Quantifying the prokaryotic resource niche

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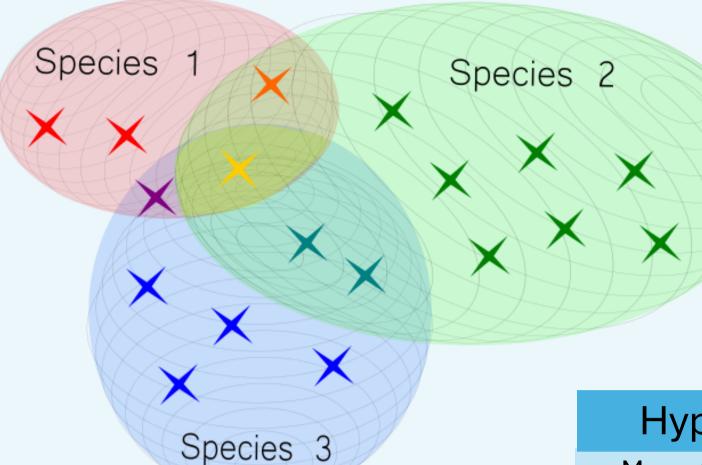


Fig 1:
Illustration of niche width (coloured circles) and niche overlap for resource requirements (x).

Background

- The ecological resource niche is the set of resources an organism requires for growth within its environment (fig 1). It can be observed by studying media recipes used to culture prokaryotes for optimal growth.
- Expanding on KOMODO¹, the
 MediaDive database² from DSMZ
 standardizes media recipes with the
 microbes able to grow on them.
- There is a limited understanding of how the fundamental niche (comprising intrinsic characteristics) effects the realised prokaryotic resource niche.

Hypothesis

- More genes (larger genomes) need more nitrogen and phosphorus resources³ for DNA replication, reducing the number of suitable growth media (niche width).
- Fewer genes limit the enzyme repertoire for resource conversion, reducing the number of suitable growth media.
- Species relatedness dictates patterns of resource niche overlap in prokaryotes.

Objectives

- 1. Create a unified framework linking species to their optimal resource media and constituent ingredient requirements.
- 2. For **intrinsic characteristics**: organism genome size, organism GC content, number of genes and number of protein coding genes, are there correlations with niche width and ingredient requirements?

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Methods

- Create a combined dataset of prokaryotes and their a) optimal growth media (b) optimal ingredient requirements (c) Intrinsic characteristics, via REST API calls to the NCBI and DSMZ.
- 2. Perform niche width analysis using the number of optimal media against the four intrinsic characteristics.
- 3. Analyze correlations for intrinsic characteristics and ingredient requirements using spearman's ranked correlation coefficient

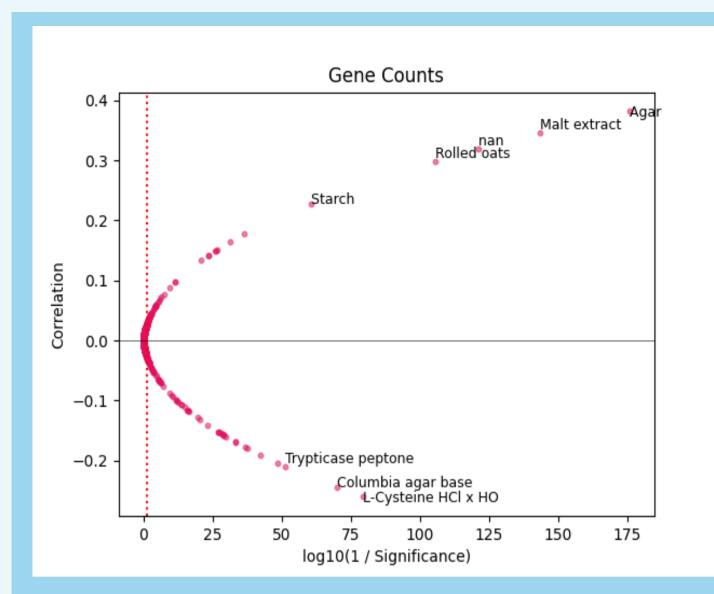


Fig 3: Relationship between log10(1/significance) and correlation coefficient for ingredient per gene count. Labels = Highly significant correlations, dotted red line = 5% significance level, solid black line = no correlation.

Preliminary Insights

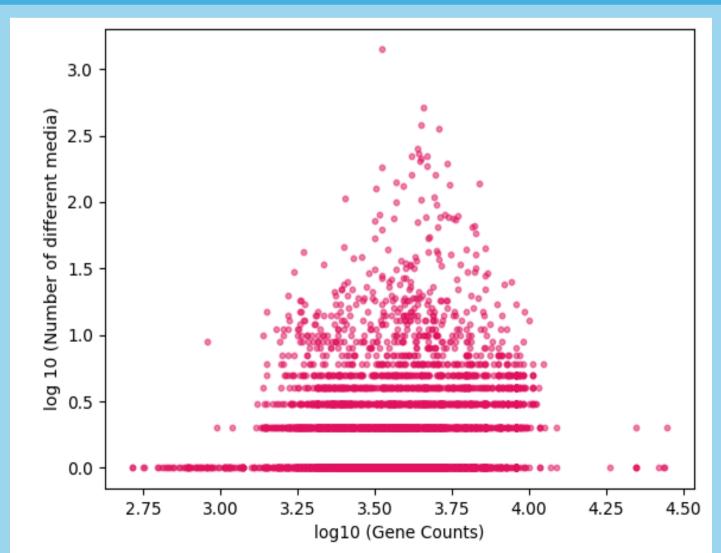


Fig 2: Relationship between log10 scaled genome size and log scaled niche width (denoted by number of different media). Discrete values on the y-axis are caused by log scaling for lower values.

Next Steps

- Microbes will fall into set life history strategies due to evolutionary trade-offs⁴.
- Investigate whether resource niche clustering occurs based on life-history strategies using PCA.
- Determine phylogenetic causes for the relationships involved.

References

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