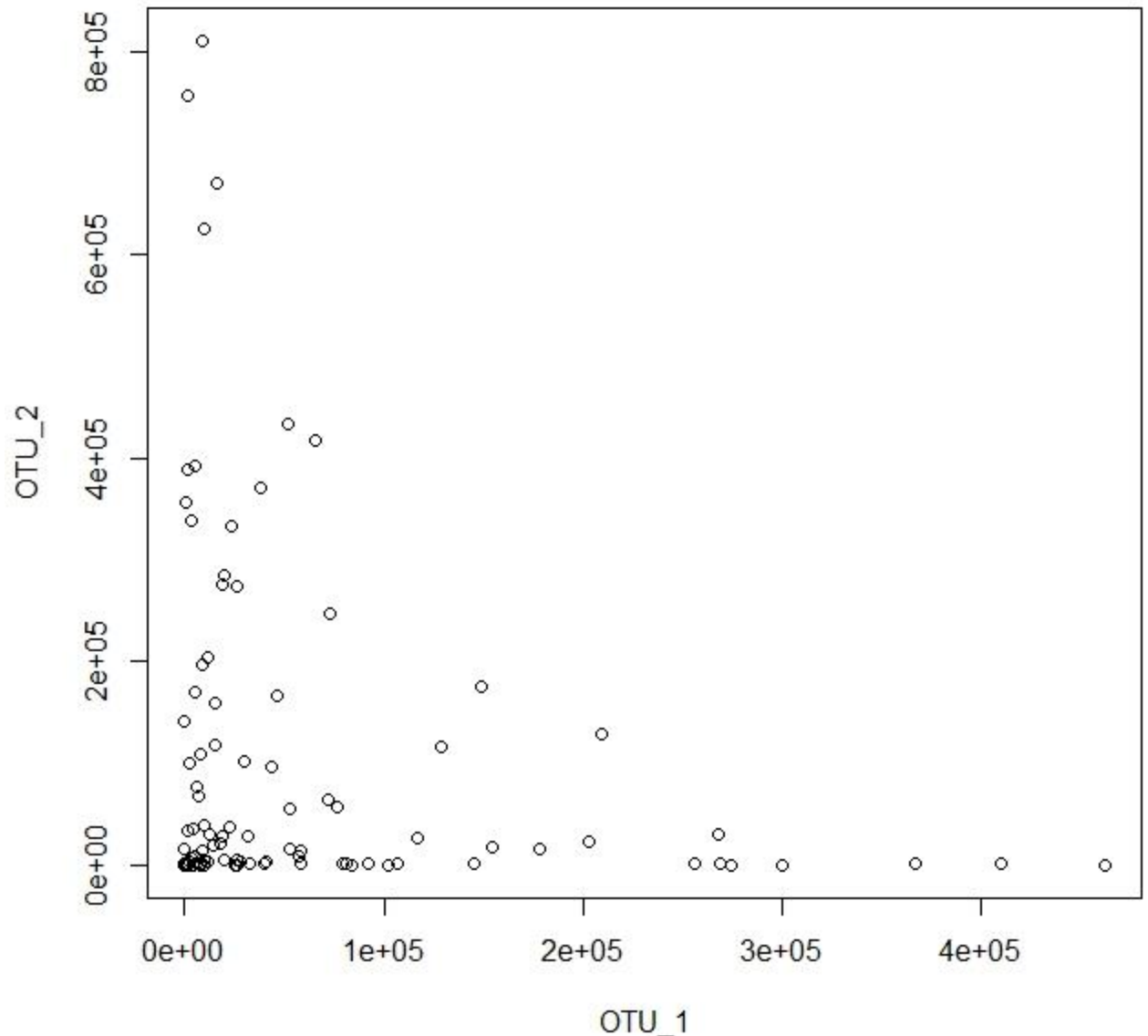
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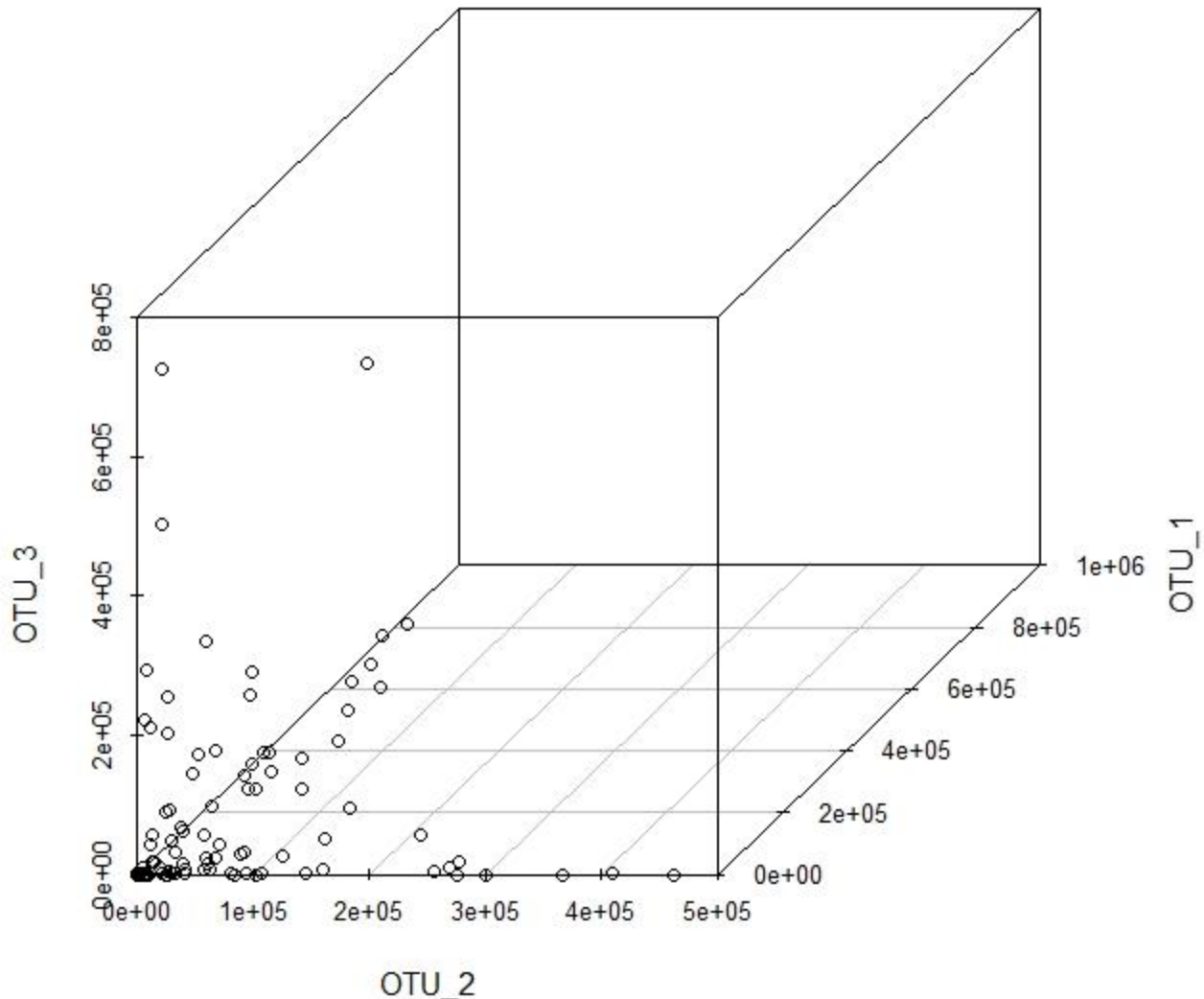
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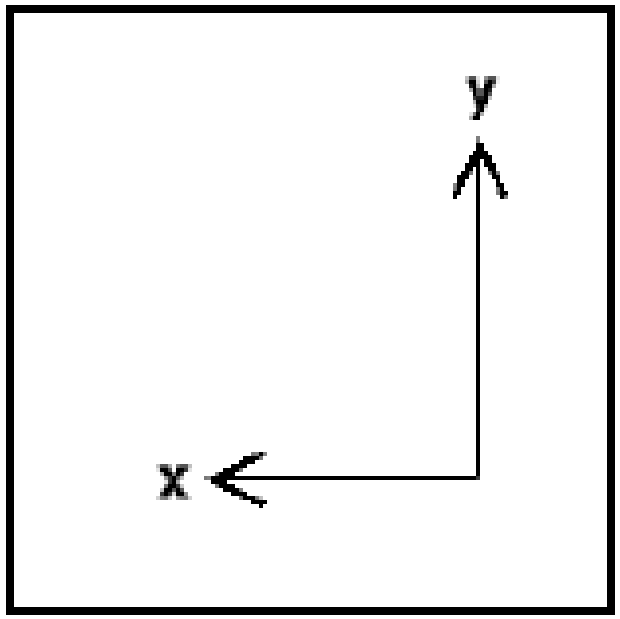
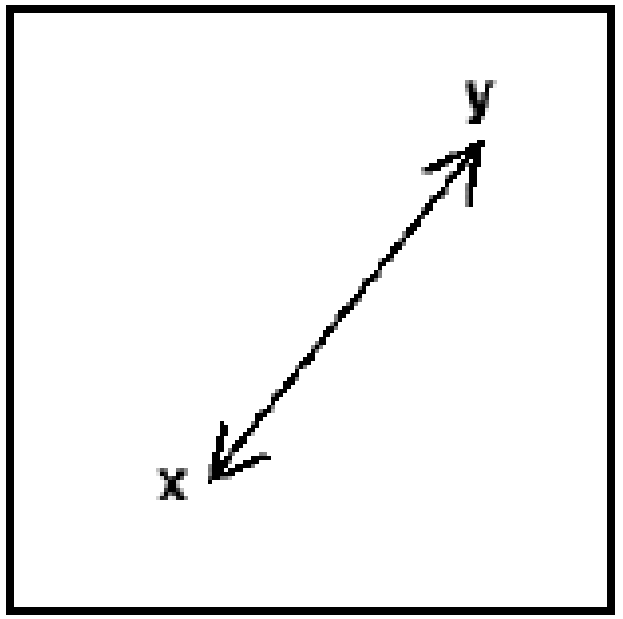


