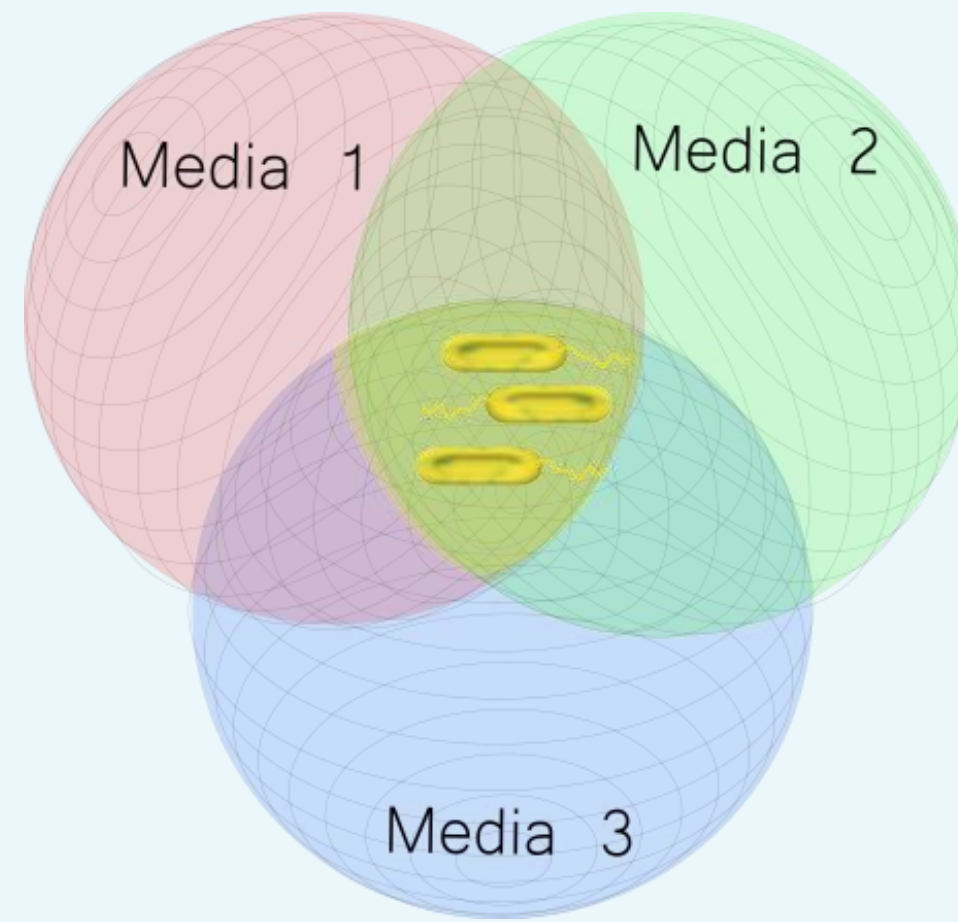


## Background

- The ecological resource niche defines the **set of resources an organism requires for growth within its environment**. It can be observed by studying media recipes used to culture bacteria for optimal growth.
- Expanding on KOMODO<sup>1</sup>, the MediaDive database<sup>2</sup> from DSMZ creates a standardized database linking media recipes with the prokaryotes able to grow on them.
- There is a limited understanding of how intrinsic organism characteristics (such as gene counts) effect the prokaryotic resource niche.



## Hypothesis

- Organisms with larger genomes (and more genes) need more nitrogen and phosphorus resources<sup>3</sup> for DNA replication, reducing their resource niche width.
- Equally, organisms with smaller genomes (and fewer genes) may lack certain enzymes required for resource conversion, thus also reducing their resource niche.

## Objectives

- Create a unified framework linking species to their optimal resource media and constituent ingredient requirements.
- For the four **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?

