V_17_2	-0.85	Vietnam
1248	V_16_2	V_17_2	-0.98	Vietnam
1249	V_17_1	V_17_2	-0.47	Vietnam
1250	V_17_2	V_17_2	0	Vietnam
1251	V_18_1	V_17_2	-0.96	Vietnam
1252	V_18_2	V_17_2	-0.54	Vietnam
1253	V_18_4	V_17_2	1	Vietnam
1254	V_19_1	V_17_2	1	Vietnam
1255	V_19_3	V_17_2	1	Vietnam
1256	V_20_1	V_17_2	0.92	Vietnam
1257	V_21_1	V_17_2	0.98	Vietnam
1258	V_22_1	V_17_2	1	Vietnam
1259	V_22_3	V_17_2	1	Vietnam
1260	V_22_4	V_17_2	1	Vietnam
1261	V_1_2	V_18_1	0.47	Vietnam
1262	V_2_2	V_18_1	1	Vietnam
1263	V_3_1	V_18_1	1	Vietnam
1264	V_3_2	V_18_1	1	Vietnam
1265	V_5_3	V_18_1	0.98	Vietnam
1266	V_6_1	V_18_1	1	Vietnam
1267	V_6_2	V_18_1	-0.52	Vietnam
1268	V_6_3	V_18_1	1	Vietnam
1269	V_7_1	V_18_1	0.4	Vietnam
1270	V_7_2	V_18_1	1	Vietnam
1271	V_7_3	V_18_1	1	Vietnam
1272	V_8_2	V_18_1	1	Vietnam
1273	V_9_1	V_18_1	-0.6	Vietnam
1274	V_9_2	V_18_1	1	Vietnam
1275	V_9_4	V_18_1	1	Vietnam

1276	V_10_1	V_18_1	-0.72	Vietnam
1277	V_11_1	V_18_1	1	Vietnam
1278	V_11_3	V_18_1	1	Vietnam
1279	V_12_1	V_18_1	0.88	Vietnam
1280	V_13_2	V_18_1	0.23	Vietnam
1281	V_14_1	V_18_1	0.04	Vietnam
1282	V_15_1	V_18_1	-0.7	Vietnam
1283	V_15_2	V_18_1	-0.72	Vietnam
1284	V_15_3	V_18_1	-0.66	Vietnam
1285	V_16_1	V_18_1	-0.97	Vietnam
1286	V_16_2	V_18_1	-0.97	Vietnam
1287	V_17_1	V_18_1	-0.61	Vietnam
1288	V_17_2	V_18_1	-0.96	Vietnam
1289	V_18_1	V_18_1	0	Vietnam
1290	V_18_2	V_18_1	-1	Vietnam
1291	V_18_4	V_18_1	0.98	Vietnam
1292	V_19_1	V_18_1	1	Vietnam
1293	V_19_3	V_18_1	0.99	Vietnam
1294	V_20_1	V_18_1	0.76	Vietnam
1295	V_21_1	V_18_1	0.28	Vietnam
1296	V_22_1	V_18_1	1	Vietnam
1297	V_22_3	V_18_1	1	Vietnam
1298	V_22_4	V_18_1	1	Vietnam
1299	V_1_2	V_18_2	0.81	Vietnam
1300	V_2_2	V_18_2	1	Vietnam
1301	V_3_1	V_18_2	1	Vietnam
1302	V_3_2	V_18_2	1	Vietnam
1303	V_5_3	V_18_2	1	Vietnam
1304	V_6_1	V_18_2	1	Vietnam
1305	V_6_2	V_18_2	-0.65	Vietnam
1306	V_6_3	V_18_2	1	Vietnam
1307	V_7_1	V_18_2	0.91	Vietnam
1308	V_7_2	V_18_2	1	Vietnam
1309	V_7_3	V_18_2	1	Vietnam
1310	V_8_2	V_18_2	1	Vietnam
1311	V_9_1	V_18_2	-0.15	Vietnam
1312	V_9_2	V_18_2	1	Vietnam
1313	V_9_4	V_18_2	1	Vietnam
1314	V_10_1	V_18_2	0.18	Vietnam
1315	V_11_1	V_18_2	1	Vietnam
1316	V_11_3	V_18_2	1	Vietnam
1317	V_12_1	V_18_2	0.96	Vietnam
1318	V_13_2	V_18_2	0.69	Vietnam

1319	V_14_1	V_18_2	0.71	Vietnam
1320	V_15_1	V_18_2	-0.11	Vietnam
1321	V_15_2	V_18_2	0.04	Vietnam
1322	V_15_3	V_18_2	0.14	Vietnam
1323	V_16_1	V_18_2	-0.48	Vietnam
1324	V_16_2	V_18_2	-0.33	Vietnam
1325	V_17_1	V_18_2	0.03	Vietnam
1326	V_17_2	V_18_2	-0.54	Vietnam
1327	V_18_1	V_18_2	-1	Vietnam
1328	V_18_2	V_18_2	0	Vietnam
1329	V_18_4	V_18_2	1	Vietnam
1330	V_19_1	V_18_2	1	Vietnam
1331	V_19_3	V_18_2	1	Vietnam
1332	V_20_1	V_18_2	0.96	Vietnam
1333	V_21_1	V_18_2	0.63	Vietnam
1334	V_22_1	V_18_2	1	Vietnam
1335	V_22_3	V_18_2	1	Vietnam
1336	V_22_4	V_18_2	1	Vietnam
1337	V_1_2	V_18_4	0.99	Vietnam
1338	V_2_2	V_18_4	1	Vietnam
1339	V_3_1	V_18_4	1	Vietnam
1340	V_3_2	V_18_4	1	Vietnam
1341	V_5_3	V_18_4	1	Vietnam
1342	V_6_1	V_18_4	1	Vietnam
1343	V_6_2	V_18_4	1	Vietnam
1344	V_6_3	V_18_4	1	Vietnam
1345	V_7_1	V_18_4	1	Vietnam
1346	V_7_2	V_18_4	1	Vietnam
1347	V_7_3	V_18_4	1	Vietnam
1348	V_8_2	V_18_4	0.99	Vietnam
1349	V_9_1	V_18_4	1	Vietnam
1350	V_9_2	V_18_4	1	Vietnam
1351	V_9_4	V_18_4	1	Vietnam
1352	V_10_1	V_18_4	1	Vietnam
1353	V_11_1	V_18_4	1	Vietnam
1354	V_11_3	V_18_4	1	Vietnam
1355	V_12_1	V_18_4	1	Vietnam
1356	V_13_2	V_18_4	1	Vietnam
1357	V_14_1	V_18_4	1	Vietnam
1358	V_15_1	V_18_4	1	Vietnam
1359	V_15_2	V_18_4	1	Vietnam
1360	V_15_3	V_18_4	1	Vietnam
1361	V_16_1	V_18_4	1	Vietnam

1362	V_16_2	V_18_4	1	Vietnam
1363	V_17_1	V_18_4	1	Vietnam
1364	V_17_2	V_18_4	1	Vietnam
1365	V_18_1	V_18_4	0.98	Vietnam
1366	V_18_2	V_18_4	1	Vietnam
1367	V_18_4	V_18_4	0	Vietnam
1368	V_19_1	V_18_4	1	Vietnam
1369	V_19_3	V_18_4	0.21	Vietnam
1370	V_20_1	V_18_4	1	Vietnam
1371	V_21_1	V_18_4	0.99	Vietnam
1372	V_22_1	V_18_4	1	Vietnam
1373	V_22_3	V_18_4	1	Vietnam
1374	V_22_4	V_18_4	1	Vietnam
1375	V_1_2	V_19_1	0.99	Vietnam
1376	V_2_2	V_19_1	1	Vietnam
1377	V_3_1	V_19_1	1	Vietnam
1378	V_3_2	V_19_1	1	Vietnam
1379	V_5_3	V_19_1	1	Vietnam
1380	V_6_1	V_19_1	1	Vietnam
1381	V_6_2	V_19_1	1	Vietnam
1382	V_6_3	V_19_1	1	Vietnam
1383	V_7_1	V_19_1	1	Vietnam
1384	V_7_2	V_19_1	1	Vietnam
1385	V_7_3	V_19_1	1	Vietnam
1386	V_8_2	V_19_1	1	Vietnam
1387	V_9_1	V_19_1	1	Vietnam
1388	V_9_2	V_19_1	1	Vietnam
1389	V_9_4	V_19_1	1	Vietnam
1390	V_10_1	V_19_1	1	Vietnam
1391	V_11_1	V_19_1	1	Vietnam
1392	V_11_3	V_19_1	1	Vietnam
1393	V_12_1	V_19_1	1	Vietnam
1394	V_13_2	V_19_1	0.98	Vietnam
1395	V_14_1	V_19_1	0.92	Vietnam
1396	V_15_1	V_19_1	1	Vietnam
1397	V_15_2	V_19_1	1	Vietnam
1398	V_15_3	V_19_1	1	Vietnam
1399	V_16_1	V_19_1	1	Vietnam
1400	V_16_2	V_19_1	1	Vietnam
1401	V_17_1	V_19_1	1	Vietnam
1402	V_17_2	V_19_1	1	Vietnam
1403	V_18_1	V_19_1	1	Vietnam
1404	V_18_2	V_19_1	1	Vietnam