Manhattan



Euclidean

ECOLOGY LETTERS

Ecology Letters, (2013) **16**: 951–963 doi: 10.1111/ele.12141

IDEA AND PERSPECTIVE

Beta diversity as the variance of community data: dissimilarity coefficients and partitioning

Pierre Legendre[1]* and Miquel De Cáceres[2,3]

Abstract

Beta diversity can be measured in different ways. Among these, the total variance of the community data table **Y** can be used as an estimate of beta diversity. We show how the total variance of **Y** can be calculated either directly or through a dissimilarity matrix obtained using any dissimilarity index deemed appropriate for pairwise comparisons of community composition data. We addressed the question of which index to use by coding 16 indices using 14 properties that are necessary for beta assessment, comparability among data sets, sampling issues and ordination. Our comparison analysis classified the coefficients under study into five types, three of which are appropriate for beta diversity assessment. Our approach links the concept of beta diversity with the analysis of community data by commonly used methods like ordination and ANOVA. Total beta can be partitioned into Species Contributions (SCBD: degree of variation of individual species across the study area) and Local Contributions (LCBD: comparative indicators of the ecological

frontiers in Microbiology

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Check for updates

Microbiome Datasets Are Compositional: And This Is Not Optional

Gregory B. Gloor[1], Jean M. Macklaim[1], Vera Pawlowsky-Glahn[2] and Juan J. Egozcue[3]*

