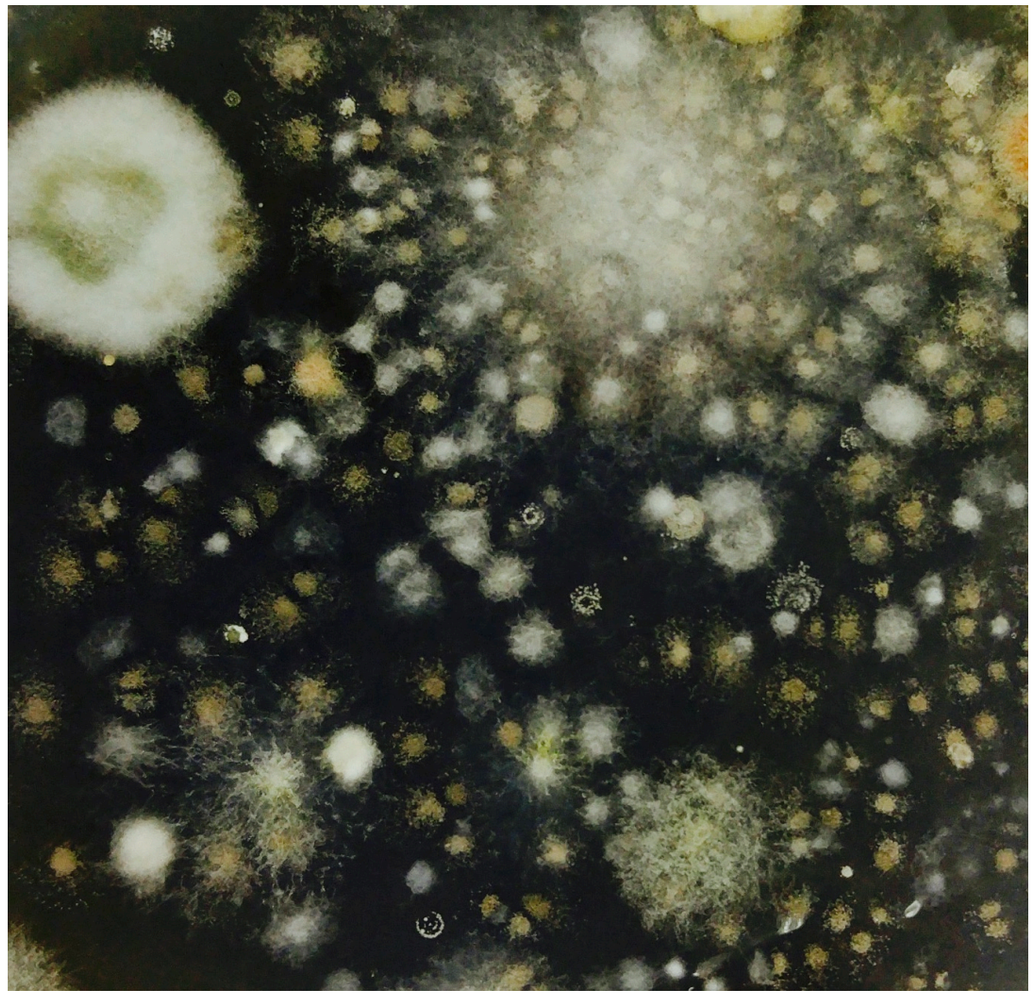
A rigorous & rational approach to

Microbial differential abundance



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Slides: github.com/statdivlab/presentations

Paradigms for microbiome data analysis

- Two statistical paradigms:

1. “How do we *model the data?*”

2. “How do we *learn about biology?*”

Paradigm 1: Model the data

- “Modeling the data” conversations sound like
  - compositional? overdispersed? zero-inflated? Negative binomial? Multinomial-Dirichlet? …
- rarefy?
- best α- and β-diversity metrics?
- best transformation / “normalization”?

Paradigm 2:
Learn about biology

- “Learning about biology” conversations sound like
  - What exists in the environment?
  - What would we like to learn?
  - How does our data reflect that environment?
  - What can we learn from our data? Under what assumptions?

Today: Paradigm 2 for differential abundance

Statistics > Methodology

[Submitted on 7 Feb 2024 (v1), last revised 14 Mar 2025 (this version, v2)]

Estimating Fold Changes from Partially Observed Outcomes with Applications in Microbial Metagenomics

David S Clausen, Sarah Teichman, Amy D Willis

We consider the problem of estimating fold-changes in the expected value of a multivariate outcome observed with unknown sample-specific and category-specific perturbations. This challenge arises in high-throughput sequencing studies of the abundance of microbial taxa because microbes are systematically over- and under-detected relative to their true abundances. Our model admits a partially identifiable estimand, and we establish full identifiability by imposing interpretable parameter constraints. To reduce bias and guarantee

Software: github.com/**statdivlab/radEmu**

What exists in the environment?

- "There is some number of a given biological quantity in every environment"

- "There are 54,601 *S. epidermidis* cells on my index finger"

- "There are 0 transcripts of the gene *Core RC1 subunit PsaA* on this podium”

- "There are 874,455,469 genomes circulating in 100 mL seawater with the 16S variant CGGAGGGTGCA…”

What exists in the environment?

Y_{ij} = true number of genomic unit j in environment i

$X_i \in \mathbb{R}^p$ covariate information
(treatment vs control, age, sex, diet…)

😻 Y_{ij} 💸	1	2	…	J
ENV 1				
ENV 2				
…				
ENV M				
ENV M+1				
…				
ENV N-1				
ENV N				

What would we like to know?