1405	V_18_4	V_19_1	1	Vietnam
1406	V_19_1	V_19_1	0	Vietnam
1407	V_19_3	V_19_1	1	Vietnam
1408	V_20_1	V_19_1	0.36	Vietnam
1409	V_21_1	V_19_1	0.93	Vietnam
1410	V_22_1	V_19_1	1	Vietnam
1411	V_22_3	V_19_1	1	Vietnam
1412	V_22_4	V_19_1	1	Vietnam
1413	V_1_2	V_19_3	0.99	Vietnam
1414	V_2_2	V_19_3	1	Vietnam
1415	V_3_1	V_19_3	1	Vietnam
1416	V_3_2	V_19_3	1	Vietnam
1417	V_5_3	V_19_3	0.99	Vietnam
1418	V_6_1	V_19_3	1	Vietnam
1419	V_6_2	V_19_3	1	Vietnam
1420	V_6_3	V_19_3	1	Vietnam
1421	V_7_1	V_19_3	1	Vietnam
1422	V_7_2	V_19_3	1	Vietnam
1423	V_7_3	V_19_3	1	Vietnam
1424	V_8_2	V_19_3	0.53	Vietnam
1425	V_9_1	V_19_3	1	Vietnam
1426	V_9_2	V_19_3	1	Vietnam
1427	V_9_4	V_19_3	1	Vietnam
1428	V_10_1	V_19_3	1	Vietnam
1429	V_11_1	V_19_3	1	Vietnam
1430	V_11_3	V_19_3	1	Vietnam
1431	V_12_1	V_19_3	1	Vietnam
1432	V_13_2	V_19_3	1	Vietnam
1433	V_14_1	V_19_3	1	Vietnam
1434	V_15_1	V_19_3	1	Vietnam
1435	V_15_2	V_19_3	0.93	Vietnam
1436	V_15_3	V_19_3	0.96	Vietnam
1437	V_16_1	V_19_3	1	Vietnam
1438	V_16_2	V_19_3	1	Vietnam
1439	V_17_1	V_19_3	1	Vietnam
1440	V_17_2	V_19_3	1	Vietnam
1441	V_18_1	V_19_3	0.99	Vietnam
1442	V_18_2	V_19_3	1	Vietnam
1443	V_18_4	V_19_3	0.21	Vietnam
1444	V_19_1	V_19_3	1	Vietnam
1445	V_19_3	V_19_3	0	Vietnam
1446	V_20_1	V_19_3	1	Vietnam
1447	V_21_1	V_19_3	0.29	Vietnam

1448	V_22_1	V_19_3	1	Vietnam
1449	V_22_3	V_19_3	0.88	Vietnam
1450	V_22_4	V_19_3	1	Vietnam
1451	V_1_2	V_20_1	0.98	Vietnam
1452	V_2_2	V_20_1	1	Vietnam
1453	V_3_1	V_20_1	1	Vietnam
1454	V_3_2	V_20_1	1	Vietnam
1455	V_5_3	V_20_1	1	Vietnam
1456	V_6_1	V_20_1	1	Vietnam
1457	V_6_2	V_20_1	1	Vietnam
1458	V_6_3	V_20_1	1	Vietnam
1459	V_7_1	V_20_1	1	Vietnam
1460	V_7_2	V_20_1	1	Vietnam
1461	V_7_3	V_20_1	1	Vietnam
1462	V_8_2	V_20_1	1	Vietnam
1463	V_9_1	V_20_1	0.99	Vietnam
1464	V_9_2	V_20_1	1	Vietnam
1465	V_9_4	V_20_1	1	Vietnam
1466	V_10_1	V_20_1	0.94	Vietnam
1467	V_11_1	V_20_1	1	Vietnam
1468	V_11_3	V_20_1	1	Vietnam
1469	V_12_1	V_20_1	1	Vietnam
1470	V_13_2	V_20_1	0.98	Vietnam
1471	V_14_1	V_20_1	0.8	Vietnam
1472	V_15_1	V_20_1	0.98	Vietnam
1473	V_15_2	V_20_1	0.99	Vietnam
1474	V_15_3	V_20_1	0.99	Vietnam
1475	V_16_1	V_20_1	1	Vietnam
1476	V_16_2	V_20_1	1	Vietnam
1477	V_17_1	V_20_1	0.9	Vietnam
1478	V_17_2	V_20_1	0.92	Vietnam
1479	V_18_1	V_20_1	0.76	Vietnam
1480	V_18_2	V_20_1	0.96	Vietnam
1481	V_18_4	V_20_1	1	Vietnam
1482	V_19_1	V_20_1	0.36	Vietnam
1483	V_19_3	V_20_1	1	Vietnam
1484	V_20_1	V_20_1	0	Vietnam
1485	V_21_1	V_20_1	1	Vietnam
1486	V_22_1	V_20_1	1	Vietnam
1487	V_22_3	V_20_1	1	Vietnam
1488	V_22_4	V_20_1	1	Vietnam
1489	V_1_2	V_21_1	0.74	Vietnam
1490	V_2_2	V_21_1	1	Vietnam

1491	V_3_1	V_21_1	1	Vietnam
1492	V_3_2	V_21_1	1	Vietnam
1493	V_5_3	V_21_1	0.35	Vietnam
1494	V_6_1	V_21_1	0.97	Vietnam
1495	V_6_2	V_21_1	0.26	Vietnam
1496	V_6_3	V_21_1	0.98	Vietnam
1497	V_7_1	V_21_1	1	Vietnam
1498	V_7_2	V_21_1	1	Vietnam
1499	V_7_3	V_21_1	1	Vietnam
1500	V_8_2	V_21_1	0.91	Vietnam
1501	V_9_1	V_21_1	0.98	Vietnam
1502	V_9_2	V_21_1	1	Vietnam
1503	V_9_4	V_21_1	1	Vietnam
1504	V_10_1	V_21_1	1	Vietnam
1505	V_11_1	V_21_1	0.99	Vietnam
1506	V_11_3	V_21_1	0.77	Vietnam
1507	V_12_1	V_21_1	0.55	Vietnam
1508	V_13_2	V_21_1	0.13	Vietnam
1509	V_14_1	V_21_1	0.46	Vietnam
1510	V_15_1	V_21_1	0.85	Vietnam
1511	V_15_2	V_21_1	0.08	Vietnam
1512	V_15_3	V_21_1	0.33	Vietnam
1513	V_16_1	V_21_1	0.99	Vietnam
1514	V_16_2	V_21_1	0.98	Vietnam
1515	V_17_1	V_21_1	1	Vietnam
1516	V_17_2	V_21_1	0.98	Vietnam
1517	V_18_1	V_21_1	0.28	Vietnam
1518	V_18_2	V_21_1	0.63	Vietnam
1519	V_18_4	V_21_1	0.99	Vietnam
1520	V_19_1	V_21_1	0.93	Vietnam
1521	V_19_3	V_21_1	0.29	Vietnam
1522	V_20_1	V_21_1	1	Vietnam
1523	V_21_1	V_21_1	0	Vietnam
1524	V_22_1	V_21_1	1	Vietnam
1525	V_22_3	V_21_1	0.99	Vietnam
1526	V_22_4	V_21_1	1	Vietnam
1527	V_1_2	V_22_1	1	Vietnam
1528	V_2_2	V_22_1	1	Vietnam
1529	V_3_1	V_22_1	1	Vietnam
1530	V_3_2	V_22_1	1	Vietnam
1531	V_5_3	V_22_1	1	Vietnam
1532	V_6_1	V_22_1	1	Vietnam
1533	V_6_2	V_22_1	1	Vietnam

1534	V_6_3	V_22_1	1	Vietnam
1535	V_7_1	V_22_1	1	Vietnam
1536	V_7_2	V_22_1	1	Vietnam
1537	V_7_3	V_22_1	1	Vietnam
1538	V_8_2	V_22_1	1	Vietnam
1539	V_9_1	V_22_1	1	Vietnam
1540	V_9_2	V_22_1	1	Vietnam
1541	V_9_4	V_22_1	1	Vietnam
1542	V_10_1	V_22_1	1	Vietnam
1543	V_11_1	V_22_1	1	Vietnam
1544	V_11_3	V_22_1	1	Vietnam
1545	V_12_1	V_22_1	1	Vietnam
1546	V_13_2	V_22_1	1	Vietnam
1547	V_14_1	V_22_1	1	Vietnam
1548	V_15_1	V_22_1	1	Vietnam
1549	V_15_2	V_22_1	1	Vietnam
1550	V_15_3	V_22_1	1	Vietnam
1551	V_16_1	V_22_1	1	Vietnam
1552	V_16_2	V_22_1	1	Vietnam
1553	V_17_1	V_22_1	1	Vietnam
1554	V_17_2	V_22_1	1	Vietnam
1555	V_18_1	V_22_1	1	Vietnam
1556	V_18_2	V_22_1	1	Vietnam
1557	V_18_4	V_22_1	1	Vietnam
1558	V_19_1	V_22_1	1	Vietnam
1559	V_19_3	V_22_1	1	Vietnam
1560	V_20_1	V_22_1	1	Vietnam
1561	V_21_1	V_22_1	1	Vietnam
1562	V_22_1	V_22_1	0	Vietnam
1563	V_22_3	V_22_1	0.61	Vietnam
1564	V_22_4	V_22_1	1	Vietnam
1565	V_1_2	V_22_3	1	Vietnam
1566	V_2_2	V_22_3	1	Vietnam
1567	V_3_1	V_22_3	1	Vietnam
1568	V_3_2	V_22_3	1	Vietnam
1569	V_5_3	V_22_3	1	Vietnam
1570	V_6_1	V_22_3	1	Vietnam
1571	V_6_2	V_22_3	1	Vietnam
1572	V_6_3	V_22_3	1	Vietnam
1573	V_7_1	V_22_3	1	Vietnam
1574	V_7_2	V_22_3	1	Vietnam
1575	V_7_3	V_22_3	1	Vietnam
1576	V_8_2	V_22_3	0.98	Vietnam