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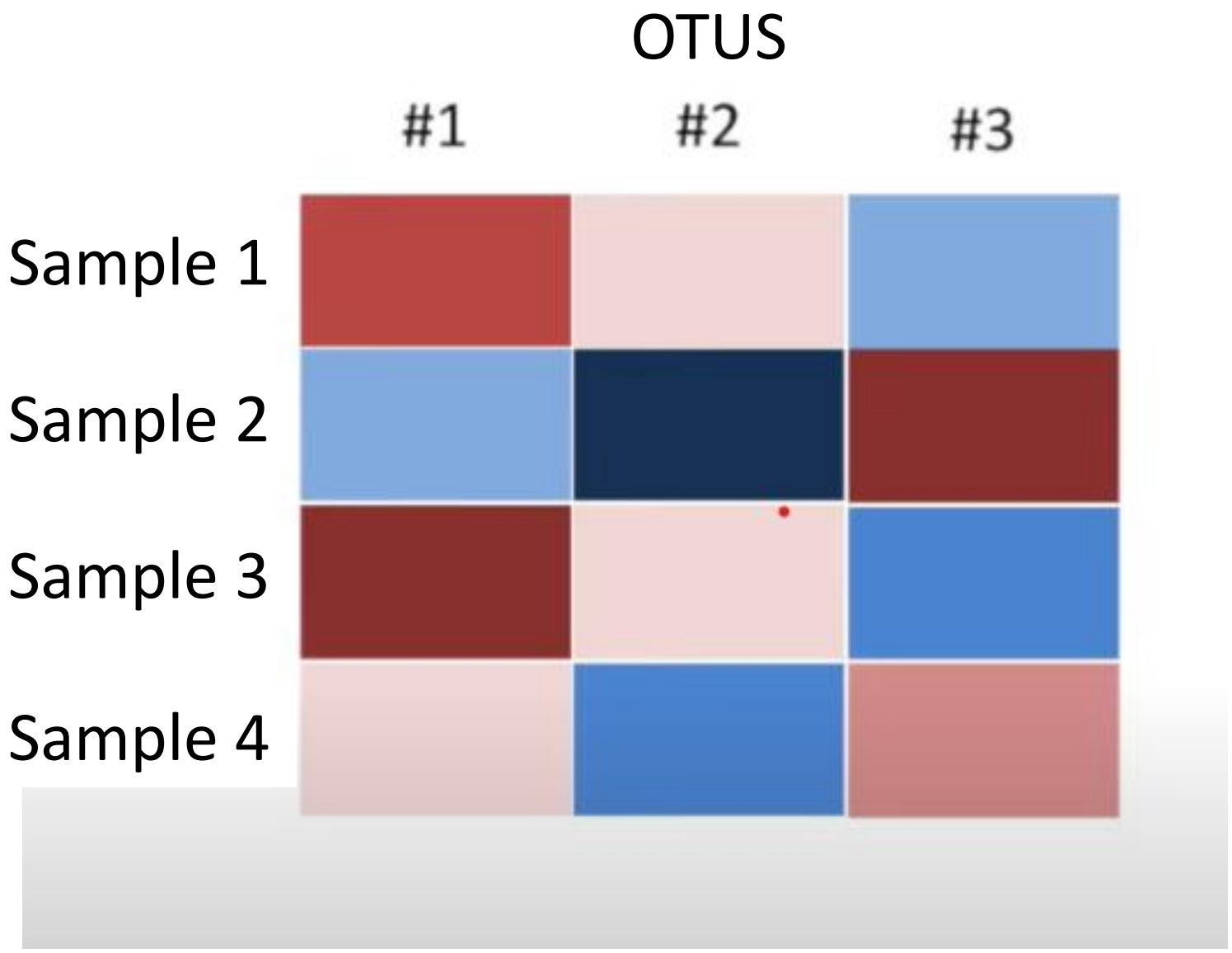
Datasets collected by high-throughput sequencing (HTS) of 16S rRNA gene amplimers, metagenomes or metatranscriptomes are commonplace and being used to study human disease states, ecological differences between sites, and the built environment. There is increasing awareness that microbiome datasets generated by HTS are compositional because they have an arbitrary total imposed by the instrument. However, many investigators are either unaware of this or assume specific properties of the compositional data. The purpose of this review is to alert investigators to the dangers inherent in ignoring the compositional nature of the data, and point out that HTS datasets derived from microbiome studies can and should be treated as compositions at all stages of

