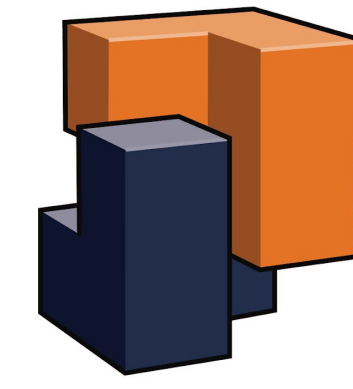# Visualizing 'omic feature rankings and log-ratios using Qurro

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Theme 3, "Scaling Applications and Making the Programmer's Life Easy"

Task 2780.023, "Precision Medicine"

CRISP
Center for Research on Intelligent Storage and Processing in Memory

Qurro

Compositionality

Usually, we only know <u>relative abundances</u> of features. We can't infer "absolute" changes.
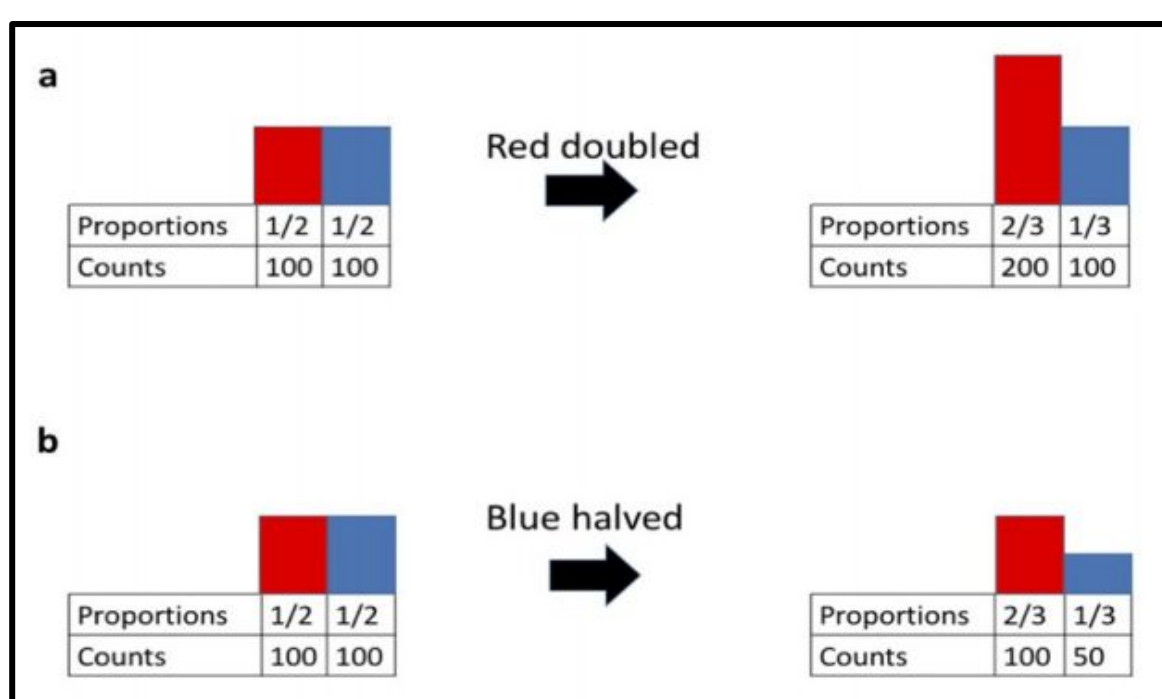

Figure from *Morton et al. 2017*. Also see *Gloor et al. 2017*.

Rankings and log-ratios

rankings: order features by some sort of (estimated) variation

ratios: cancel out "total microbial load" bias

log-ratios: center the ratio around zero (enables standard statistical testing)