1577	V_9_1	V_22_3	1	Vietnam
1578	V_9_2	V_22_3	1	Vietnam
1579	V_9_4	V_22_3	1	Vietnam
1580	V_10_1	V_22_3	1	Vietnam
1581	V_11_1	V_22_3	1	Vietnam
1582	V_11_3	V_22_3	1	Vietnam
1583	V_12_1	V_22_3	1	Vietnam
1584	V_13_2	V_22_3	1	Vietnam
1585	V_14_1	V_22_3	1	Vietnam
1586	V_15_1	V_22_3	1	Vietnam
1587	V_15_2	V_22_3	1	Vietnam
1588	V_15_3	V_22_3	1	Vietnam
1589	V_16_1	V_22_3	1	Vietnam
1590	V_16_2	V_22_3	1	Vietnam
1591	V_17_1	V_22_3	1	Vietnam
1592	V_17_2	V_22_3	1	Vietnam
1593	V_18_1	V_22_3	1	Vietnam
1594	V_18_2	V_22_3	1	Vietnam
1595	V_18_4	V_22_3	1	Vietnam
1596	V_19_1	V_22_3	1	Vietnam
1597	V_19_3	V_22_3	0.88	Vietnam
1598	V_20_1	V_22_3	1	Vietnam
1599	V_21_1	V_22_3	0.99	Vietnam
1600	V_22_1	V_22_3	0.61	Vietnam
1601	V_22_3	V_22_3	0	Vietnam
1602	V_22_4	V_22_3	0.99	Vietnam
1603	V_1_2	V_22_4	1	Vietnam
1604	V_2_2	V_22_4	1	Vietnam
1605	V_3_1	V_22_4	1	Vietnam
1606	V_3_2	V_22_4	1	Vietnam
1607	V_5_3	V_22_4	1	Vietnam
1608	V_6_1	V_22_4	1	Vietnam
1609	V_6_2	V_22_4	1	Vietnam
1610	V_6_3	V_22_4	1	Vietnam
1611	V_7_1	V_22_4	1	Vietnam
1612	V_7_2	V_22_4	1	Vietnam
1613	V_7_3	V_22_4	1	Vietnam
1614	V_8_2	V_22_4	1	Vietnam
1615	V_9_1	V_22_4	1	Vietnam
1616	V_9_2	V_22_4	0.99	Vietnam
1617	V_9_4	V_22_4	1	Vietnam
1618	V_10_1	V_22_4	1	Vietnam
1619	V_11_1	V_22_4	1	Vietnam

1620	V_11_3	V_22_4	1	Vietnam
1621	V_12_1	V_22_4	1	Vietnam
1622	V_13_2	V_22_4	1	Vietnam
1623	V_14_1	V_22_4	1	Vietnam
1624	V_15_1	V_22_4	1	Vietnam
1625	V_15_2	V_22_4	1	Vietnam
1626	V_15_3	V_22_4	1	Vietnam
1627	V_16_1	V_22_4	1	Vietnam
1628	V_16_2	V_22_4	1	Vietnam
1629	V_17_1	V_22_4	1	Vietnam
1630	V_17_2	V_22_4	1	Vietnam
1631	V_18_1	V_22_4	1	Vietnam
1632	V_18_2	V_22_4	1	Vietnam
1633	V_18_4	V_22_4	1	Vietnam
1634	V_19_1	V_22_4	1	Vietnam
1635	V_19_3	V_22_4	1	Vietnam
1636	V_20_1	V_22_4	1	Vietnam
1637	V_21_1	V_22_4	1	Vietnam
1638	V_22_1	V_22_4	1	Vietnam
1639	V_22_3	V_22_4	0.99	Vietnam
1640	V_22_4	V_22_4	0	Vietnam

Table 8：pairwise RC value of hypothesis 1.

	Var1	Var2	value	Groups
1	T_4_4	T_4_4	0	4
2	T_9_4	T_4_4	1	4
3	V_9_4	T_4_4	1	4
4	V_18_4	T_4_4	1	4
5	V_22_4	T_4_4	1	4
6	T_4_4	T_9_4	1	4
7	T_9_4	T_9_4	0	4
8	V_9_4	T_9_4	1	4
9	V_18_4	T_9_4	1	4
10	V_22_4	T_9_4	1	4
11	T_4_4	V_9_4	1	4
12	T_9_4	V_9_4	1	4
13	V_9_4	V_9_4	0	4
14	V_18_4	V_9_4	0.99	4
15	V_22_4	V_9_4	1	4
16	T_4_4	V_18_4	1	4
17	T_9_4	V_18_4	1	4
18	V_9_4	V_18_4	0.99	4
19	V_18_4	V_18_4	0	4

20	V_22_4	V_18_4	1	4
21	T_4_4	V_22_4	1	4
22	T_9_4	V_22_4	1	4
23	V_9_4	V_22_4	1	4
24	V_18_4	V_22_4	1	4
25	V_22_4	V_22_4	0	4
26	T_2_3	T_2_3	0	3
27	T_4_3	T_2_3	0.63	3
28	T_5_3	T_2_3	-0.38	3
29	V_5_3	T_2_3	1	3
30	V_6_3	T_2_3	1	3
31	V_7_3	T_2_3	1	3
32	V_11_3	T_2_3	1	3
33	V_15_3	T_2_3	1	3
34	V_19_3	T_2_3	1	3
35	V_22_3	T_2_3	1	3
36	T_2_3	T_4_3	0.63	3
37	T_4_3	T_4_3	0	3
38	T_5_3	T_4_3	-0.63	3
39	V_5_3	T_4_3	0.99	3
40	V_6_3	T_4_3	0.91	3
41	V_7_3	T_4_3	0.98	3
42	V_11_3	T_4_3	0.96	3
43	V_15_3	T_4_3	0.95	3
44	V_19_3	T_4_3	0.98	3
45	V_22_3	T_4_3	0.91	3
46	T_2_3	T_5_3	-0.38	3
47	T_4_3	T_5_3	-0.63	3
48	T_5_3	T_5_3	0	3
49	V_5_3	T_5_3	1	3
50	V_6_3	T_5_3	1	3
51	V_7_3	T_5_3	1	3
52	V_11_3	T_5_3	1	3
53	V_15_3	T_5_3	1	3
54	V_19_3	T_5_3	1	3
55	V_22_3	T_5_3	1	3
56	T_2_3	V_5_3	1	3
57	T_4_3	V_5_3	0.99	3
58	T_5_3	V_5_3	1	3
59	V_5_3	V_5_3	0	3
60	V_6_3	V_5_3	1	3
61	V_7_3	V_5_3	1	3
62	V_11_3	V_5_3	0.89	3

63	V_15_3	V_5_3	1	3
64	V_19_3	V_5_3	0.62	3
65	V_22_3	V_5_3	0.97	3
66	T_2_3	V_6_3	1	3
67	T_4_3	V_6_3	0.91	3
68	T_5_3	V_6_3	1	3
69	V_5_3	V_6_3	1	3
70	V_6_3	V_6_3	0	3
71	V_7_3	V_6_3	1	3
72	V_11_3	V_6_3	1	3
73	V_15_3	V_6_3	0.99	3
74	V_19_3	V_6_3	0.92	3
75	V_22_3	V_6_3	0.98	3
76	T_2_3	V_7_3	1	3
77	T_4_3	V_7_3	0.98	3
78	T_5_3	V_7_3	1	3
79	V_5_3	V_7_3	1	3
80	V_6_3	V_7_3	1	3
81	V_7_3	V_7_3	0	3
82	V_11_3	V_7_3	1	3
83	V_15_3	V_7_3	1	3
84	V_19_3	V_7_3	1	3
85	V_22_3	V_7_3	1	3
86	T_2_3	V_11_3	1	3
87	T_4_3	V_11_3	0.96	3
88	T_5_3	V_11_3	1	3
89	V_5_3	V_11_3	0.89	3
90	V_6_3	V_11_3	1	3
91	V_7_3	V_11_3	1	3
92	V_11_3	V_11_3	0	3
93	V_15_3	V_11_3	1	3
94	V_19_3	V_11_3	1	3
95	V_22_3	V_11_3	1	3
96	T_2_3	V_15_3	1	3
97	T_4_3	V_15_3	0.95	3
98	T_5_3	V_15_3	1	3
99	V_5_3	V_15_3	1	3
100	V_6_3	V_15_3	0.99	3
101	V_7_3	V_15_3	1	3
102	V_11_3	V_15_3	1	3
103	V_15_3	V_15_3	0	3
104	V_19_3	V_15_3	0.61	3
105	V_22_3	V_15_3	0.95	3