OPEN ACCESS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#3
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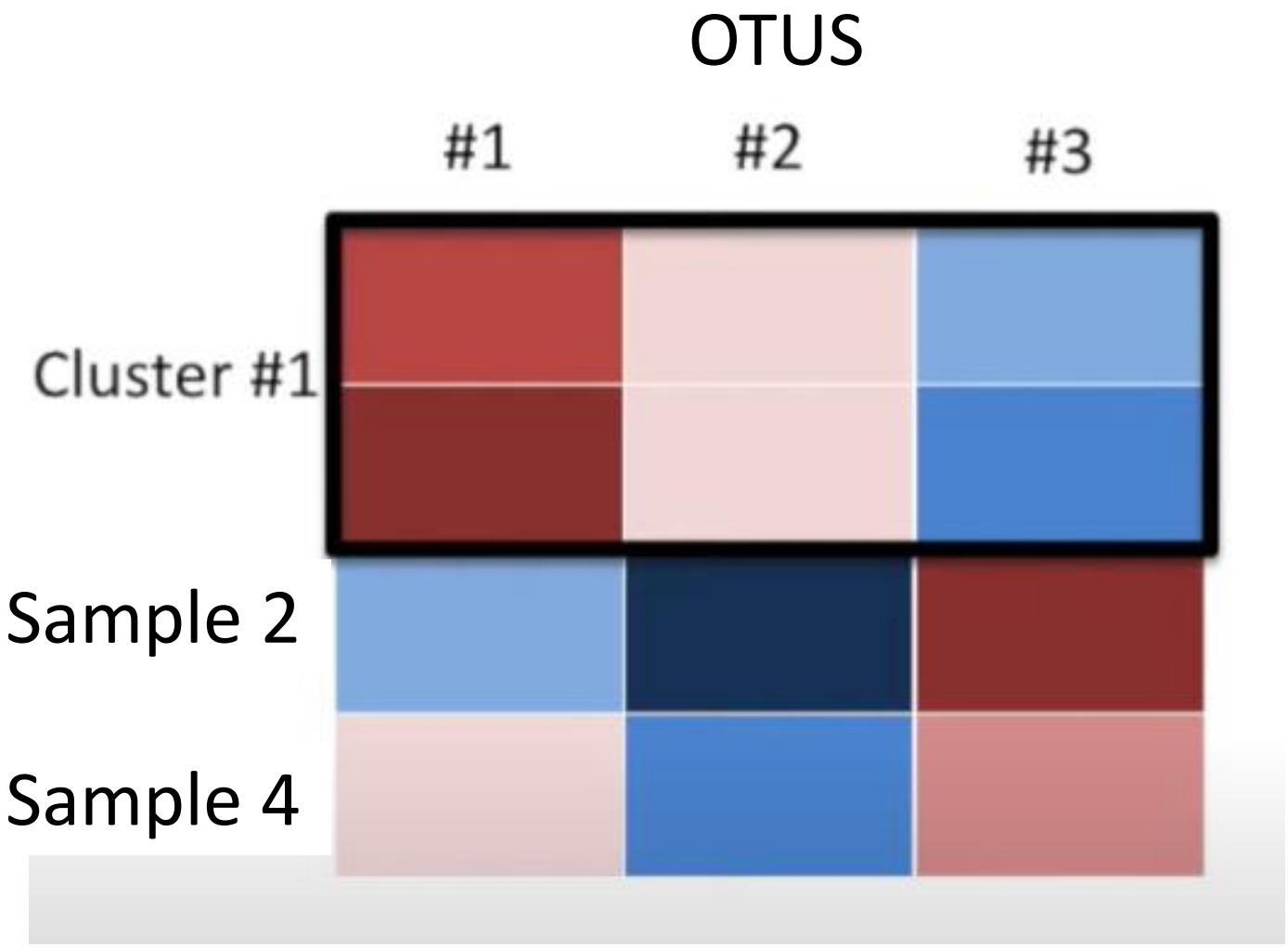
Sample 2
