# Using Dendritic Heat Maps to Simultaneously Display Genotype Divergence with Phenotype Divergence.

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Introduction:

The visualization of sequencing data is an integral part of the analysis and communication of genomics-based research. A key advance in microbial ecology in both modern and ancient ecosystems will be connecting genotypic lineages and metabolisms to environmental dynamics. This has become a daunting task in light of the burgeoning repositories of -omics sequence data, calling on entirely new methods for analyzing and visualizing complex biogeochemical datasets. The effects of environment on biology are often shown as heat maps of sequence abundance, where the responses of distinct sequence groups are measured and compared. However, the grouping process of heat map construction is performed at a single, often arbitrary, level of inclusiveness. Here, we introduce dendritic heat maps (DHMs) that simultaneously display multiple heat maps over a range of binning specificities, arranged in a dendrogram-like configuration, to show the effects of environment on sequence homology and relative abundance. Importantly, tracking changes in relative abundance can be particularly useful for observing the levels at which genotypic divergence (cluster branching) correlates with gene expression (differing heat map bin response), helping to better understand the effects of environment on metabolism and genotypic lineages.

Figure 1: Representative DHM using simulated data:
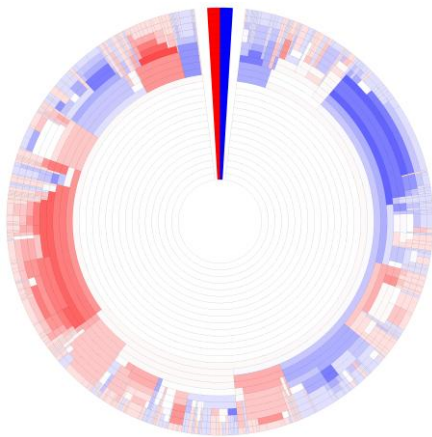
Results/Discussion:

We demonstrate that dendritic heat maps give freedom to scrutinize specific clustering levels across a range of cutoffs, track changes in phenotype inequity across multiple levels of sequence clustering specificity, and easily visualize how deeply rooted changes in phenotype inequity are in a dataset. As genotypes diverge in sample populations, clusters are shown to break apart into smaller clusters at higher identity cutoff levels, similar to a dendrogram. Phenotype divergence, which is shown as a heat map of relative abundance bin response, may or may not follow genotype divergences.

To make relationships that may emerge across hierarchical cutoffs more apparent, heat maps at each cutoff level are aligned, so that clusters may be directly compared across multiple cutoff levels. By aligning and clustering DNA molecules across these multiple cutoff levels, the aligned heat maps take on a radial dendrogram configuration (Seen in Figure 1). This is particularly useful, as the branching of a cluster into progressively more fine-grained clusters can be tracked and further annotated with heat map bin responses to reveal salient features of the clusters.

Overlaying phenotype shifts on genotype divergence creates a way to visually compare how deeply rooted observed phenotype ratios are across multiple genotypes. Displaying how deeply rooted a response is can be informative in many comparative studies that seek to better understand both the general and more finely detailed structures of the data by elucidating divergence points. Work that focuses on multi-scale genomic changes, such as evolution of microbial or viral populations, could benefit from the visualizations of DHMs.

Reference:

Kellom M., Raymond J. 2016. Using Dendritic Heat Maps to Simultaneously Display Genotype Divergence with Phenotype Divergence. PLOS ONE 11:e0161292. DOI: 10.1371/journal.pone.0161292.