106	T_2_3	V_19_3	1	3
107	T_4_3	V_19_3	0.98	3
108	T_5_3	V_19_3	1	3
109	V_5_3	V_19_3	0.62	3
110	V_6_3	V_19_3	0.92	3
111	V_7_3	V_19_3	1	3
112	V_11_3	V_19_3	1	3
113	V_15_3	V_19_3	0.61	3
114	V_19_3	V_19_3	0	3
115	V_22_3	V_19_3	0.44	3
116	T_2_3	V_22_3	1	3
117	T_4_3	V_22_3	0.91	3
118	T_5_3	V_22_3	1	3
119	V_5_3	V_22_3	0.97	3
120	V_6_3	V_22_3	0.98	3
121	V_7_3	V_22_3	1	3
122	V_11_3	V_22_3	1	3
123	V_15_3	V_22_3	0.95	3
124	V_19_3	V_22_3	0.44	3
125	V_22_3	V_22_3	0	3
126	T_2_2	T_2_2	0	2
127	T_5_2	T_2_2	0.15	2
128	T_9_2	T_2_2	1	2
129	V_1_2	T_2_2	0.99	2
130	V_2_2	T_2_2	1	2
131	V_3_2	T_2_2	1	2
132	V_6_2	T_2_2	1	2
133	V_7_2	T_2_2	1	2
134	V_8_2	T_2_2	1	2
135	V_9_2	T_2_2	1	2
136	V_13_2	T_2_2	0.99	2
137	V_15_2	T_2_2	0.99	2
138	V_16_2	T_2_2	0.05	2
139	V_17_2	T_2_2	0.82	2
140	V_18_2	T_2_2	0.85	2
141	T_2_2	T_5_2	0.15	2
142	T_5_2	T_5_2	0	2
143	T_9_2	T_5_2	0.48	2
144	V_1_2	T_5_2	1	2
145	V_2_2	T_5_2	1	2
146	V_3_2	T_5_2	1	2
147	V_6_2	T_5_2	1	2
148	V_7_2	T_5_2	1	2

149	V_8_2	T_5_2	1	2
150	V_9_2	T_5_2	1	2
151	V_13_2	T_5_2	1	2
152	V_15_2	T_5_2	1	2
153	V_16_2	T_5_2	0.93	2
154	V_17_2	T_5_2	1	2
155	V_18_2	T_5_2	0.96	2
156	T_2_2	T_9_2	1	2
157	T_5_2	T_9_2	0.48	2
158	T_9_2	T_9_2	0	2
159	V_1_2	T_9_2	1	2
160	V_2_2	T_9_2	1	2
161	V_3_2	T_9_2	1	2
162	V_6_2	T_9_2	1	2
163	V_7_2	T_9_2	1	2
164	V_8_2	T_9_2	1	2
165	V_9_2	T_9_2	1	2
166	V_13_2	T_9_2	1	2
167	V_15_2	T_9_2	1	2
168	V_16_2	T_9_2	1	2
169	V_17_2	T_9_2	1	2
170	V_18_2	T_9_2	1	2
171	T_2_2	V_1_2	0.99	2
172	T_5_2	V_1_2	1	2
173	T_9_2	V_1_2	1	2
174	V_1_2	V_1_2	0	2
175	V_2_2	V_1_2	1	2
176	V_3_2	V_1_2	1	2
177	V_6_2	V_1_2	0.5	2
178	V_7_2	V_1_2	1	2
179	V_8_2	V_1_2	1	2
180	V_9_2	V_1_2	1	2
181	V_13_2	V_1_2	0.4	2
182	V_15_2	V_1_2	0.05	2
183	V_16_2	V_1_2	0.82	2
184	V_17_2	V_1_2	0.75	2
185	V_18_2	V_1_2	0.57	2
186	T_2_2	V_2_2	1	2
187	T_5_2	V_2_2	1	2
188	T_9_2	V_2_2	1	2
189	V_1_2	V_2_2	1	2
190	V_2_2	V_2_2	0	2
191	V_3_2	V_2_2	1	2

192	V_6_2	V_2_2	1	2
193	V_7_2	V_2_2	1	2
194	V_8_2	V_2_2	1	2
195	V_9_2	V_2_2	1	2
196	V_13_2	V_2_2	1	2
197	V_15_2	V_2_2	1	2
198	V_16_2	V_2_2	1	2
199	V_17_2	V_2_2	1	2
200	V_18_2	V_2_2	1	2
201	T_2_2	V_3_2	1	2
202	T_5_2	V_3_2	1	2
203	T_9_2	V_3_2	1	2
204	V_1_2	V_3_2	1	2
205	V_2_2	V_3_2	1	2
206	V_3_2	V_3_2	0	2
207	V_6_2	V_3_2	1	2
208	V_7_2	V_3_2	1	2
209	V_8_2	V_3_2	1	2
210	V_9_2	V_3_2	1	2
211	V_13_2	V_3_2	1	2
212	V_15_2	V_3_2	1	2
213	V_16_2	V_3_2	1	2
214	V_17_2	V_3_2	1	2
215	V_18_2	V_3_2	1	2
216	T_2_2	V_6_2	1	2
217	T_5_2	V_6_2	1	2
218	T_9_2	V_6_2	1	2
219	V_1_2	V_6_2	0.5	2
220	V_2_2	V_6_2	1	2
221	V_3_2	V_6_2	1	2
222	V_6_2	V_6_2	0	2
223	V_7_2	V_6_2	1	2
224	V_8_2	V_6_2	1	2
225	V_9_2	V_6_2	1	2
226	V_13_2	V_6_2	0.57	2
227	V_15_2	V_6_2	0.42	2
228	V_16_2	V_6_2	0.75	2
229	V_17_2	V_6_2	0.86	2
230	V_18_2	V_6_2	-0.82	2
231	T_2_2	V_7_2	1	2
232	T_5_2	V_7_2	1	2
233	T_9_2	V_7_2	1	2
234	V_1_2	V_7_2	1	2

235	V_2_2	V_7_2	1	2
236	V_3_2	V_7_2	1	2
237	V_6_2	V_7_2	1	2
238	V_7_2	V_7_2	0	2
239	V_8_2	V_7_2	1	2
240	V_9_2	V_7_2	1	2
241	V_13_2	V_7_2	1	2
242	V_15_2	V_7_2	1	2
243	V_16_2	V_7_2	1	2
244	V_17_2	V_7_2	1	2
245	V_18_2	V_7_2	1	2
246	T_2_2	V_8_2	1	2
247	T_5_2	V_8_2	1	2
248	T_9_2	V_8_2	1	2
249	V_1_2	V_8_2	1	2
250	V_2_2	V_8_2	1	2
251	V_3_2	V_8_2	1	2
252	V_6_2	V_8_2	1	2
253	V_7_2	V_8_2	1	2
254	V_8_2	V_8_2	0	2
255	V_9_2	V_8_2	1	2
256	V_13_2	V_8_2	1	2
257	V_15_2	V_8_2	1	2
258	V_16_2	V_8_2	1	2
259	V_17_2	V_8_2	1	2
260	V_18_2	V_8_2	1	2
261	T_2_2	V_9_2	1	2
262	T_5_2	V_9_2	1	2
263	T_9_2	V_9_2	1	2
264	V_1_2	V_9_2	1	2
265	V_2_2	V_9_2	1	2
266	V_3_2	V_9_2	1	2
267	V_6_2	V_9_2	1	2
268	V_7_2	V_9_2	1	2
269	V_8_2	V_9_2	1	2
270	V_9_2	V_9_2	0	2
271	V_13_2	V_9_2	1	2
272	V_15_2	V_9_2	1	2
273	V_16_2	V_9_2	1	2
274	V_17_2	V_9_2	1	2
275	V_18_2	V_9_2	1	2
276	T_2_2	V_13_2	0.99	2
277	T_5_2	V_13_2	1	2

278	T_9_2	V_13_2	1	2
279	V_1_2	V_13_2	0.4	2
280	V_2_2	V_13_2	1	2
281	V_3_2	V_13_2	1	2
282	V_6_2	V_13_2	0.57	2
283	V_7_2	V_13_2	1	2
284	V_8_2	V_13_2	1	2
285	V_9_2	V_13_2	1	2
286	V_13_2	V_13_2	0	2
287	V_15_2	V_13_2	0.55	2
288	V_16_2	V_13_2	0.51	2
289	V_17_2	V_13_2	0.79	2
290	V_18_2	V_13_2	0.45	2
291	T_2_2	V_15_2	0.99	2
292	T_5_2	V_15_2	1	2
293	T_9_2	V_15_2	1	2
294	V_1_2	V_15_2	0.05	2
295	V_2_2	V_15_2	1	2
296	V_3_2	V_15_2	1	2
297	V_6_2	V_15_2	0.42	2
298	V_7_2	V_15_2	1	2
299	V_8_2	V_15_2	1	2
300	V_9_2	V_15_2	1	2
301	V_13_2	V_15_2	0.55	2
302	V_15_2	V_15_2	0	2
303	V_16_2	V_15_2	0.16	2
304	V_17_2	V_15_2	0.68	2
305	V_18_2	V_15_2	-0.2	2
306	T_2_2	V_16_2	0.05	2
307	T_5_2	V_16_2	0.93	2
308	T_9_2	V_16_2	1	2
309	V_1_2	V_16_2	0.82	2
310	V_2_2	V_16_2	1	2
311	V_3_2	V_16_2	1	2
312	V_6_2	V_16_2	0.75	2
313	V_7_2	V_16_2	1	2
314	V_8_2	V_16_2	1	2
315	V_9_2	V_16_2	1	2
316	V_13_2	V_16_2	0.51	2
317	V_15_2	V_16_2	0.16	2
318	V_16_2	V_16_2	0	2
319	V_17_2	V_16_2	-0.97	2
320	V_18_2	V_16_2	-0.54	2