Sample 3
Sample 4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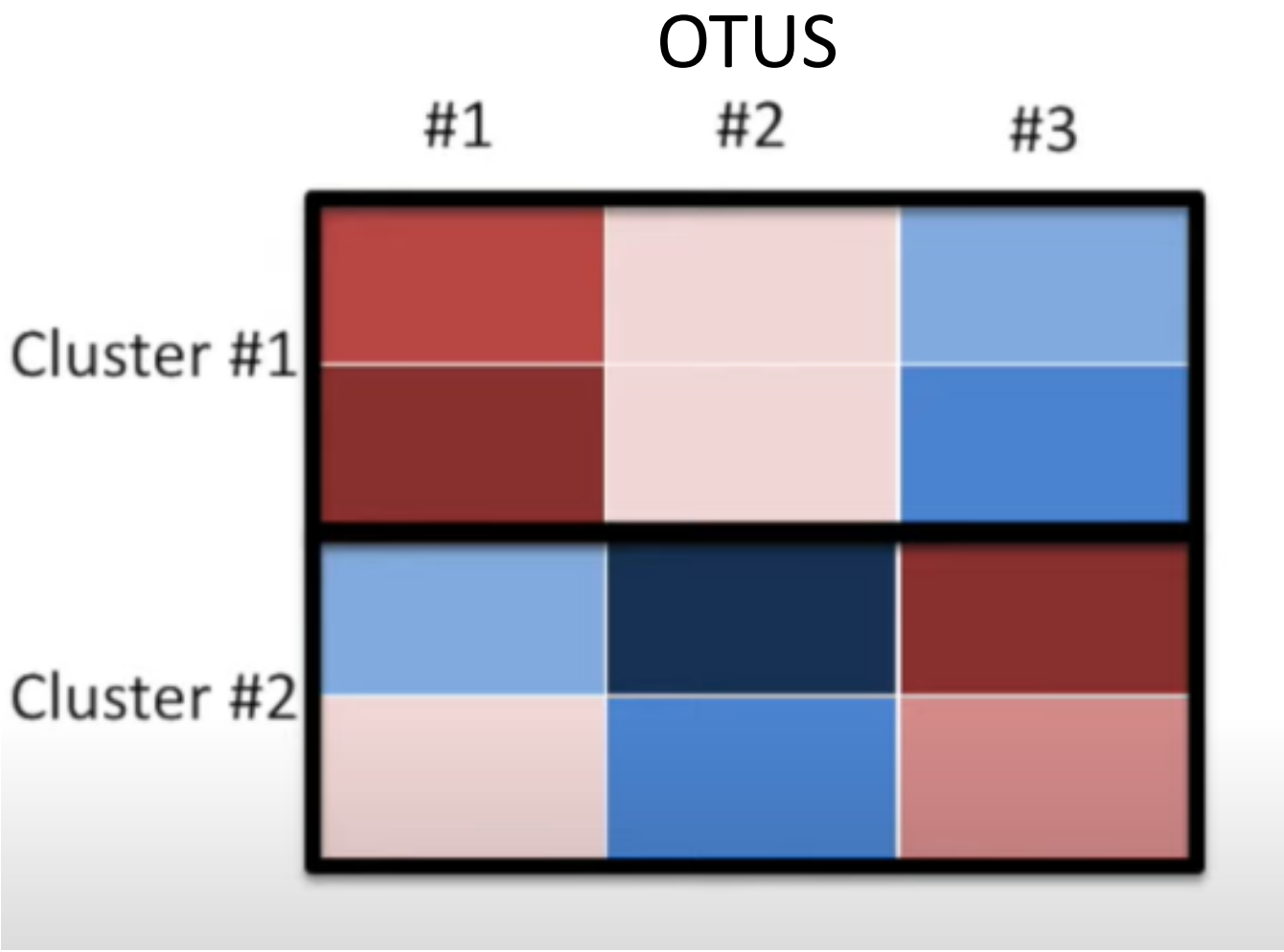
#3
Cluster #1
Sample 2
Sample 4