Y_{ij} = true number of unit j in sample i

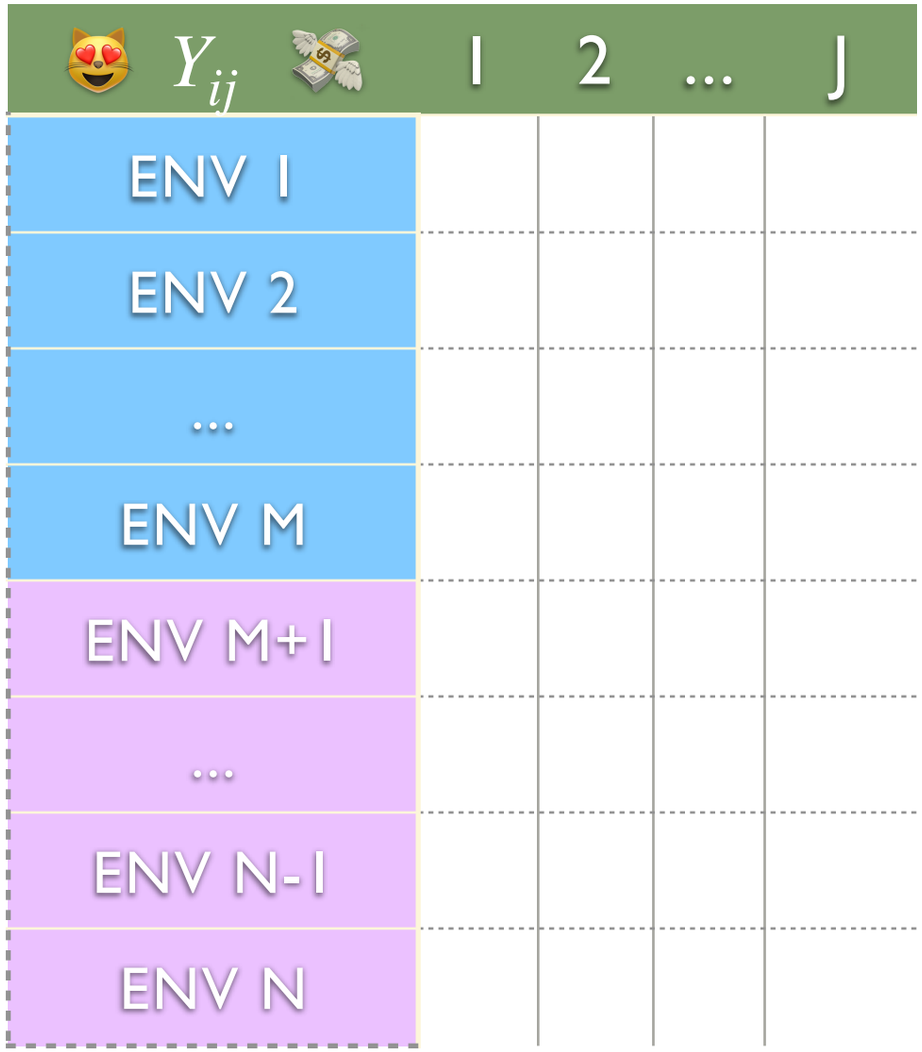
We do **not** observe $\{Y_{ij}\}$…

…but if we did, what would we do?

😻 Y_{ij} 💸	1	2	…	J
ENV 1				
ENV 2				
…				
ENV M				
ENV M+1				
…				
ENV N-1				
ENV N				

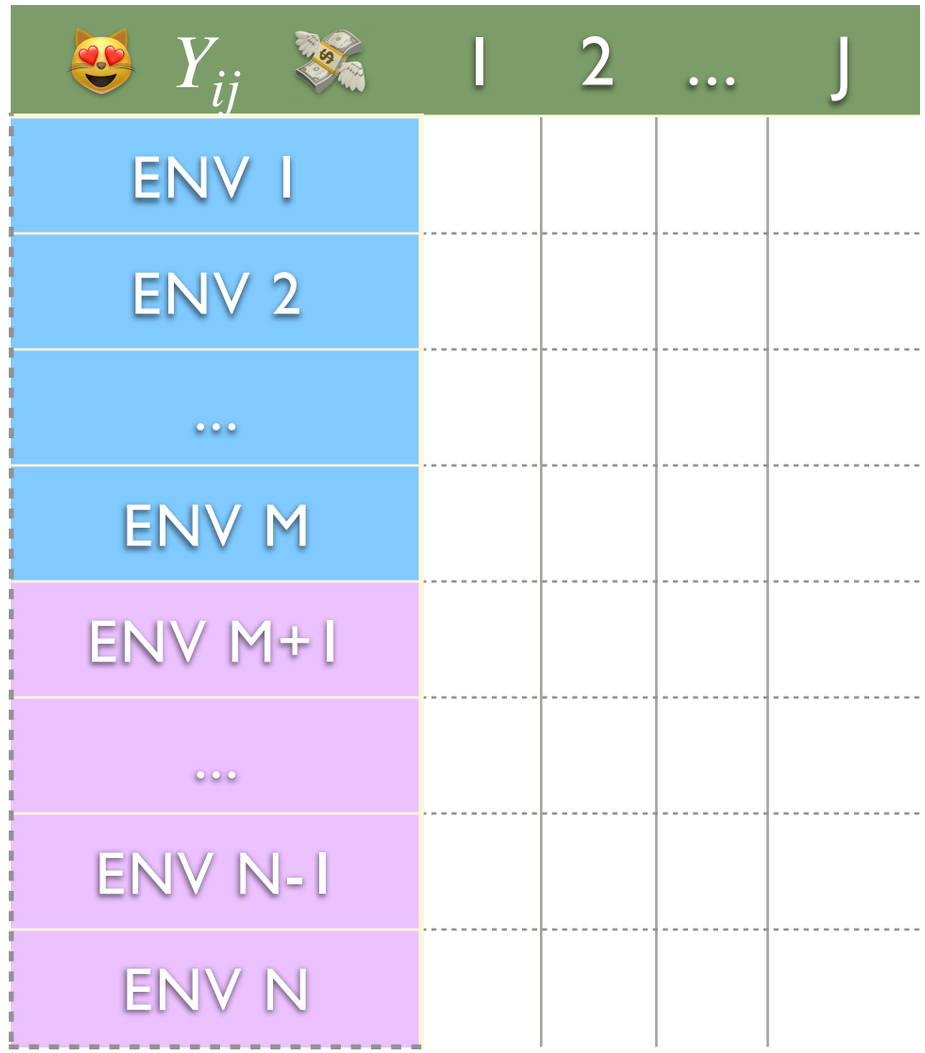
What would we like to know?

- How *abundant* are species?
  - Average of Y_{i4} across environments
- How *present* are species?
  - % of environments in which $Y_{i2} > 0$
- How *diverse* are communities?
  - $\#\{j : Y_{ij} > 0\}$
  - $-\sum_{j=1}^{J} p_{ij} \log p_{ij}$ for $p_{ij} := \frac{Y_{ij}}{\sum_j Y_{ij}}$
- ...



What would we like to know?

- Which species differ in their average abundance?
  - All?
- By how much?
  - 0.1%? 50%? 500%?



What data do we have?

Y_{ij} = true number of unit j in sample i

W_{ij} = number of times unit j observed in sample i from HTS

🌧️ W_{ij} 😿	1	2	…	J
SAMPLE 1				
SAMPLE 2				
…				
SAMPLE M				
SAMPLE M+1				
…				
SAMPLE N-1				
SAMPLE N				

How do we connect the Y_{ij}'s and the W_{ij}'s?

Connecting data to reality

- Traditionally, DA methods assume

$$\mathbb{E}[W_{ij}] = c_i Y_{ij}$$

- Is this reasonable?

Connecting data to reality

- Mock community: An artificially constructed community of known composition

	L.crispatus	L.iners	A.vaginae	S.agalactiae	G.vaginalis	S.amnii	P.bivia
1	0	0	0	1.00	0	0	0
2	0	0	0.5	0	0	0	0.5
3	0.33	0.33	0	0	0	0	0.33
4	0.33	0.33	0	0.33	0	0	0

Connecting data to reality

	L.crispatus	L.iners	A.vaginae	S.agalactiae	G.vaginalis	S.amnii	P.bivia
1	19	4	2	51332	1	14	1
2	0	1	1424	0	0	7	21708
3	4775	11234	0	0	0	1	3249
4	1644	5497	1	4521	0	7	0

	L.crispatus	L.iners	A.vaginae	S.agalactiae	G.vaginalis	S.amnii	P.bivia
1	0	0	0	1.00	0	0	0
2	0	0	0.5	0	0	0	0.5
3	0.33	0.33	0	0	0	0	0.33
4	0.33	0.33	0	0.33	0	0	0