321	T_2_2	V_17_2	0.82	2
322	T_5_2	V_17_2	1	2
323	T_9_2	V_17_2	1	2
324	V_1_2	V_17_2	0.75	2
325	V_2_2	V_17_2	1	2
326	V_3_2	V_17_2	1	2
327	V_6_2	V_17_2	0.86	2
328	V_7_2	V_17_2	1	2
329	V_8_2	V_17_2	1	2
330	V_9_2	V_17_2	1	2
331	V_13_2	V_17_2	0.79	2
332	V_15_2	V_17_2	0.68	2
333	V_16_2	V_17_2	-0.97	2
334	V_17_2	V_17_2	0	2
335	V_18_2	V_17_2	-0.64	2
336	T_2_2	V_18_2	0.85	2
337	T_5_2	V_18_2	0.96	2
338	T_9_2	V_18_2	1	2
339	V_1_2	V_18_2	0.57	2
340	V_2_2	V_18_2	1	2
341	V_3_2	V_18_2	1	2
342	V_6_2	V_18_2	-0.82	2
343	V_7_2	V_18_2	1	2
344	V_8_2	V_18_2	1	2
345	V_9_2	V_18_2	1	2
346	V_13_2	V_18_2	0.45	2
347	V_15_2	V_18_2	-0.2	2
348	V_16_2	V_18_2	-0.54	2
349	V_17_2	V_18_2	-0.64	2
350	V_18_2	V_18_2	0	2
351	T_2_1	T_2_1	0	1
352	V_3_1	T_2_1	1	1
353	V_6_1	T_2_1	1	1
354	V_7_1	T_2_1	1	1
355	V_9_1	T_2_1	0.32	1
356	V_10_1	T_2_1	0.28	1
357	V_11_1	T_2_1	1	1
358	V_12_1	T_2_1	1	1
359	V_14_1	T_2_1	1	1
360	V_15_1	T_2_1	1	1
361	V_16_1	T_2_1	0.75	1
362	V_17_1	T_2_1	0.69	1
363	V_18_1	T_2_1	0.27	1

364	V_19_1	T_2_1	1	1
365	V_20_1	T_2_1	1	1
366	V_21_1	T_2_1	1	1
367	V_22_1	T_2_1	1	1
368	T_2_1	V_3_1	1	1
369	V_3_1	V_3_1	0	1
370	V_6_1	V_3_1	1	1
371	V_7_1	V_3_1	1	1
372	V_9_1	V_3_1	1	1
373	V_10_1	V_3_1	1	1
374	V_11_1	V_3_1	1	1
375	V_12_1	V_3_1	1	1
376	V_14_1	V_3_1	1	1
377	V_15_1	V_3_1	1	1
378	V_16_1	V_3_1	1	1
379	V_17_1	V_3_1	1	1
380	V_18_1	V_3_1	1	1
381	V_19_1	V_3_1	1	1
382	V_20_1	V_3_1	1	1
383	V_21_1	V_3_1	1	1
384	V_22_1	V_3_1	1	1
385	T_2_1	V_6_1	1	1
386	V_3_1	V_6_1	1	1
387	V_6_1	V_6_1	0	1
388	V_7_1	V_6_1	1	1
389	V_9_1	V_6_1	1	1
390	V_10_1	V_6_1	1	1
391	V_11_1	V_6_1	1	1
392	V_12_1	V_6_1	0.98	1
393	V_14_1	V_6_1	1	1
394	V_15_1	V_6_1	1	1
395	V_16_1	V_6_1	1	1
396	V_17_1	V_6_1	1	1
397	V_18_1	V_6_1	1	1
398	V_19_1	V_6_1	1	1
399	V_20_1	V_6_1	1	1
400	V_21_1	V_6_1	1	1
401	V_22_1	V_6_1	1	1
402	T_2_1	V_7_1	1	1
403	V_3_1	V_7_1	1	1
404	V_6_1	V_7_1	1	1
405	V_7_1	V_7_1	0	1
406	V_9_1	V_7_1	0.75	1

407	V_10_1	V_7_1	-0.05	1
408	V_11_1	V_7_1	1	1
409	V_12_1	V_7_1	1	1
410	V_14_1	V_7_1	1	1
411	V_15_1	V_7_1	1	1
412	V_16_1	V_7_1	0.98	1
413	V_17_1	V_7_1	0.8	1
414	V_18_1	V_7_1	0.85	1
415	V_19_1	V_7_1	1	1
416	V_20_1	V_7_1	1	1
417	V_21_1	V_7_1	1	1
418	V_22_1	V_7_1	1	1
419	T_2_1	V_9_1	0.32	1
420	V_3_1	V_9_1	1	1
421	V_6_1	V_9_1	1	1
422	V_7_1	V_9_1	0.75	1
423	V_9_1	V_9_1	0	1
424	V_10_1	V_9_1	-0.77	1
425	V_11_1	V_9_1	1	1
426	V_12_1	V_9_1	1	1
427	V_14_1	V_9_1	0.97	1
428	V_15_1	V_9_1	0.86	1
429	V_16_1	V_9_1	-0.95	1
430	V_17_1	V_9_1	-1	1
431	V_18_1	V_9_1	-0.03	1
432	V_19_1	V_9_1	1	1
433	V_20_1	V_9_1	1	1
434	V_21_1	V_9_1	1	1
435	V_22_1	V_9_1	1	1
436	T_2_1	V_10_1	0.28	1
437	V_3_1	V_10_1	1	1
438	V_6_1	V_10_1	1	1
439	V_7_1	V_10_1	-0.05	1
440	V_9_1	V_10_1	-0.77	1
441	V_10_1	V_10_1	0	1
442	V_11_1	V_10_1	1	1
443	V_12_1	V_10_1	1	1
444	V_14_1	V_10_1	0.97	1
445	V_15_1	V_10_1	0.79	1
446	V_16_1	V_10_1	-0.89	1
447	V_17_1	V_10_1	-0.72	1
448	V_18_1	V_10_1	-0.31	1
449	V_19_1	V_10_1	1	1

450	V_20_1	V_10_1	0.99	1
451	V_21_1	V_10_1	1	1
452	V_22_1	V_10_1	1	1
453	T_2_1	V_11_1	1	1
454	V_3_1	V_11_1	1	1
455	V_6_1	V_11_1	1	1
456	V_7_1	V_11_1	1	1
457	V_9_1	V_11_1	1	1
458	V_10_1	V_11_1	1	1
459	V_11_1	V_11_1	0	1
460	V_12_1	V_11_1	1	1
461	V_14_1	V_11_1	1	1
462	V_15_1	V_11_1	1	1
463	V_16_1	V_11_1	1	1
464	V_17_1	V_11_1	1	1
465	V_18_1	V_11_1	1	1
466	V_19_1	V_11_1	1	1
467	V_20_1	V_11_1	1	1
468	V_21_1	V_11_1	1	1
469	V_22_1	V_11_1	1	1
470	T_2_1	V_12_1	1	1
471	V_3_1	V_12_1	1	1
472	V_6_1	V_12_1	0.98	1
473	V_7_1	V_12_1	1	1
474	V_9_1	V_12_1	1	1
475	V_10_1	V_12_1	1	1
476	V_11_1	V_12_1	1	1
477	V_12_1	V_12_1	0	1
478	V_14_1	V_12_1	1	1
479	V_15_1	V_12_1	1	1
480	V_16_1	V_12_1	1	1
481	V_17_1	V_12_1	1	1
482	V_18_1	V_12_1	1	1
483	V_19_1	V_12_1	1	1
484	V_20_1	V_12_1	1	1
485	V_21_1	V_12_1	0.89	1
486	V_22_1	V_12_1	1	1
487	T_2_1	V_14_1	1	1
488	V_3_1	V_14_1	1	1
489	V_6_1	V_14_1	1	1
490	V_7_1	V_14_1	1	1
491	V_9_1	V_14_1	0.97	1
492	V_10_1	V_14_1	0.97	1