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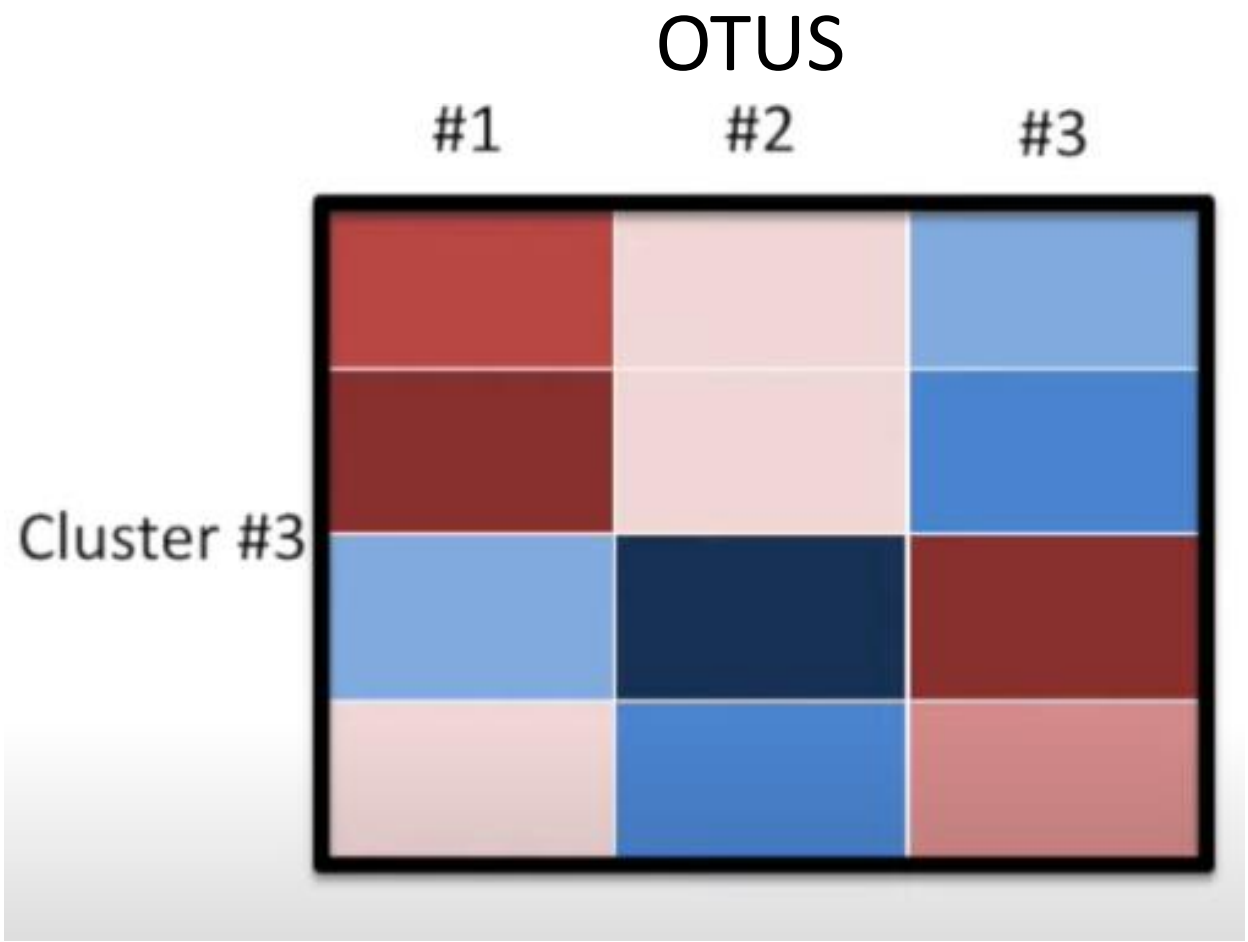
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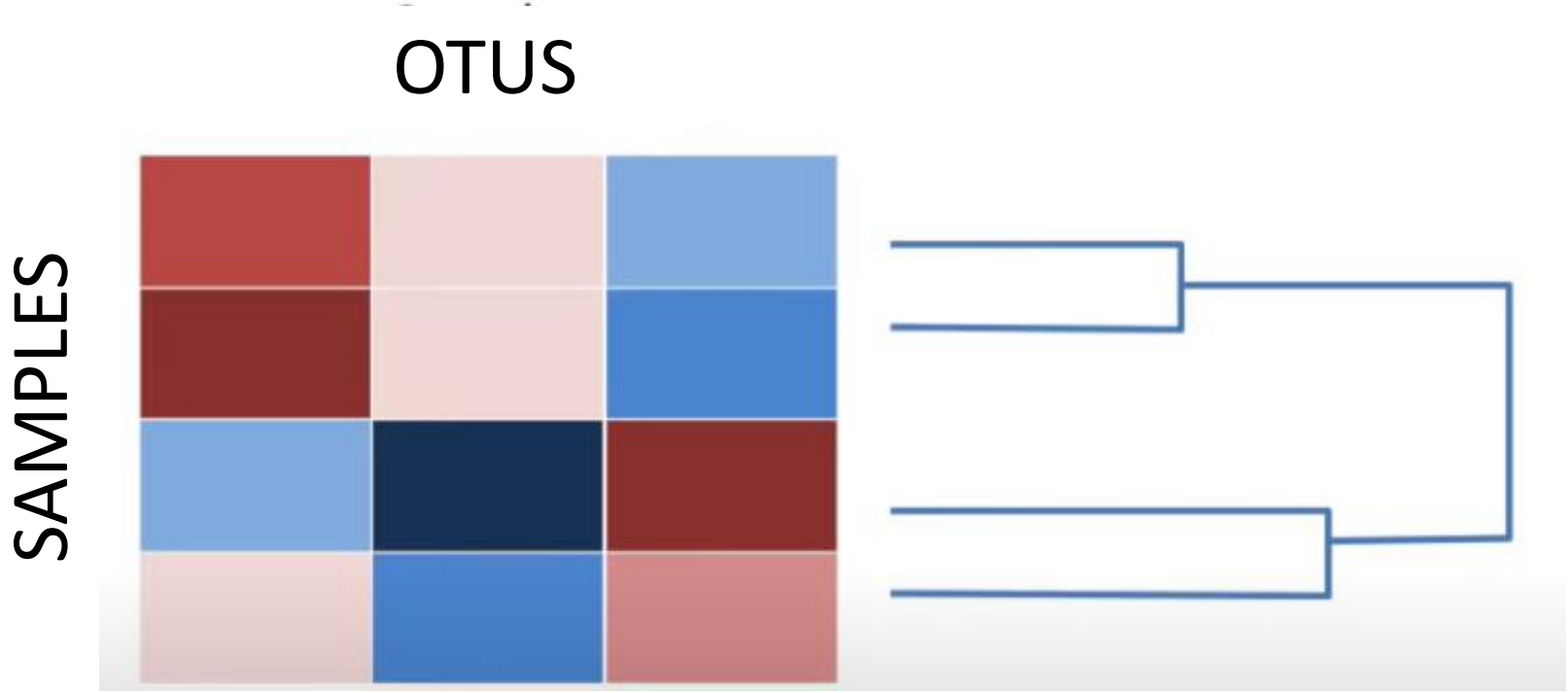