## Methods

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

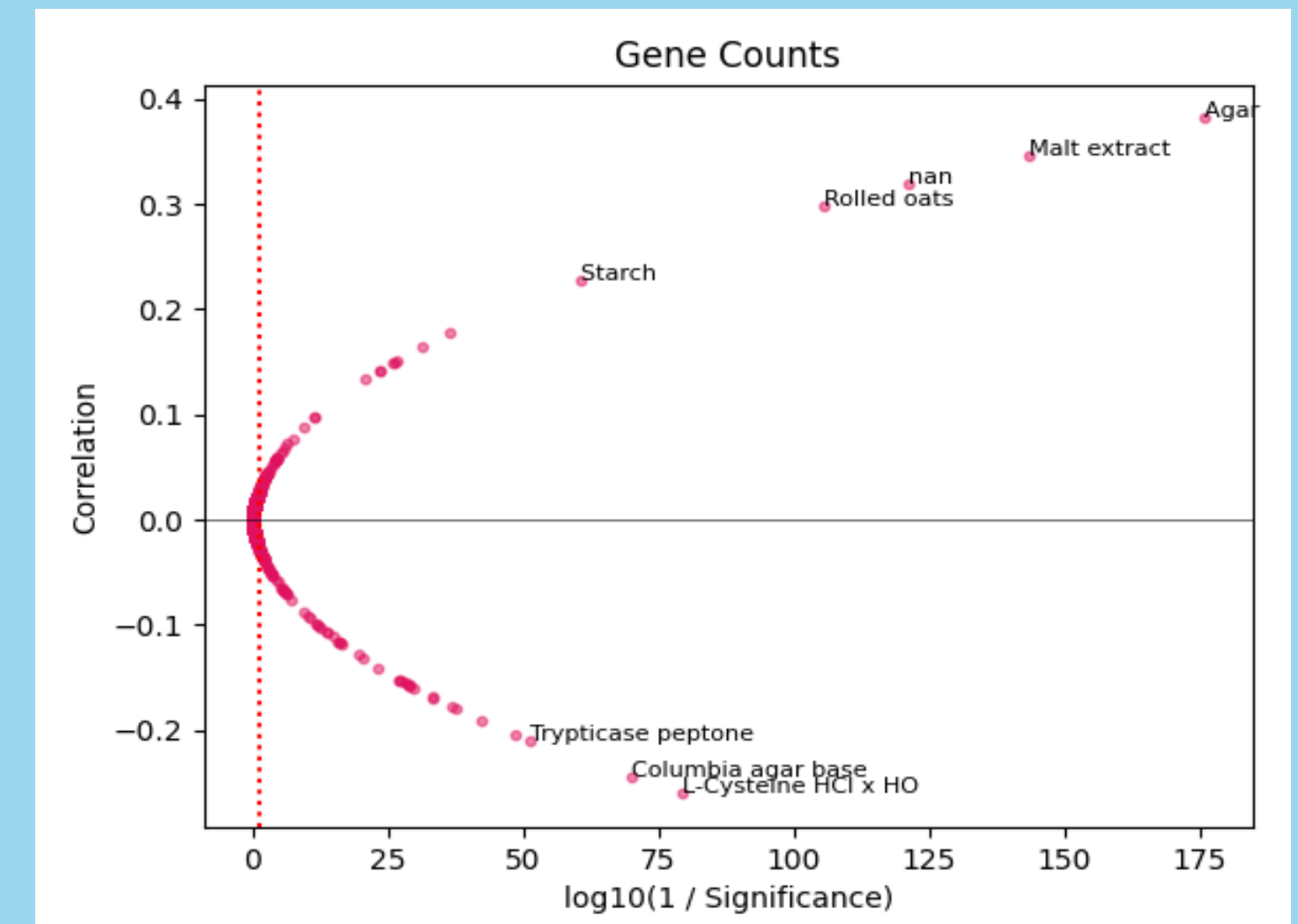


Fig 2: Plot detailing the spearman's ranked correlation coefficient of each ingredient requirement with respect to gene count. Highly significant correlations are labelled. The 5% significance level is highlighted by the dotted red line and the solid horizontal black line indicates the line of no correlation.