493	V_11_1	V_14_1	1	1
494	V_12_1	V_14_1	1	1
495	V_14_1	V_14_1	0	1
496	V_15_1	V_14_1	0.89	1
497	V_16_1	V_14_1	0.96	1
498	V_17_1	V_14_1	1	1
499	V_18_1	V_14_1	0.66	1
500	V_19_1	V_14_1	0.99	1
501	V_20_1	V_14_1	0.91	1
502	V_21_1	V_14_1	0.84	1
503	V_22_1	V_14_1	1	1
504	T_2_1	V_15_1	1	1
505	V_3_1	V_15_1	1	1
506	V_6_1	V_15_1	1	1
507	V_7_1	V_15_1	1	1
508	V_9_1	V_15_1	0.86	1
509	V_10_1	V_15_1	0.79	1
510	V_11_1	V_15_1	1	1
511	V_12_1	V_15_1	1	1
512	V_14_1	V_15_1	0.89	1
513	V_15_1	V_15_1	0	1
514	V_16_1	V_15_1	0.99	1
515	V_17_1	V_15_1	0.93	1
516	V_18_1	V_15_1	-0.11	1
517	V_19_1	V_15_1	1	1
518	V_20_1	V_15_1	1	1
519	V_21_1	V_15_1	0.98	1
520	V_22_1	V_15_1	1	1
521	T_2_1	V_16_1	0.75	1
522	V_3_1	V_16_1	1	1
523	V_6_1	V_16_1	1	1
524	V_7_1	V_16_1	0.98	1
525	V_9_1	V_16_1	-0.95	1
526	V_10_1	V_16_1	-0.89	1
527	V_11_1	V_16_1	1	1
528	V_12_1	V_16_1	1	1
529	V_14_1	V_16_1	0.96	1
530	V_15_1	V_16_1	0.99	1
531	V_16_1	V_16_1	0	1
532	V_17_1	V_16_1	-0.96	1
533	V_18_1	V_16_1	-0.56	1
534	V_19_1	V_16_1	1	1
535	V_20_1	V_16_1	1	1

536	V_21_1	V_16_1	1	1
537	V_22_1	V_16_1	1	1
538	T_2_1	V_17_1	0.69	1
539	V_3_1	V_17_1	1	1
540	V_6_1	V_17_1	1	1
541	V_7_1	V_17_1	0.8	1
542	V_9_1	V_17_1	-1	1
543	V_10_1	V_17_1	-0.72	1
544	V_11_1	V_17_1	1	1
545	V_12_1	V_17_1	1	1
546	V_14_1	V_17_1	1	1
547	V_15_1	V_17_1	0.93	1
548	V_16_1	V_17_1	-0.96	1
549	V_17_1	V_17_1	0	1
550	V_18_1	V_17_1	-0.28	1
551	V_19_1	V_17_1	1	1
552	V_20_1	V_17_1	0.99	1
553	V_21_1	V_17_1	1	1
554	V_22_1	V_17_1	1	1
555	T_2_1	V_18_1	0.27	1
556	V_3_1	V_18_1	1	1
557	V_6_1	V_18_1	1	1
558	V_7_1	V_18_1	0.85	1
559	V_9_1	V_18_1	-0.03	1
560	V_10_1	V_18_1	-0.31	1
561	V_11_1	V_18_1	1	1
562	V_12_1	V_18_1	1	1
563	V_14_1	V_18_1	0.66	1
564	V_15_1	V_18_1	-0.11	1
565	V_16_1	V_18_1	-0.56	1
566	V_17_1	V_18_1	-0.28	1
567	V_18_1	V_18_1	0	1
568	V_19_1	V_18_1	1	1
569	V_20_1	V_18_1	0.99	1
570	V_21_1	V_18_1	0.82	1
571	V_22_1	V_18_1	1	1
572	T_2_1	V_19_1	1	1
573	V_3_1	V_19_1	1	1
574	V_6_1	V_19_1	1	1
575	V_7_1	V_19_1	1	1
576	V_9_1	V_19_1	1	1
577	V_10_1	V_19_1	1	1
578	V_11_1	V_19_1	1	1

579	V_12_1	V_19_1	1	1
580	V_14_1	V_19_1	0.99	1
581	V_15_1	V_19_1	1	1
582	V_16_1	V_19_1	1	1
583	V_17_1	V_19_1	1	1
584	V_18_1	V_19_1	1	1
585	V_19_1	V_19_1	0	1
586	V_20_1	V_19_1	0.62	1
587	V_21_1	V_19_1	1	1
588	V_22_1	V_19_1	1	1
589	T_2_1	V_20_1	1	1
590	V_3_1	V_20_1	1	1
591	V_6_1	V_20_1	1	1
592	V_7_1	V_20_1	1	1
593	V_9_1	V_20_1	1	1
594	V_10_1	V_20_1	0.99	1
595	V_11_1	V_20_1	1	1
596	V_12_1	V_20_1	1	1
597	V_14_1	V_20_1	0.91	1
598	V_15_1	V_20_1	1	1
599	V_16_1	V_20_1	1	1
600	V_17_1	V_20_1	0.99	1
601	V_18_1	V_20_1	0.99	1
602	V_19_1	V_20_1	0.62	1
603	V_20_1	V_20_1	0	1
604	V_21_1	V_20_1	1	1
605	V_22_1	V_20_1	1	1
606	T_2_1	V_21_1	1	1
607	V_3_1	V_21_1	1	1
608	V_6_1	V_21_1	1	1
609	V_7_1	V_21_1	1	1
610	V_9_1	V_21_1	1	1
611	V_10_1	V_21_1	1	1
612	V_11_1	V_21_1	1	1
613	V_12_1	V_21_1	0.89	1
614	V_14_1	V_21_1	0.84	1
615	V_15_1	V_21_1	0.98	1
616	V_16_1	V_21_1	1	1
617	V_17_1	V_21_1	1	1
618	V_18_1	V_21_1	0.82	1
619	V_19_1	V_21_1	1	1
620	V_20_1	V_21_1	1	1
621	V_21_1	V_21_1	0	1

622	V_22_1	V_21_1	1	1
623	T_2_1	V_22_1	1	1
624	V_3_1	V_22_1	1	1
625	V_6_1	V_22_1	1	1
626	V_7_1	V_22_1	1	1
627	V_9_1	V_22_1	1	1
628	V_10_1	V_22_1	1	1
629	V_11_1	V_22_1	1	1
630	V_12_1	V_22_1	1	1
631	V_14_1	V_22_1	1	1
632	V_15_1	V_22_1	1	1
633	V_16_1	V_22_1	1	1
634	V_17_1	V_22_1	1	1
635	V_18_1	V_22_1	1	1
636	V_19_1	V_22_1	1	1
637	V_20_1	V_22_1	1	1
638	V_21_1	V_22_1	1	1
639	V_22_1	V_22_1	0	1

Table 9： pairwise RC value of hypothesis 2.

	N	value	sd	se	ci
Tanzania	196	0.004592	0.876483	0.062606	0.123472
Vietnam	1444	-0.21137	0.882114	0.023214	0.045536

Table 10： RC value of hypothesis 1.

	N	value	sd	se	ci
1	289	-0.30332	0.879952	0.051762	0.10188
2	225	-0.07591	0.884229	0.058949	0.116165
3	100	0.1976	0.845226	0.084523	0.167711
4	25	0.6584	0.54362	0.108724	0.224395

Table 11： RC value of hypothesis 2.

Appendix E

The R script and data below are related to the subset analysis and subtree.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to "To Source File Location"
#Script for finding subsets

library(phyloseq)
library(vegan)
```

```
library(ggplot2)
library(sinkr)

#PARAMETERS ###########################
which_level<-"Otus" #Phylum Class Order Family Genus Otus
top_N_abundant_OTUs<-2000
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
#/PARAMETERS ###########################


abund_table<-otu_table(physeq)
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]


OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment", and "non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") | OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") | OTU_taxonomy$Family %in% c("Mitochondria"))]


#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
```

```
#when reducing the abund_table, there is a high likelihood that an OTU was only present in a sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their dimensions should match
#/DATA IMPORT###################################################################

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE##############################
#In the hypothesis space, all you need is to select the rows in meta_table you are interested in
#and then allocate a column to meta_table$Groups that you want to use.
#additionally, allocate a column to meta_table$Connections if the data is paired

label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
    "Tanzania",
    "Vietnam"
))
PERMANOVA_variables<-c("Country","Latrine","Depth")

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
    "4",
    "3",
    "2",
    "1"
))
PERMANOVA_variables<-c("Country","Latrine","Depth")
```

```
#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE############################

#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]
#Adjust OTU taxonomy
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#COLLATE OTUS AT A PARTICULAR LEVEL#######################################
new_abund_table<-NULL
if(which_level=="Otus"){
  new_abund_table<-abund_table
} else {
  list<-unique(OTU_taxonomy[,which_level])
  new_abund_table<-NULL
  for(i in list){
    tmp<-data.frame(rowSums(abund_table[,rownames(OTU_taxonomy)[OTU_taxonomy[,which_level]==i],drop=FALSE]))
    if(i==""){colnames(tmp)<-c("__Unknowns__")} else {
      #colnames(tmp)<-paste("",i,sep="")
      colnames(tmp)<-gsub(";+$","",paste(sapply(OTU_taxonomy[OTU_taxonomy[,which_level]==i,][1,1:which(colnames(OTU_taxonomy)==which_level)],as.character),collapse=";"))
    }
    if(is.null(new_abund_table)){new_abund_table<-tmp} else {new_abund_table<-cbind(tmp,new_abund_table)}
  }
}

new_abund_table<-as.data.frame(as(new_abund_table,"matrix"))
abund_table<-new_abund_table
#/COLLATE OTUS AT A PARTICULAR LEVEL#######################################

if(which_level=="Otus"){
  at<-abund_table[,order(colSums(abund_table),decreasing=TRUE)][,1:min(top_N_abundant_OTUs,dim(abund_table)[2])]
} else{
  at<-abund_table
```