See *Gloor et al. 2017*, *Martino et al. 2019*, and *Morton et al. 2019*.
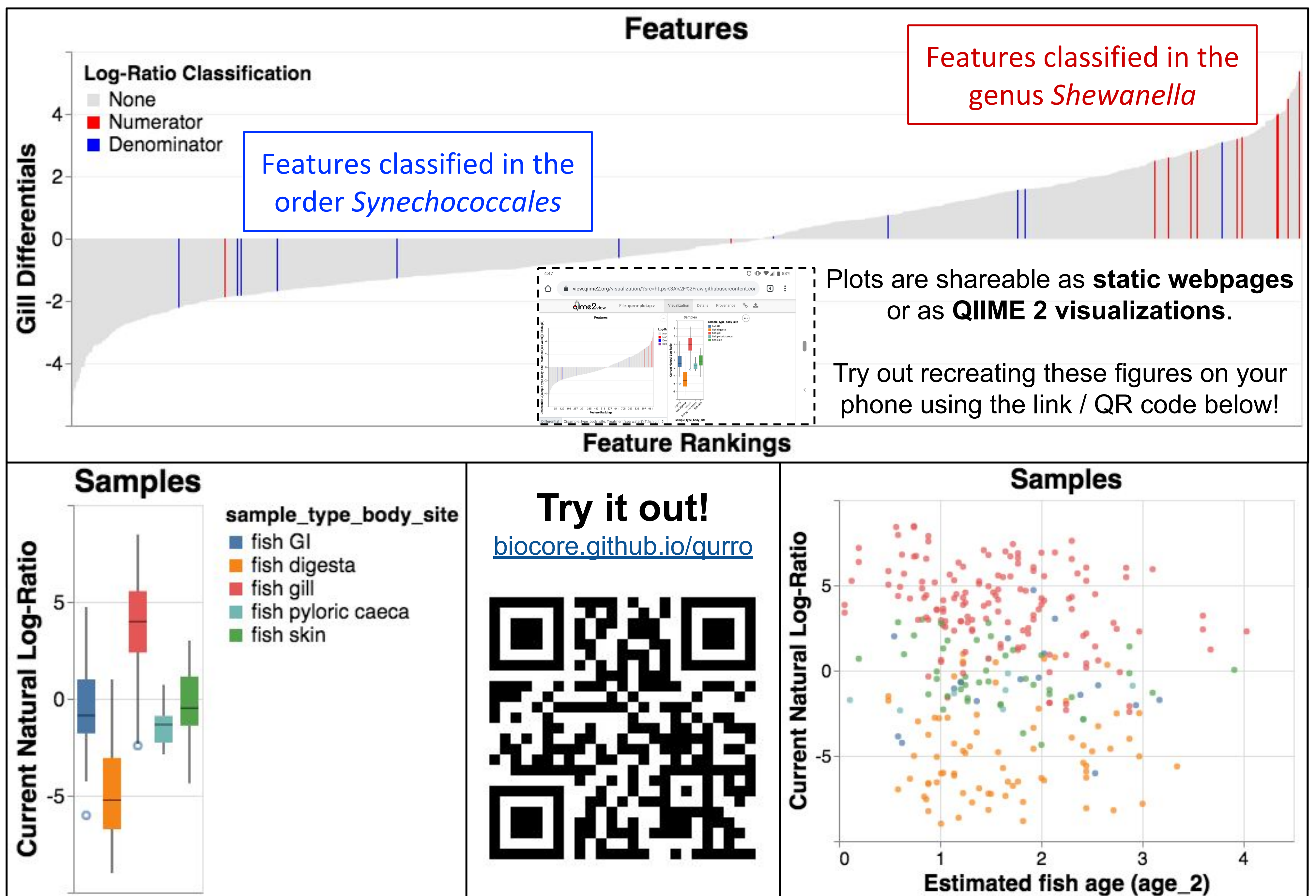
Computational hurdles

Various types of processing needed before higher-level visualizations like this, depending on dataset:

performing taxonomic classification of sequences

filtering out host DNA in metagenomic sequencing (discussed elsewhere today)

...and more!

Example: 16S rRNA marker gene sequencing data from Pacific chub mackerel (*Scomber japonicus*) samples

Features classified in the genus *Shewanella*

Features classified in the order *Synechococcales*

Plots are shareable as **static webpages** or as **QIIME 2 visualizations**.

Try out recreating these figures on your phone using the link / QR code below!

Try it out!

biocore.github.io/qurro

The log-ratio of *Shewanella* features to *Synechococcales* features is comparatively large in Pacific chub mackerel gill samples, corroborating prior research.

Demos of five real datasets—including this one—are available at the link / QR code above!

Acknowledgements