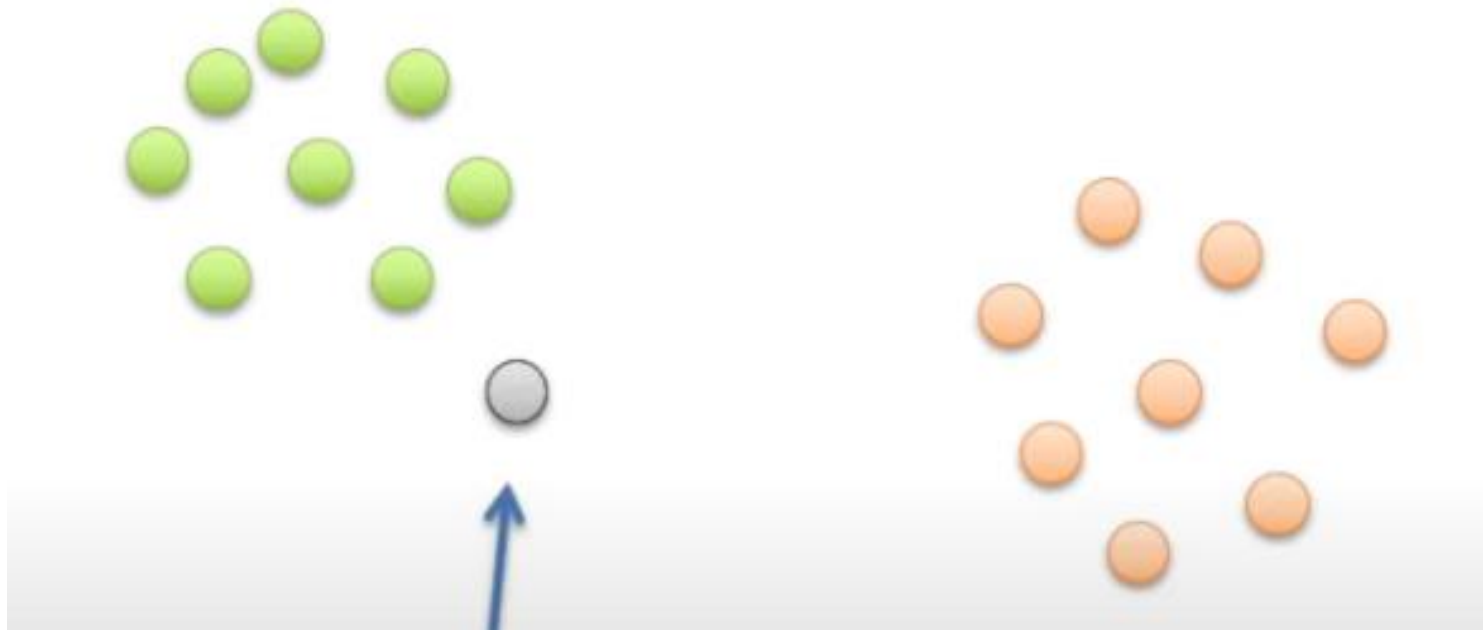
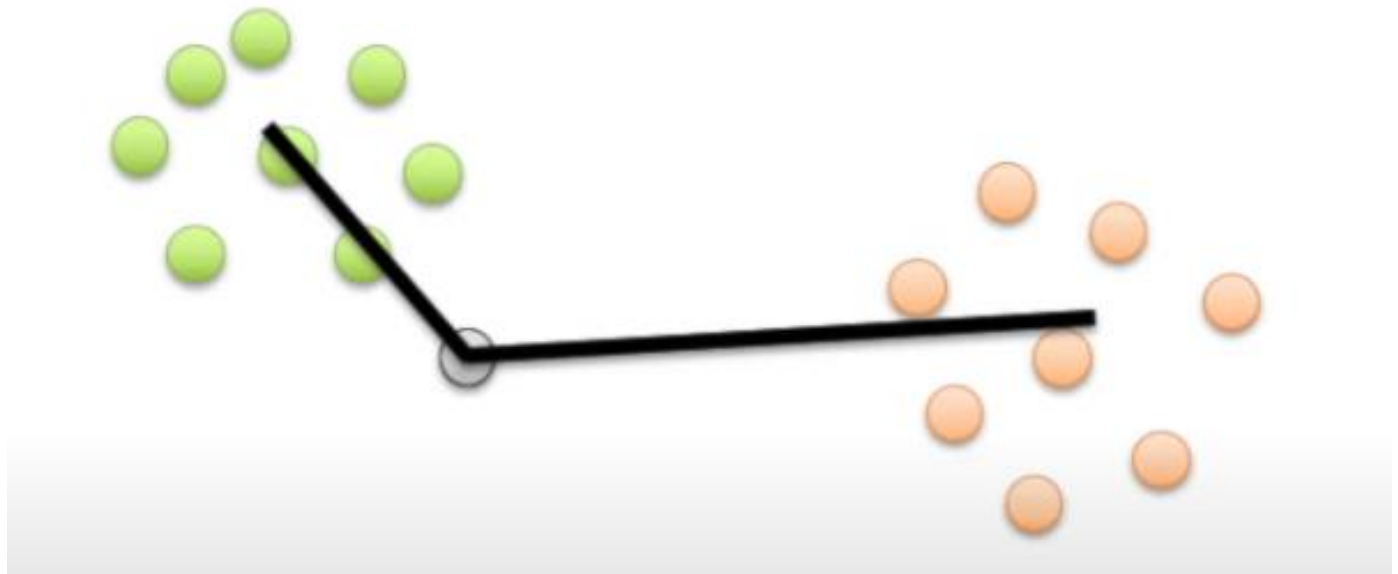
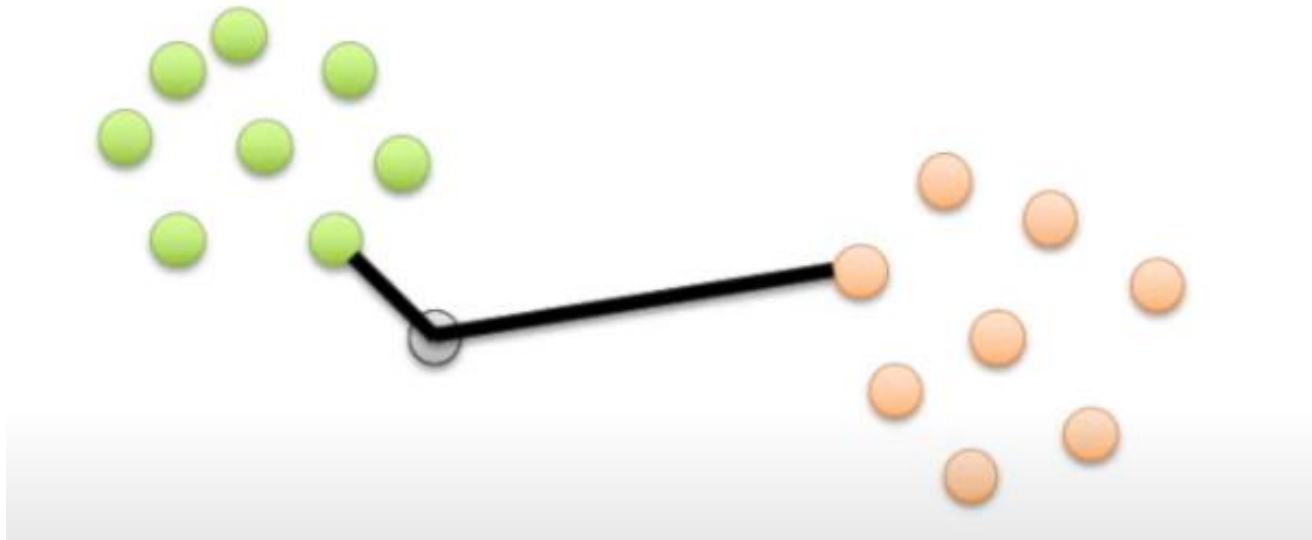
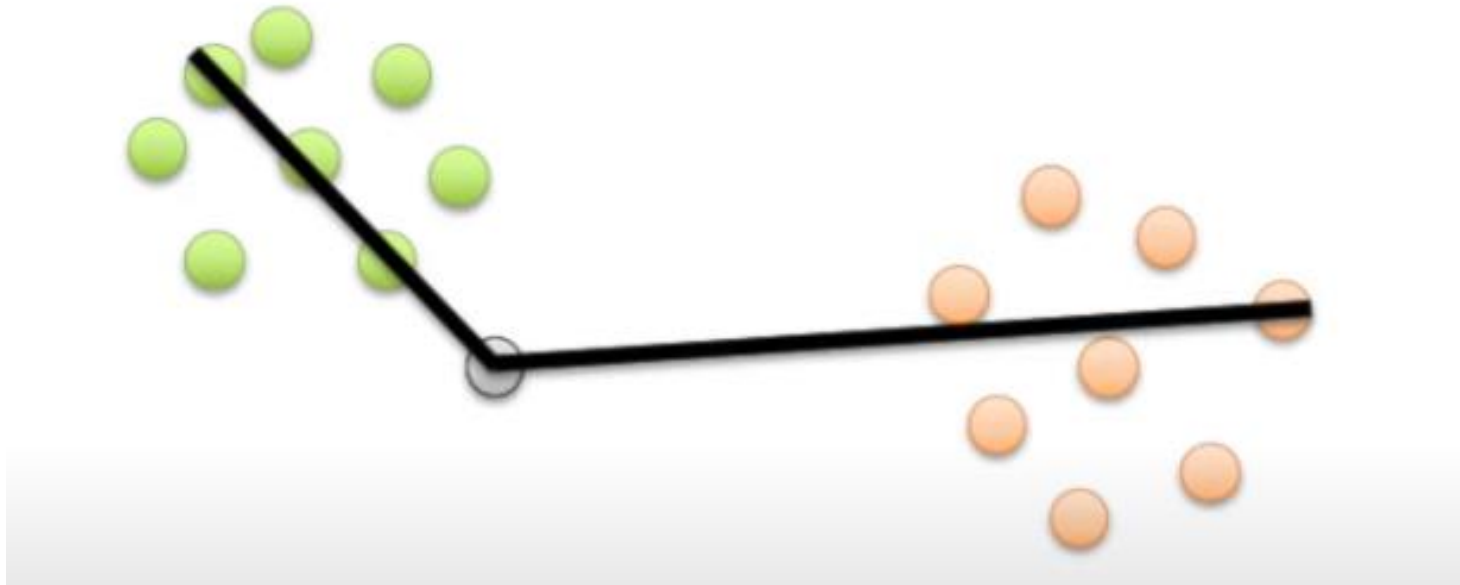
Cluster #3