```
}

res.bv.step.biobio <-bvStep(abund_table, at, fix.dist.method = "bray",
                                        var.dist.method = "bray", scale.fix = FALSE, scale.var = FALSE,
                                        max.rho = 0.95, min.delta.rho = 0.001, random.selection =
TRUE,
                                        prop.selected.var = 0.8, num.restarts = 10,
var.always.include = NULL,
                                        var.exclude = NULL, output.best = 50)

#Get the N best subset of taxa
Taxa_all_names<-colnames(abund_table)
bestTaxaFit<-""
OUTPUT<-NULL
Significant_taxa<-NULL
for(i in (1:length(res.bv.step.biobio$order.by.best$var.incl)))
{
  Taxa_list<-
Taxa_all_names[as.numeric(unlist(strsplit(res.bv.step.biobio$order.by.best$var.incl[i],
split=",")))]
  if(length(Taxa_list)>1){
    at<-abund_table[,Taxa_list]
    mt<-meta_table[,PERMANOVA_variables,drop=F]
    #Remove rows that are all zeros as a result of this filtering and adjust mt accordingly
otherwise
    #bray-curtis distance won't work
    at<-at[rowSums(at)>0,]
    mt<-mt[rownames(at),,drop=F]

    a<-capture.output(print(paste(paste(Taxa_list,collapse=' + '), " =
",res.bv.step.biobio$order.by.best$rho[i],sep="")))
    b<-capture.output(print(adonis(vegdist(at,"bray") ~ ., data=mt)))
    tmp<-c("SUBSET",a,"PERMANOVA",b,"------------------------")
    if(is.null(OUTPUT)){OUTPUT<-tmp} else {OUTPUT<-cbind(OUTPUT,tmp)}
    if(is.null(Significant_taxa)){Significant_taxa<-Taxa_list} else {Significant_taxa<-
c(Significant_taxa,Taxa_list)}
    }
}

if(which_level=="Otus"){

capture.output(c(paste(unique(Significant_taxa),as.character(apply(OTU_taxonomy[unique(Si
gnificant_taxa),],1,function(x)
paste(x,collapse=";"))),sep=":"),"===",OUTPUT),file=paste("bioenv_",which_level,"_",label,".txt
```

```
",sep=""))
} else {
  capture.output(OUTPUT,file=paste("bioenv_",which_level,"_",label,".txt",sep=""))
}
```

Script 6： R script of construct a subset anslysis.

```
#ACHTUNG: From the RStudio menu, click on "Session" and then "Set Working Directory" to
"To Source File Location"
#Script for generating files for EvolView

library(phyloseq)
library(vegan)
library(ggplot2)
library(ape)
library(phangorn)
library(stringr)

#PARAMETERS ###########################
physeq<-import_biom("../../Data/feature_w_tax.biom")
meta_table<-read.csv("../../Data/meta_data.csv",header=T,row.names=1)
#Load the tree using ape package
OTU_tree <- read.tree("../../Data/tree.nwk")
do_we_want_top_N_OTUs=FALSE #if FALSE then provide selected_OTUs.csv
how_many_abundant_OTUs=100
taxonomy_coloring_rank=5 #1:Kingdom 2:Phylum 3:Class 4:Order 5:Family 6:Genus
#/PARAMETERS ###########################

#colours to be used for EvolView
colours <- c("#F0A3FF", "#0075DC",
"#993F00","#4C005C","#2BCE48","#FFCC99","#808080","#8F7C00","#9DCC00","#C20088","#
003380","#FFA405","#FFA8BB","#426600","#FF0010","#5EF1F2","#00998F","#740AFF","#990
000","#FFFF00",as.character(sapply(rainbow(200),function(x){substr(x,1,7)})));
colours2<- c("#F0A3FF", "#0075DC",
"#993F00","#4C005C","#2BCE48","#FFCC99","#808080","#94FFB5","#8F7C00","#9DCC00","#
C20088","#003380","#FFA405","#FFA8BB","#426600","#FF0010","#5EF1F2","#00998F","#740
AFF","#990000","#FFFF00","#F0A3FF", "#0075DC",
"#993F00","#4C005C","#2BCE48","#FFCC99","#808080","#94FFB5","#8F7C00","#9DCC00","#
C20088","#003380","#FFA405","#FFA8BB","#426600","#FF0010","#5EF1F2","#00998F","#740
AFF","#990000","#FFFF00")

abund_table<-otu_table(physeq)
abund_table<-t(abund_table)
#Uncomment if you'd like to get rid of samples below a certain library size
abund_table<-abund_table[rowSums(abund_table)>=5000,]
```

```
OTU_taxonomy<-as.data.frame(tax_table(physeq))
colnames(OTU_taxonomy)<-c("Kingdom","Phylum","Class","Order","Family","Genus","Otus")

#Ensure that all columns of OTU_taxonomy are character and not factors
OTU_taxonomy[] <- lapply(OTU_taxonomy, function(x) as.character(x))
OTU_taxonomy[is.na(OTU_taxonomy)]<-""
OTU_taxonomy$Otus<-gsub("D_6__","",OTU_taxonomy$Otus)
OTU_taxonomy$Genus<-gsub("D_5__","",OTU_taxonomy$Genus)
OTU_taxonomy$Family<-gsub("D_4__","",OTU_taxonomy$Family)
OTU_taxonomy$Order<-gsub("D_3__","",OTU_taxonomy$Order)
OTU_taxonomy$Class<-gsub("D_2__","",OTU_taxonomy$Class)
OTU_taxonomy$Phylum<-gsub("D_1__","",OTU_taxonomy$Phylum)
OTU_taxonomy$Kingdom<-gsub("D_0__","",OTU_taxonomy$Kingdom)

#Remove singletons and adjust OTU_taxonomy
abund_table<-abund_table[,colSums(abund_table)>1]
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

#get rid of contaminants with "Unassigned", "Chloroplast" and "Mitochondria" assignment",
and "non classified" at Phylum level
abund_table<-abund_table[,!(OTU_taxonomy$Kingdom %in% c("Unassigned") |
OTU_taxonomy$Phylum=="" | OTU_taxonomy$Order %in% c("Chloroplast") |
OTU_taxonomy$Family %in% c("Mitochondria"))]


#extract subset of abund_table for which samples also exists in meta_table
abund_table<-abund_table[rownames(abund_table) %in% rownames(meta_table),]
#when reducing the abund_table, there is a high likelihood that an OTU was only present in
a sample that is removed, so we shrink
#the abund_table to get rid of empty columns
abund_table<-abund_table[,colSums(abund_table)>0]
#make your meta_table smaller by only considering samples that appear in abund_table
meta_table<-meta_table[rownames(abund_table),]
#make OTU_taxonomy smaller by only considering OTUs that appear in abund_table
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]
#At this point we have abund_table, meta_table, and OTU_taxonomy are ready and their
dimensions should match
#/DATA
IMPORT############################################################

#PARAMETERS CHANGE THE GROUPING COLUMN AS YOU
DESIRE############################
```

```
#In the hypothesis space, all you need is to select the rows in meta_table you are interested in
#and then allocate a column to meta_table$Groups that you want to use.

label="Hypothesis1"
meta_table<-meta_table[meta_table$Country %in% c("Tanzania","Vietnam"),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Country)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "Tanzania",
   "Vietnam"
))

label="Hypothesis2"
meta_table<-meta_table[meta_table$Depth %in% c(1,2,3,4),]
#First provide grouping column
meta_table$Groups<-as.character(meta_table$Depth)
#The colours in the the next instruction match the factors for meta_table$Groups
meta_table$Groups<-factor(meta_table$Groups,c(
   "4",
   "3",
   "2",
   "1"
))

#Note that we can supply a list of OTUs in the form of a CSV file which should have the
#following column headers
#ID,OTUs,Description,Colour_1,Colour_2,Colour_3,.......
#The names "OTUs" and "Description" are hardcoded in the script whereas the remaining
#columns can be named anything
#selected_OTUs<-read.csv("selected_features_subset_analysis1.csv",header=T,row.names=1) #Not required for N abundant OTUs
selected_OTUs<-read.csv("selected_features_subset_analysis2.csv",header=T,row.names=1) #Not required for N abundant OTUs
#/PARAMETERS CHANGE THE GROUPING COLUMN AS YOU DESIRE############################

abund_table<-as(abund_table,"matrix")
#Adjust abund_table to contain only those rows that got selected in the Hypothesis space
abund_table<-abund_table[rownames(meta_table),]
#After adjustment, get rid of OTUs that are all empty
abund_table<-abund_table[,colSums(abund_table)>0]
```

```
#Adjust OTU taxonomy
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

if(do_we_want_top_N_OTUs==TRUE){
   abund_table<-
abund_table[,order(colSums(abund_table),decreasing=TRUE)][,1:min(dim(abund_table)[2],ho
w_many_abundant_OTUs)]
}else{
   abund_table<-abund_table[,as.character(selected_OTUs$OTUs)]
}

#Adjust OTU_Taxonomy and OTU_tree as a result of filteration process
OTU_taxonomy<-OTU_taxonomy[colnames(abund_table),]

OTU_tree<-drop.tip(OTU_tree,OTU_tree$tip.label[!OTU_tree$tip.label %in%
colnames(abund_table)])

#Now apply wisconsin normalisation
abund_table<-wisconsin(abund_table)

#COLLATE SAMPLES FOR EACH
GROUP###########################################
#Find unique sample groups
group_names<-unique(as.character(unique(meta_table$Groups)))