Data from Brooks *et al* (2015) BMC Microbiology

Connecting data to reality

1. Despite equal mixing fractions, some taxa are observed many more times

2. Despite being purportedly absent, taxa are observed

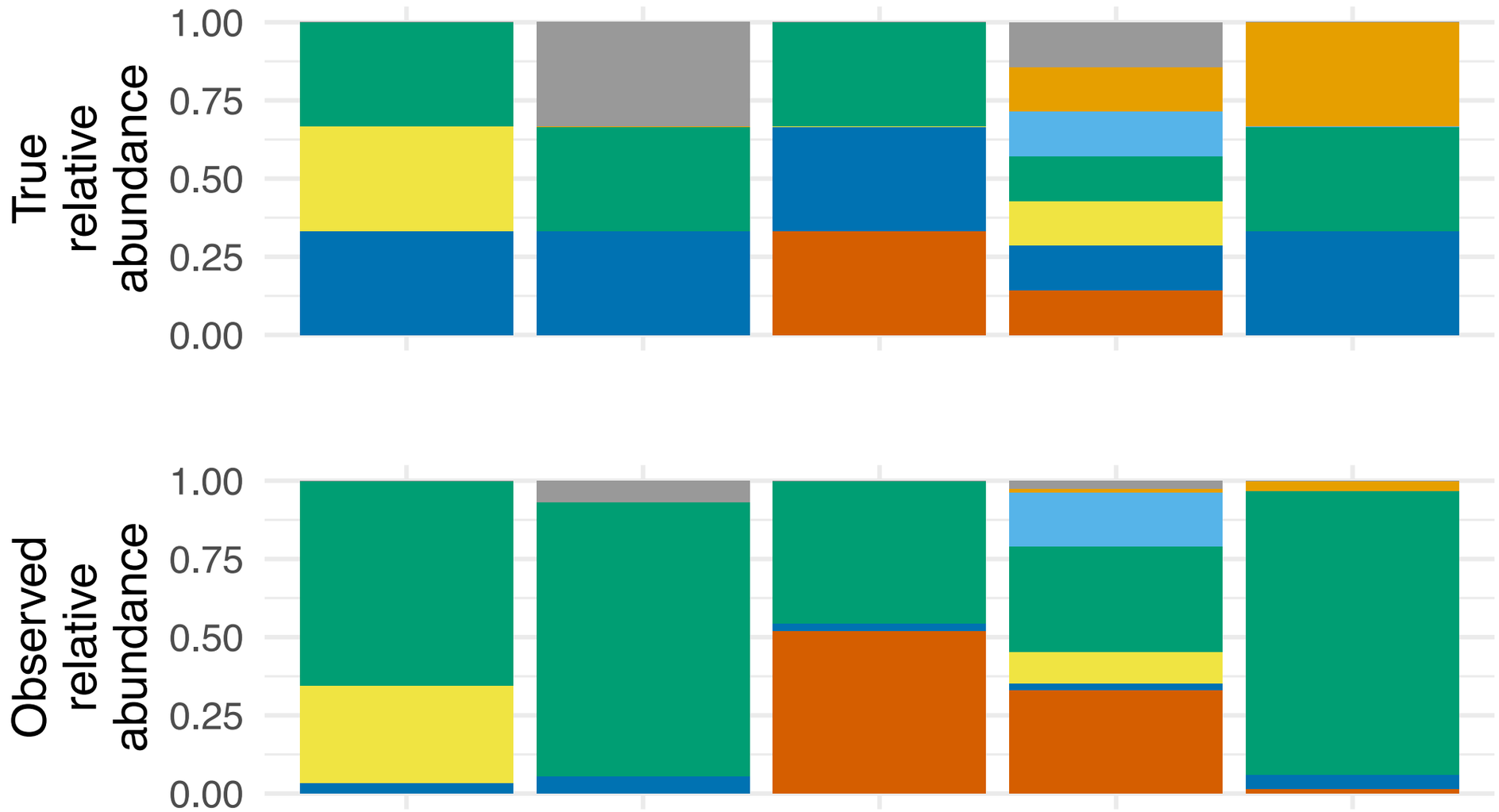
Connecting data to reality

- Despite the common assumption that

$$\mathbb{E}[W_{ij}] = c_i Y_{ij}$$

some taxa are *over-observed* for equal c_i and Y_{ij}

- What model better explains this observation?



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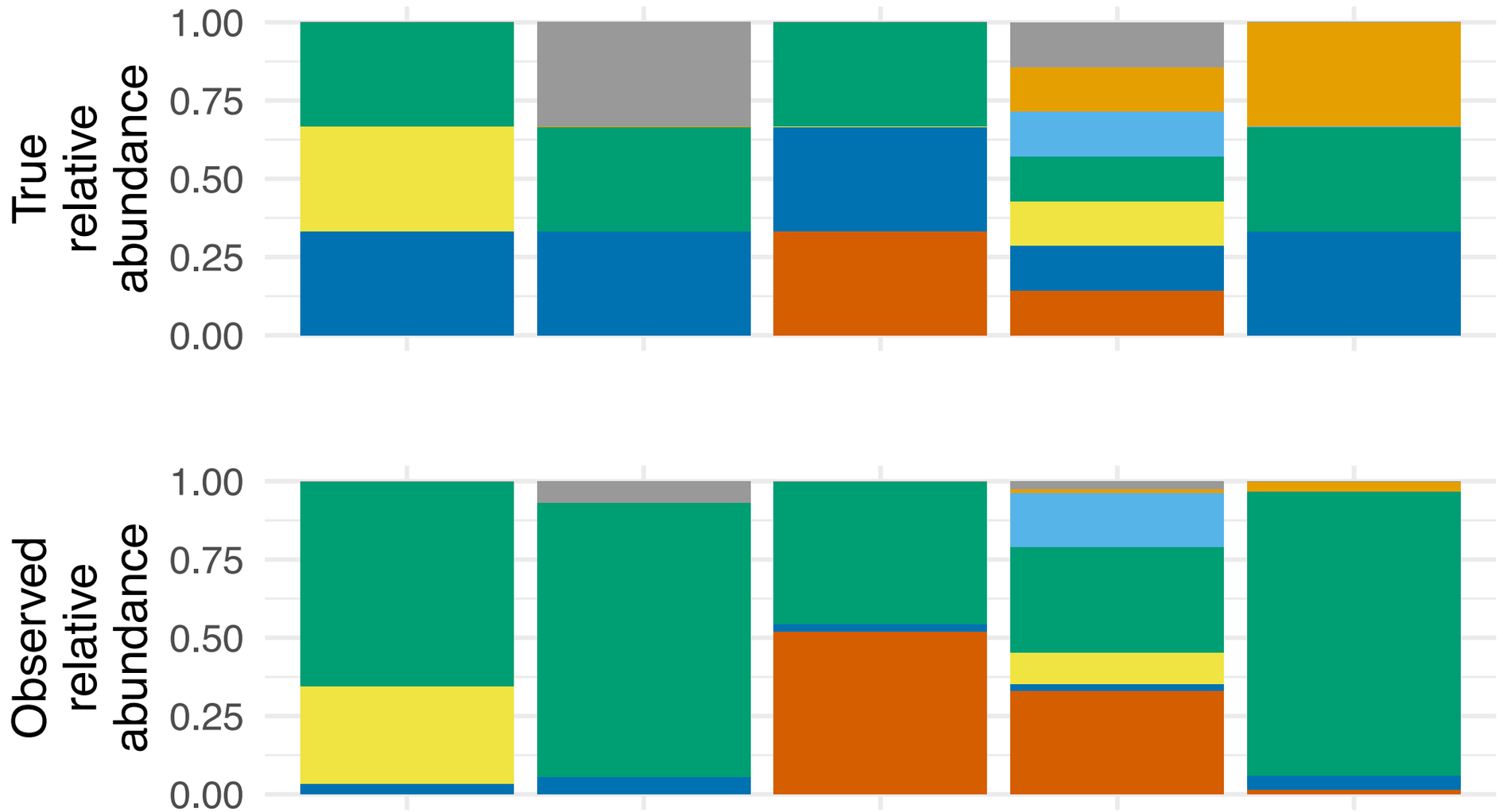