## Preliminary Insights

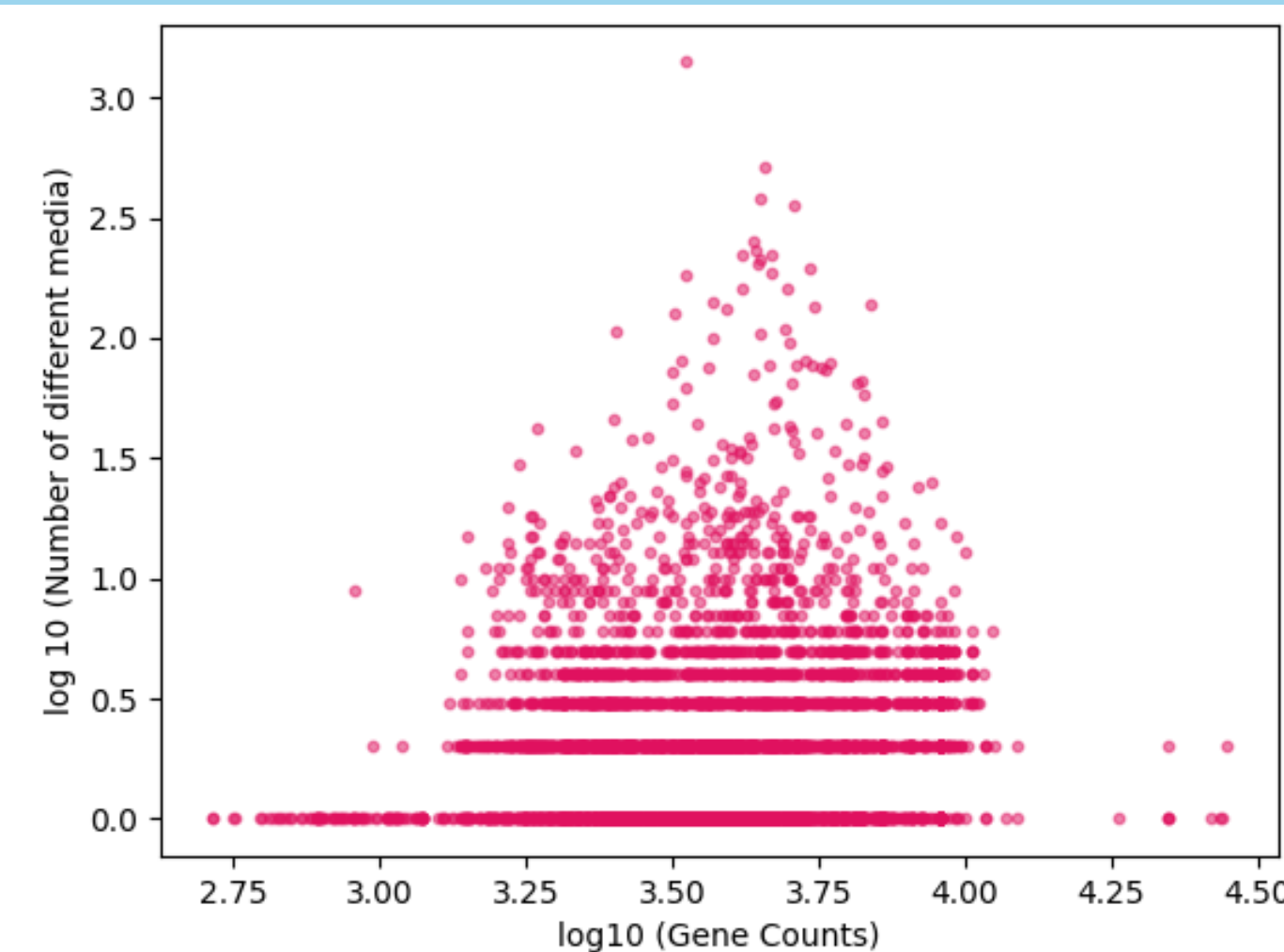


Fig 1: Relationship between log10 scaled genome size and log scaled niche width (denoted by number of different media). Discrete values on the y-axis are caused by log scaling for lower values.

## Next Steps

- Microbes will fall into set life history strategies due to evolutionary trade-offs<sup>4</sup>.
- Investigate whether resource niche clustering occurs based on life-history strategies using PCA.
- Determine phylogenetic causes for the relationships involved.

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