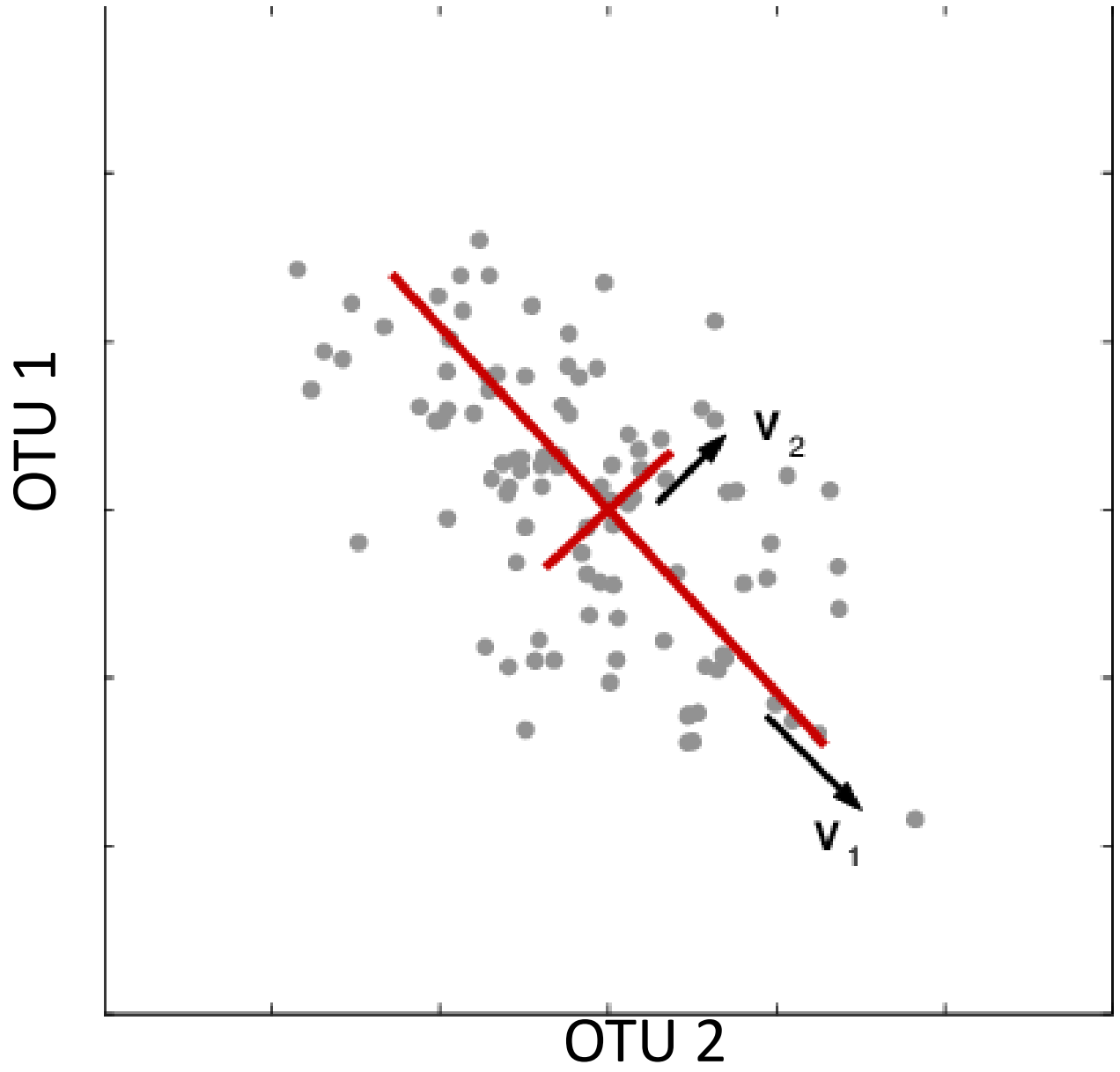

OTUS
SAMPLES



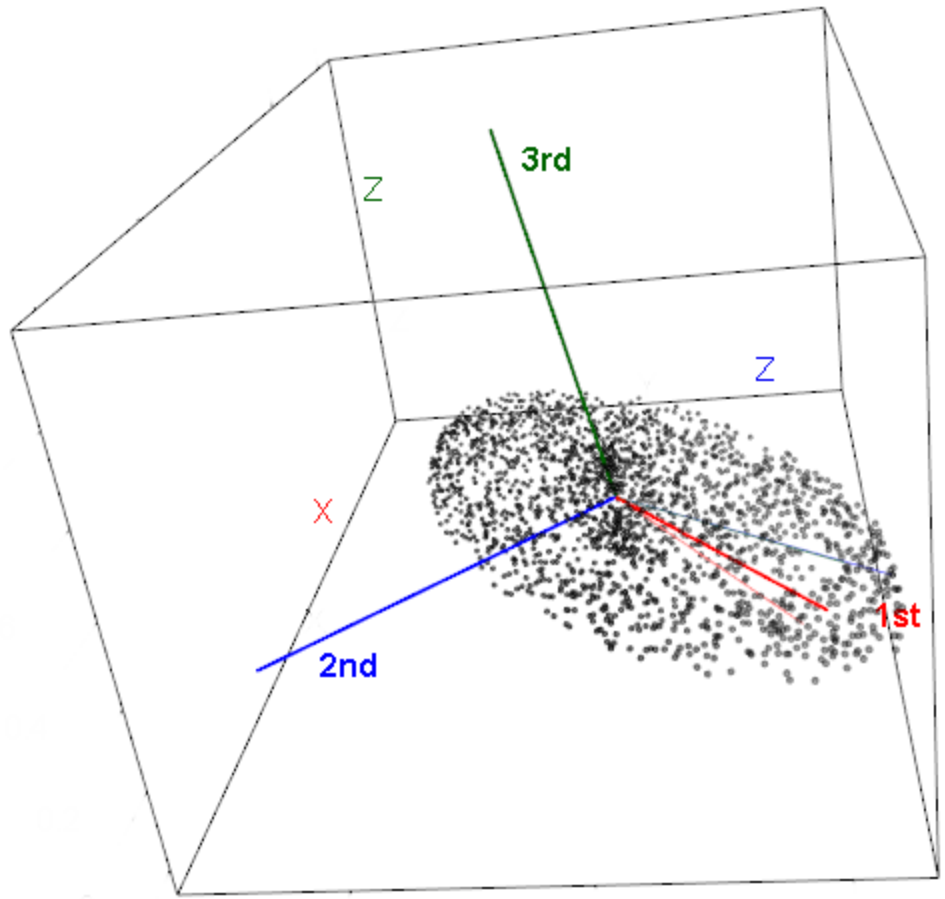







OTU 1
OTU 2
v 2
v 1

PCA applied to an ellipsoidically shaped point cloud



more information: www.joyofdata.de/blog/illustration-of-principal-component-analysis-pca

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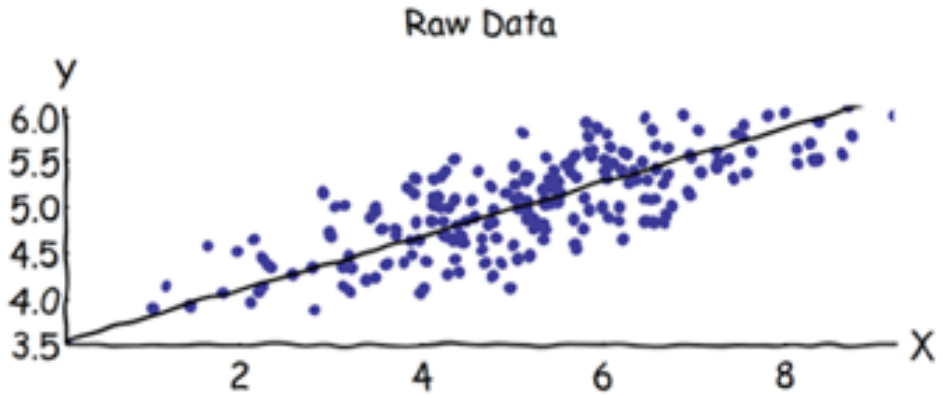
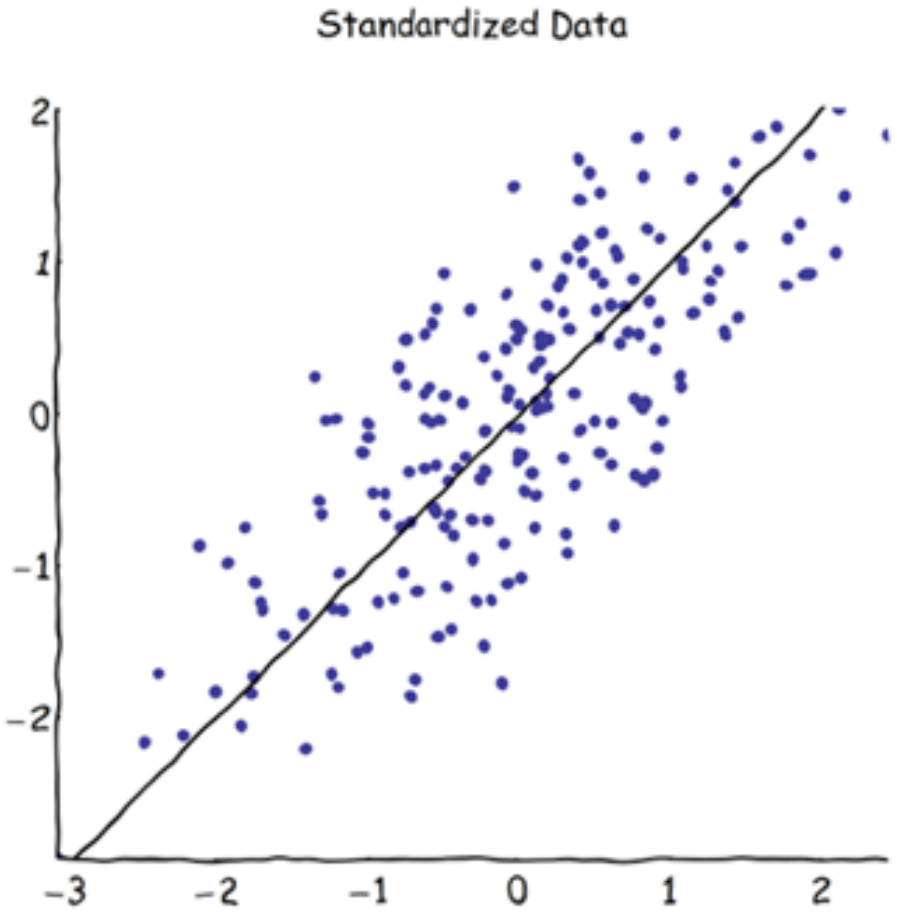
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