L.iners/S.agalactiae						
	19.5	16.1	18.9	17.4	19.9	**18.3 (1.6)**

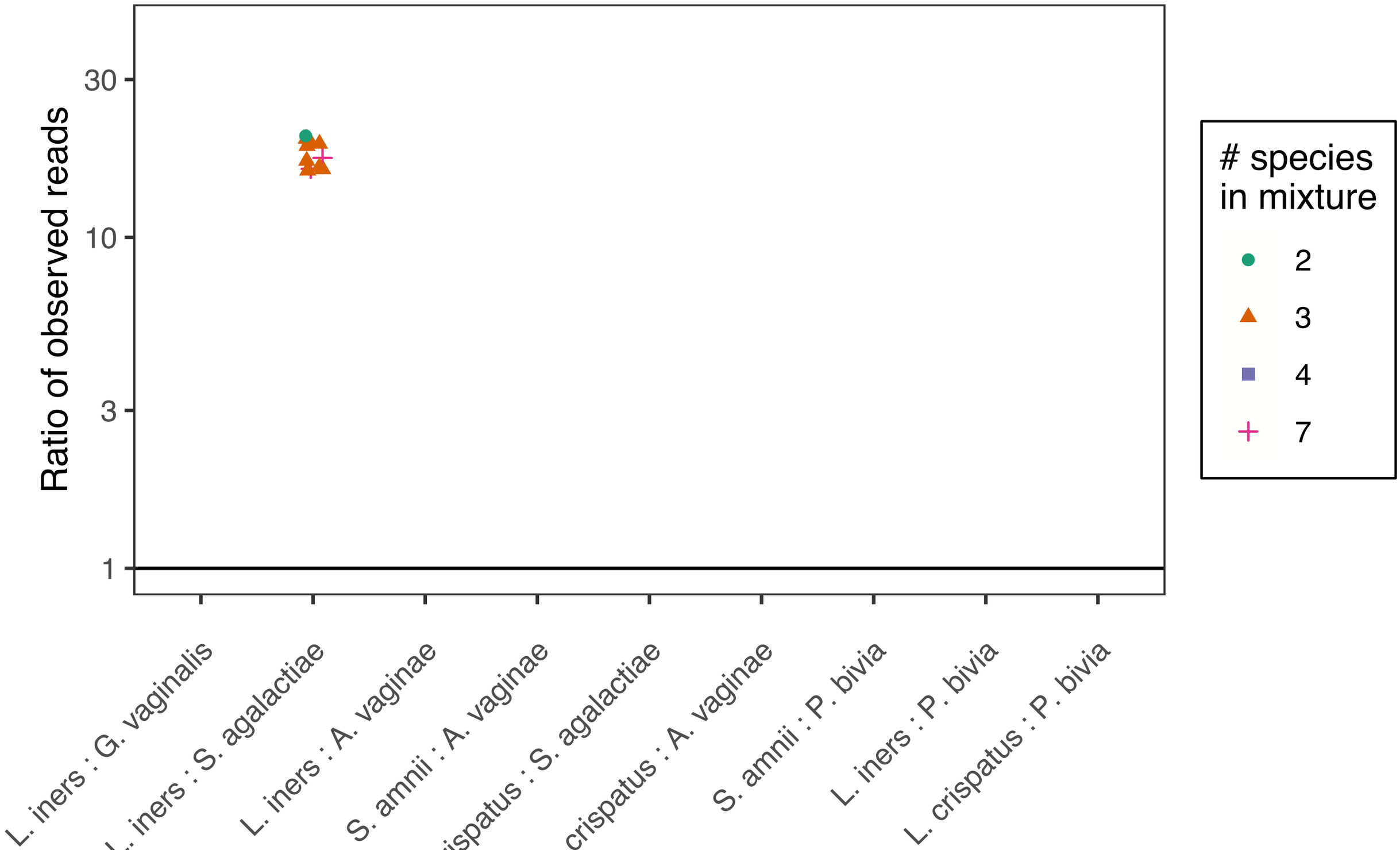


 Figure adapted from McLaren, Willis & Callahan, 2019, *eLife*

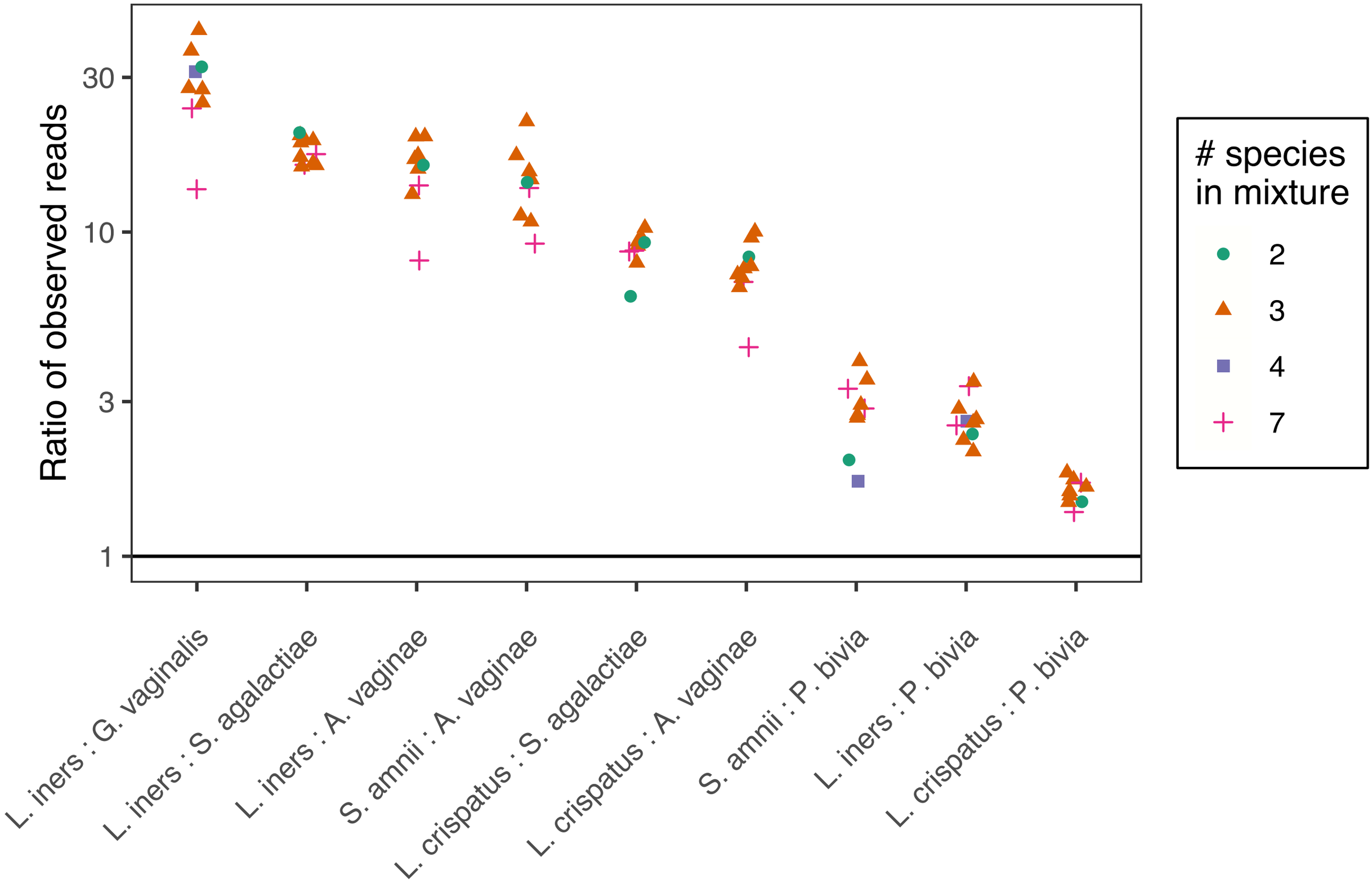


 Figure adapted from McLaren, Willis & Callahan, 2019, *eLife*

Connecting data to reality

- Evidence *against*

$$\mathbb{E}[W_{ij}] = c_i \times Y_{ij}$$