#Collated all the fractions together
abund_table_collated<-NULL
meta_table_collated<-NULL
for(i in group_names){
   tmp<-
colMeans(abund_table[rownames(abund_table)[grepl(paste("^",i,"$",sep=""),meta_table$Gro
ups)],,drop=F])
   tmp<-data.frame(row.names=i,t(as.matrix(tmp)),check.names=FALSE)
   tmp2<-
data.frame(row.names=i,meta_table[rownames(abund_table)[grepl(paste("^",i,"$",sep=""),m
eta_table$Groups)],,drop=F][1,,drop=F])
   if(is.null(abund_table_collated)){abund_table_collated<-tmp}else{abund_table_collated<-
rbind(abund_table_collated,tmp)}
   if(is.null(meta_table_collated)){meta_table_collated<-tmp2}else{meta_table_collated<-
rbind(meta_table_collated,tmp2)}
}
meta_table<-meta_table_collated[,c("Groups"),drop=F]
abund_table<-abund_table_collated
#sort abund_table and meta_table based on meta_table$Groups
```

```
abund_table<-abund_table[order(meta_table$Groups,decreasing=F),]
meta_table<-meta_table[rownames(abund_table),,drop=F]
#/COLLATE SAMPLES FOR EACH GROUP##############################################

#GENERATE FILES FOR EVOLVIEW##################################################

#Step 1: Write a tree for EvolView to upload to
write.tree(OTU_tree,paste("EvolView_",label,".tre",sep=""))
tmp<-t(abund_table)


#Step 2: Write abundances to a file (barplots)
https://github.com/evolgeniusteam/EvolviewDocumentation/blob/master/datasets/03_bar/DatasetBars.md
fileConn<-file(paste("EvolView_",label,"_barplots.txt",sep=""))
writeLines("##barplots", fileConn)
close(fileConn)
fileConn<-file(paste("EvolView_",label,"_barplots.txt",sep=""),open="at")
writeLines(paste("!groups\t",paste(meta_table[rownames(abund_table),"Groups"],collapse=","),sep=""),fileConn)
writeLines(paste("!colors\t",paste(colours2[as.numeric(meta_table$Groups)],collapse=","),sep=""),fileConn)
writeLines("!showLegends\t0",fileConn)
writeLines("!plotwidth\t1600",fileConn)
writeLines("!style\trect",fileConn)
writeLines("!grid",fileConn)
writeLines("!align",fileConn)
writeLines("!title\tmean(wisconsin(abundance))",fileConn)
for(i in 1:nrow(tmp)){
writeLines(paste(paste(rownames(tmp)[i],"\t",sep=""),paste(tmp[i,],collapse=","),sep=""),fileConn)
}
close(fileConn)

#Step 3: Write abundances to a file (heatmap)
http://evdocs.medgenius.info/#DatasetHeatmap
fileConn<-file(paste("EvolView_",label,"_heatmap.txt",sep=""))
writeLines("#heatmap", fileConn)
close(fileConn)
fileConn<-file(paste("EvolView_",label,"_heatmap.txt",sep=""),open="at")
writeLines("!title\tmean(wisconsin(abundance))",fileConn)
writeLines("!showLegends\t1",fileConn)
```

```
writeLines("#!defaultStrokeColor\tgold",fileConn)
writeLines("#!defaultStrokeWidth\t0",fileConn)
writeLines("!colorgradient\tblue,#007FFF,#007FFF,cyan,cyan,cyan,#7FFF7F,#7FFF7F,#7FFF7F,
#7FFF7F,yellow,yellow,yellow,yellow,yellow,#FF7F00,#FF7F00,#FF7F00,#FF7F00,#FF7F00,#FF
7F00,red,red,red,red,red,red,red",fileConn)
writeLines("!showHeatMapColumnLabel\t1",fileConn)
writeLines(paste("!heatmapColumnLabels\t",paste(meta_table[rownames(abund_table),"Grou
ps"],collapse=","),sep=""),fileConn)
writeLines("!heatmap\tmargin=1,colwidth=30,roundedcorner=0",fileConn)
writeLines("!showdataValue\tshow=0",fileConn)
for(i in 1:nrow(tmp)){

writeLines(paste(paste(rownames(tmp)[i],"\t",sep=""),paste(tmp[i,],collapse=","),sep=""),fileC
onn)
}
close(fileConn)

#Step 4: Write taxonomy to a file (grouplabels)
https://github.com/evolgeniusteam/EvolviewDocumentation/blob/master/datasets/08_grou
p_label/DatasetGroupLabel.md
taxonomy_to_put<-
as.factor(sapply(1:nrow(tmp),function(x){gsub(";+$","",paste(OTU_taxonomy[rownames(tmp)[
x],],collapse=";"))}))
taxonomy_to_put_colours<-
as.factor(sapply(1:nrow(tmp),function(x){gsub(";+$","",paste(OTU_taxonomy[rownames(tmp)[
x],1:taxonomy_coloring_rank],collapse=";"))}))
fileConn<-file(paste("EvolView_",label,"_taxonomy_grouplabels.txt",sep=""))
writeLines("!grouplabel\tstyle=2,color=pink,show=1,marginPCT=0.05,fontsize=10,fontcolor
=white,fontitalic=0,textalign=middle,textorientation=horizontal,linewidth=2", fileConn)
close(fileConn)
fileConn<-file(paste("EvolView_",label,"_taxonomy_grouplabels.txt",sep=""),open="at")
writeLines("!op\t1.0",fileConn)
for(i in 1:nrow(tmp)){

writeLines(paste(paste(rownames(tmp)[i],"\t",sep=""),paste("fontcolor=black,bkcolor=",colou
rs[taxonomy_to_put_colours[i]],",text=",as.character(taxonomy_to_put[i]),sep=""),sep=""),fileC
onn)
}
close(fileConn)

if(do_we_want_top_N_OTUs==FALSE){

   #Write OTUs$Description to a file (grouplabels)
https://github.com/evolgeniusteam/EvolviewDocumentation/blob/master/datasets/08_grou
```

```
p_label/DatasetGroupLabel.md
    fileConn<-file(paste("EvolView_",label,"_OTUs_text_grouplabels.txt",sep=""))

writeLines("!grouplabel\tstyle=2,color=pink,show=1,marginPCT=0.05,fontsize=14,fontcolor
=white,fontitalic=0,textalign=middle,textorientation=horizontal,linewidth=2", fileConn)
    close(fileConn)
    fileConn<-file(paste("EvolView_",label,"_OTUs_text_grouplabels.txt",sep=""),open="at")
    writeLines("!op\t1.0",fileConn)
    for(i in 1:nrow(tmp)){

writeLines(paste(paste(rownames(tmp)[i],"\t",sep=""),paste("bkcolor=#FFFFFF,fontcolor=blac
k,text=",as.character(selected_OTUs[as.character(selected_OTUs[,"OTUs"])==rownames(tmp)
[i],"Description"]),sep=""),sep=""),fileConn)
    }
    close(fileConn)

    #Loop through all the colour annotations and generate a file for each
    for(k in 3:dim(selected_OTUs)[2]){
        #Write all colour annotations to a file (grouplabels)
https://github.com/evolgeniusteam/EvolviewDocumentation/blob/master/datasets/08_grou
p_label/DatasetGroupLabel.md
        fileConn<-
file(paste("EvolView_",label,"_OTUs_",colnames(selected_OTUs)[k],"_grouplabels.txt",sep=""))

writeLines("!grouplabel\tstyle=2,color=pink,show=1,marginPCT=0.05,fontsize=14,fontcolor
=white,fontitalic=0,textalign=middle,textorientation=horizontal,linewidth=2", fileConn)
        close(fileConn)
        fileConn<-
file(paste("EvolView_",label,"_OTUs_",colnames(selected_OTUs)[k],"_grouplabels.txt",sep=""),
open="at")
        writeLines("!op\t1.0",fileConn)
        for(i in 1:nrow(tmp)){

writeLines(paste(paste(rownames(tmp)[i],"\t",sep=""),paste("bkcolor=",as.character(selected_
OTUs[as.character(selected_OTUs[,"OTUs"])==rownames(tmp)[i],k]),",fontcolor=",as.characte
r(selected_OTUs[as.character(selected_OTUs[,"OTUs"])==rownames(tmp)[i],k]),",text=","ooo",
sep=""),sep=""),fileConn)
        }
        close(fileConn)
        }
}
#/GENERATE FILES FOR
EVOLVIEW##################################################
```

Script 7: R script of subset tree.

ID	OTUs	Description	Colour_1
1	C8	Subset Analysis	#FF0000
2	C9	Subset Analysis	#FF0000
3	C10	Subset Analysis	#FF0000
4	C13	Subset Analysis	#FF0000
5	C16	Subset Analysis	#FF0000
6	C12	Subset Analysis	#FF0000
7	C22	Subset Analysis	#FF0000

Table 12： selected features and subset analysis of hypothesis 1.

ID	OTUs	Description	Colour_1
1	C8	Subset Analysis	#FF0000
2	C9	Subset Analysis	#FF0000
3	C10	Subset Analysis	#FF0000
4	C13	Subset Analysis	#FF0000
5	C14	Subset Analysis	#FF0000
6	C12	Subset Analysis	#FF0000

Table 13： selected features and subset analysis of hypothesis 2.