- Better support for

$$\mathbb{E}[W_{ij}] = c_i \times e_j \times Y_{ij}$$

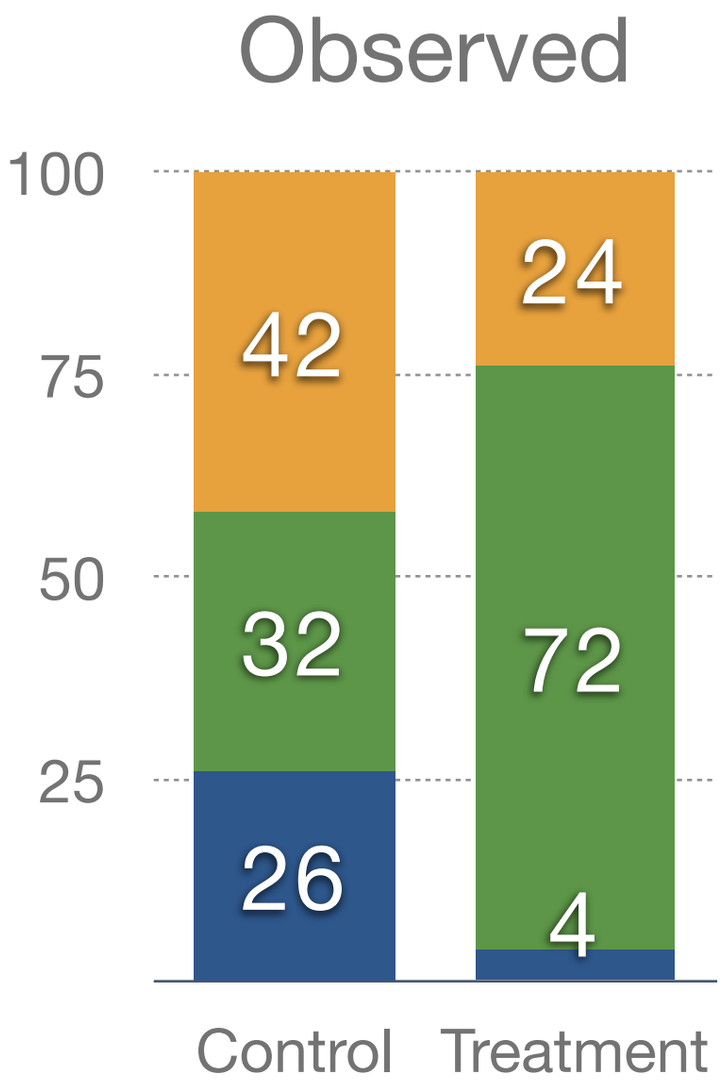
Why is this so important for data analysis?

Connecting data to reality

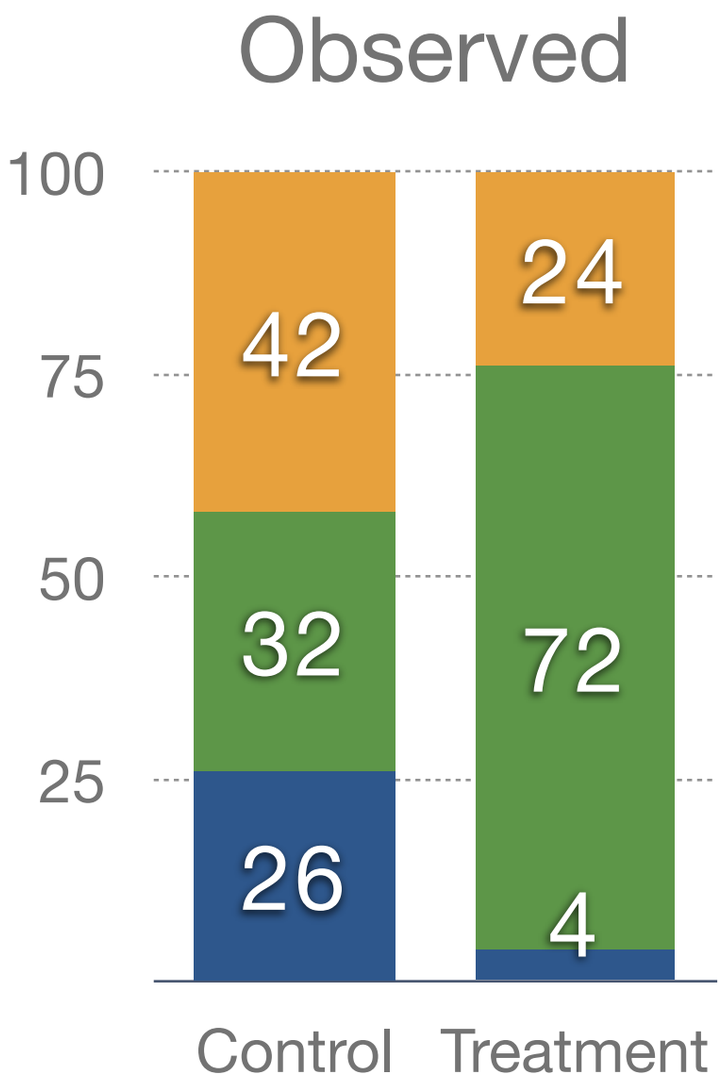
- Stated differently,

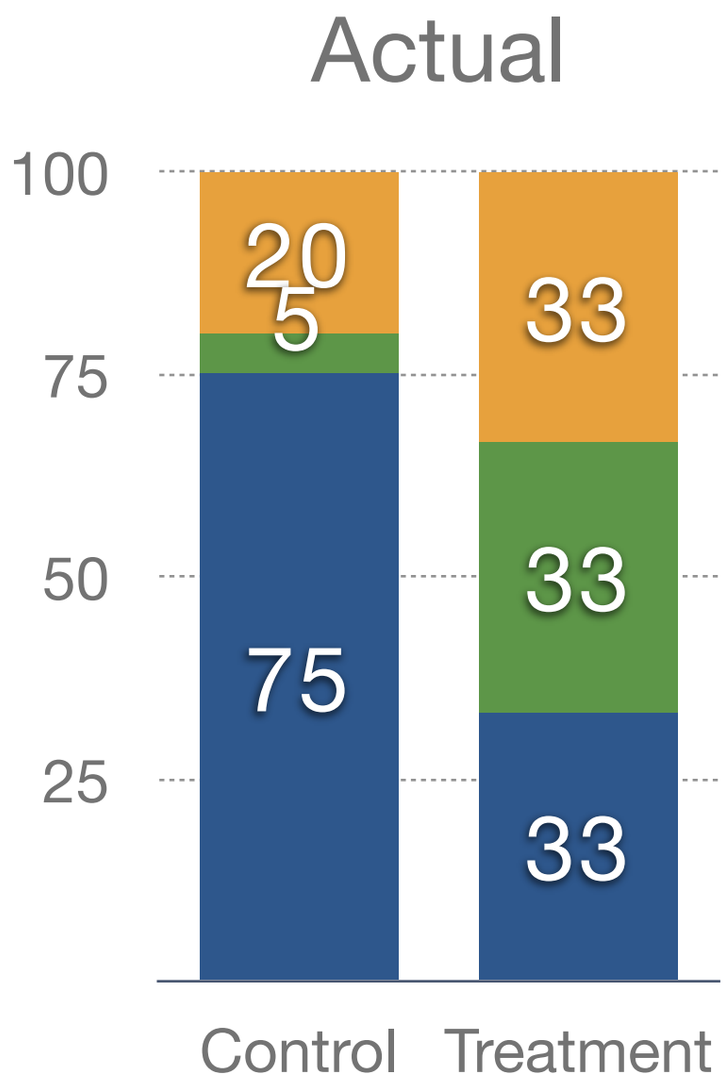
Observed relative abundance $\propto$ True relative abundance $\times$ Taxon-specific efficiencies

Expected value of $\frac{W_{ij}}{\sum_{j'} W_{ij'}} = \frac{p_{ij} e_j}{\sum_{j'} p_{ij'} e_{j'}}$



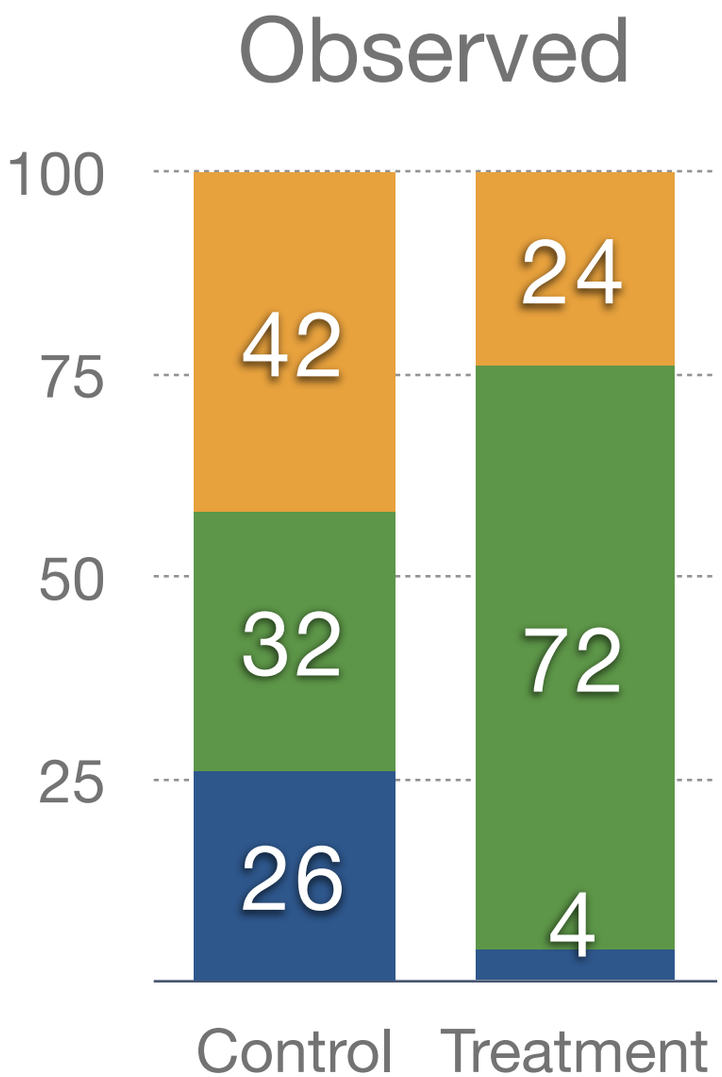
- A tempting conclusion:
  - The relative abundance of **orange** *<u>decreased</u>* in the Treatment sample (right) compared to the Control sample (left)

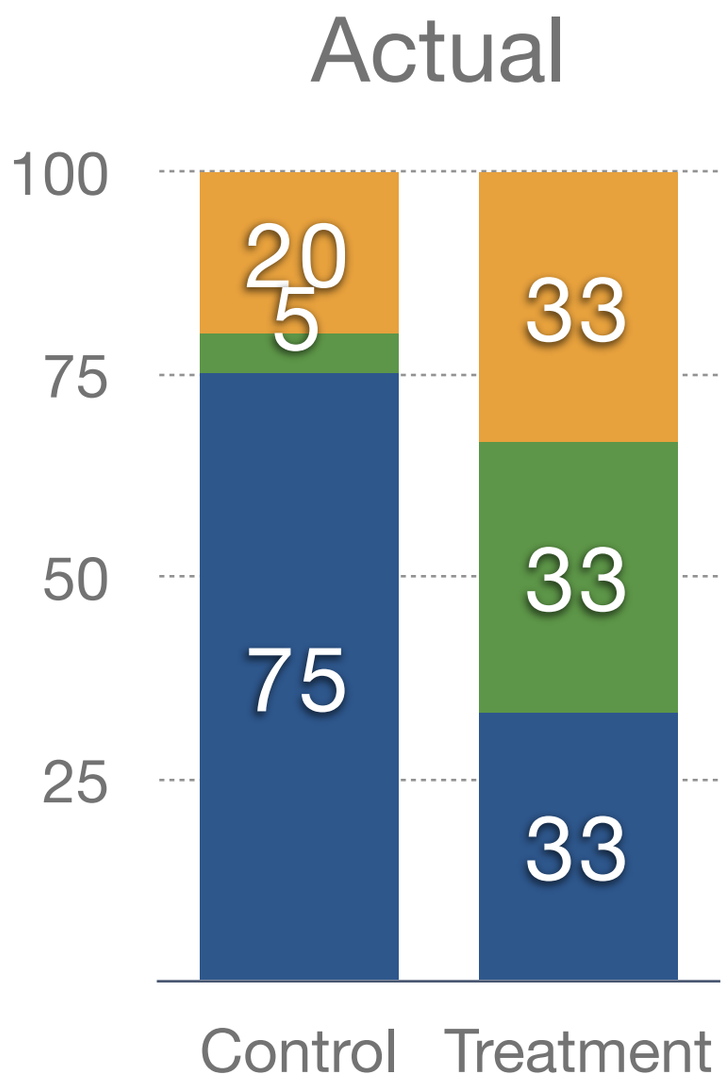


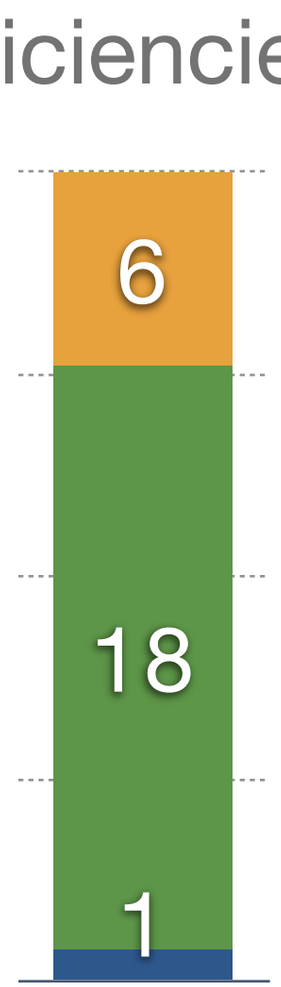


- In fact, the relative abundance of **orange** *increased* in the Treatment sample compared to the Control sample

For more details, see McLaren *et al* (2022+) "Implications of taxonomic bias..."







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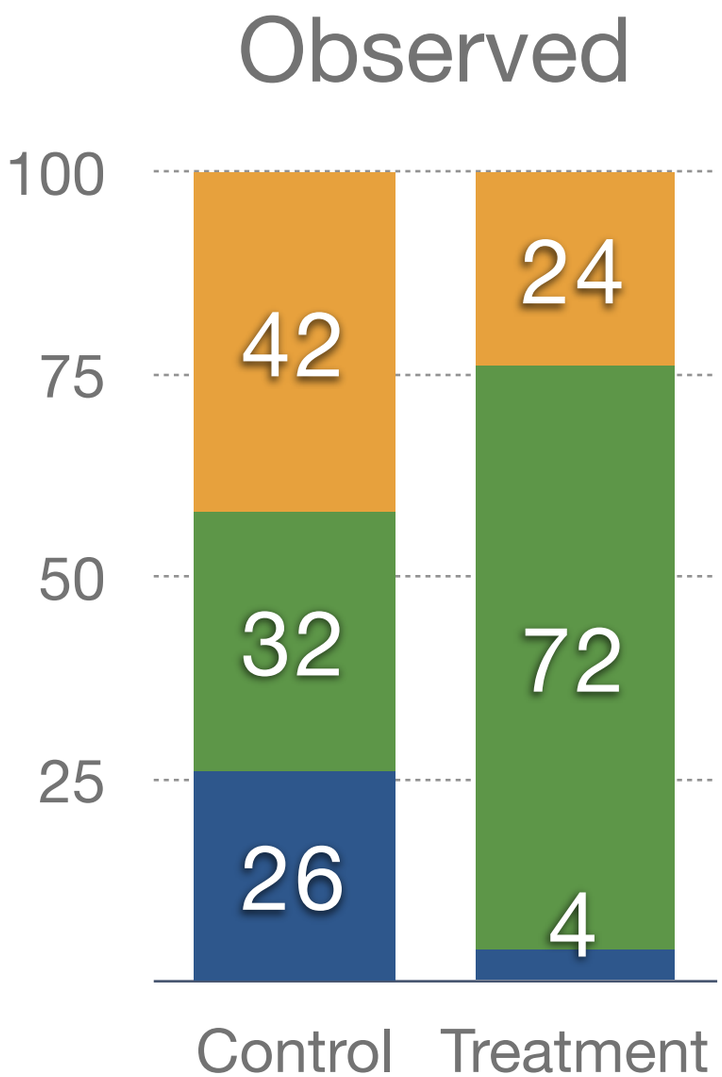
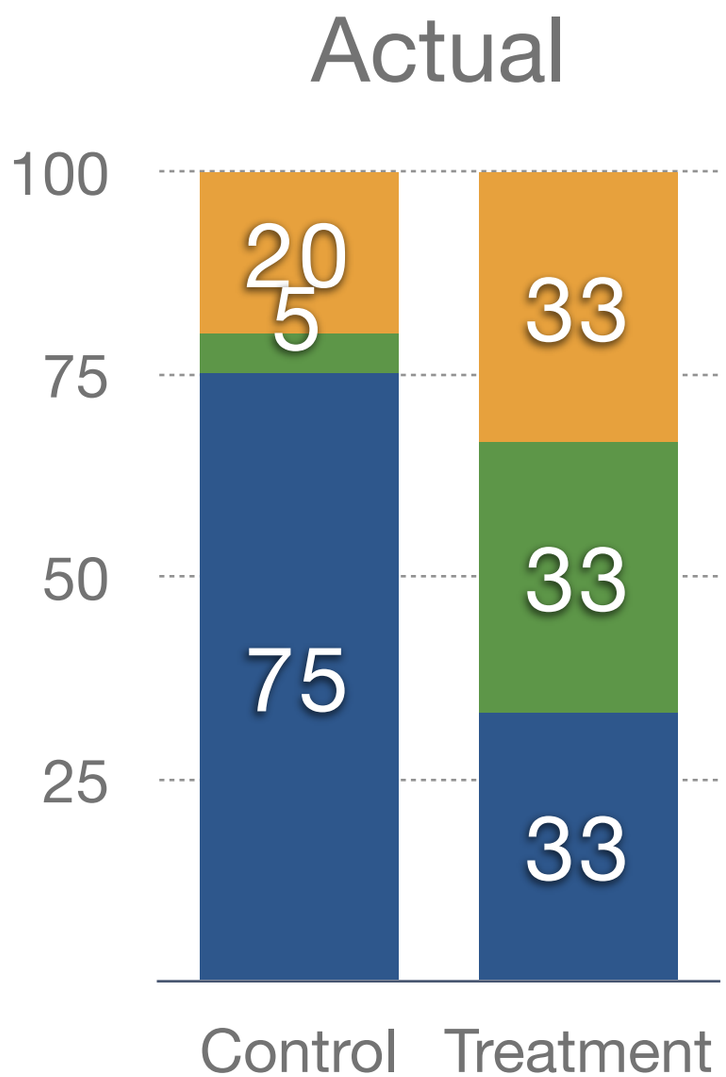
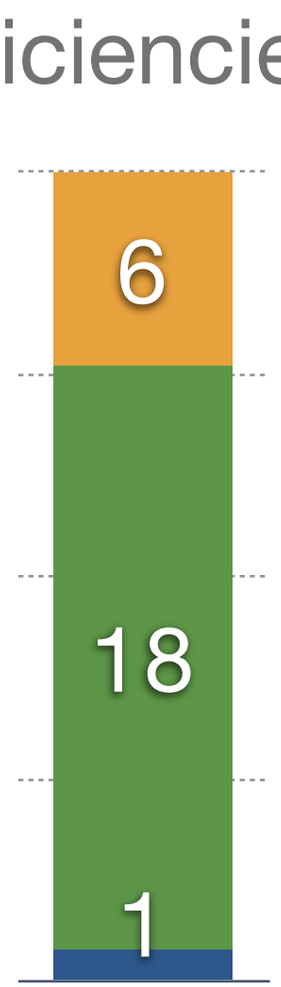






- **Green** is high efficiency; its abundance increased.
  Blue is low efficiency, and its abundance decreased.

- **Orange**'s abundance depends on the abundance of **the other taxa**.

For more details, see McLaren *et al* (2022+) "Implications of taxonomic bias..."

What can't we learn?

- Result: Under the model

$$\mathbb{E}W_{ij} = c_i \times e_j \times Y_{ij}$$

we *cannot* learn about:

- $\mathbb{E}Y_{\{X_i=1\}j} - \mathbb{E}Y_{\{X_i=0\}j}$
- $\mathbb{E}\left[\frac{Y_{\{X_i=1\}j}}{\sum_{j'} Y_{\{X_i=1\}j'}}\right] - \mathbb{E}\left[\frac{Y_{\{X_i=0\}j}}{\sum_{j'} Y_{\{X_i=0\}j'}}\right]$
- $\frac{\mathbb{E}Y_{\{X_i=1\}j}}{\mathbb{E}Y_{\{X_i=0\}j}}$ and $\log\left(\frac{\mathbb{E}Y_{\{X_i=1\}j}}{\mathbb{E}Y_{\{X_i=0\}j}}\right)$

What can we learn?

- Result: Under the model

$$\mathbb{E}W_{ij} = c_i \times e_j \times Y_{ij}$$

we *can* learn about:

- $$\log\left(\frac{\mathbb{E}Y_{\{X_i=1\}j}}{\mathbb{E}Y_{\{X_i=0\}j}}\right) - \log\left(\frac{\mathbb{E}Y_{\{X_i=1\}j'}}{\mathbb{E}Y_{\{X_i=0\}j'}}\right)$$

- $$\log\left(\frac{\mathbb{E}Y_{\{X_i=1\}j}}{\mathbb{E}Y_{\{X_i=0\}j}}\right) - \text{average}_{j'} \log\left(\frac{\mathbb{E}Y_{\{X_i=1\}j'}}{\mathbb{E}Y_{\{X_i=0\}j'}}\right)$$

What can we learn?

- Res

we

We can identify
groups (taxa, genes, etc.)
that are
changing the **most**
in abundance
from HTS

What can we learn?

- Result: Under the model

$$\mathbb{E}W_{ij} = c_i \times e_j \times Y_{ij}$$

$$\log Y_{ij} = X_i^T \beta_j$$

we *can* learn about

- $\beta_{kj} - \beta_{kj'}$ log ratios-of-ratios
- $\beta_{kj} -$ average$(\beta_{k.})$ log ratios *relative* to average log ratios

🦤 radEmu 🦤

- We propose an estimator of β_{kj} – average($\beta_{k.}$) under the model

$$\mathbb{E}W_{ij} = c_i \times e_j \times Y_{ij}$$

$$\log Y_{ij} = X_i^T \beta_j$$

- Estimator is *consistent* under weak conditions, *efficient* under stronger conditions

🦤 radEmu 🦤

✅ Estimates a ecologically-relevant, model-agnostic, interpretable parameter

"We estimate that the average abundance of *Oliverpabstia intestinalis** in metagenomes is 11 times greater after commencing dairy work, when compared to the typical fold-differences in the average abundance of taxa across these visits."

"Under the assumption that most taxa do not differ in average abundance between visits post and prior exposure, we estimate that the abundance of *Oliverpabstia intestinalis* in metagenomes from post exposure visits is 11 times greater than prior exposure visits."

✅ Robust to differential detection

✅ Adjusts for differential sequencing depth

✅ ...

*Or, you know, GCF_009696065.1, whatever…

 radEmu 

✅ Model-robust inference controls Type 1 error unlike DESeq2, ANCOM-BC2, t-tests…

✅ Handles zeroes without pseudocounts $\mathbb{E}(\log Y_{ij})$ vs $\log \mathbb{E} Y_{ij}$

✅ Simulation: Smallest estimation error out of methods that control T1E beats ALDEx2

✅ Covariate adjustment + inference under independence & cluster correlation

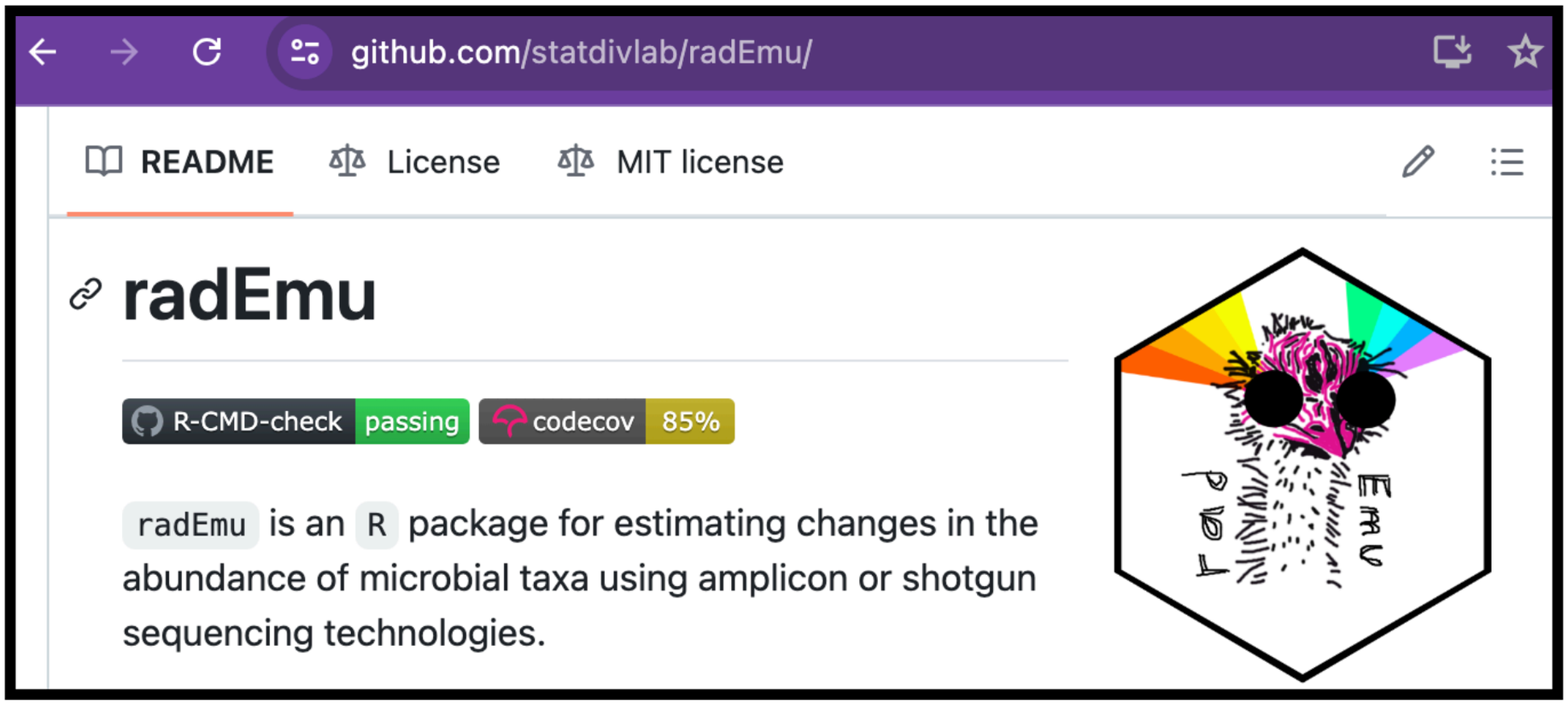
✅ Spike-ins + radEmu = you can interpret fold-differences on the absolute scale

❌ Slower than other methods

Summary

- ~~"How do we *model the data?*"~~
- "How do we *learn about biology?*"
- Want: estimate β in $\log Y_{ij} = X_i^T \beta_j$
- Have: distorted data $W_{ij} \approx c_i \times e_j \times Y_{ij}$
- Result: $\beta_{kj} -$ average$(\beta_{k.})$ is identifiable
- Method: model-robust estimation & inference with 🦤radEmu🦤

Software




```
emuFit(formula = ~ cases + age + sex,
       data = my_metadata,
       Y = my_counts)
```

arXiv > stat > arXiv:2402.05231

Search... Help | Adv

Statistics > Methodology

[Submitted on 7 Feb 2024 (v1), last revised 14 Mar 2025 (this version, v2)]

Estimating Fold Changes from Partially Observed Outcomes with Applications in Microbial Metagenomics

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David Clausen

Sarah Teichman

eLIFE elifesciences.org

RESEARCH ARTICLE

Consistent and correctable bias in metagenomic sequencing experiments

Michael R McLaren[1], Amy D Willis[2], Benjamin J Callahan[1,3]*

Michael McLaren (MIT, SecureBio)

NIH NIGMS

Implications of taxonomic bias for microbial differential-abundance analysis

Michael R. McLaren, Jacob T. Nearing, Amy D. Willis, Karen G. Lloyd, Benjamin J. Callahan

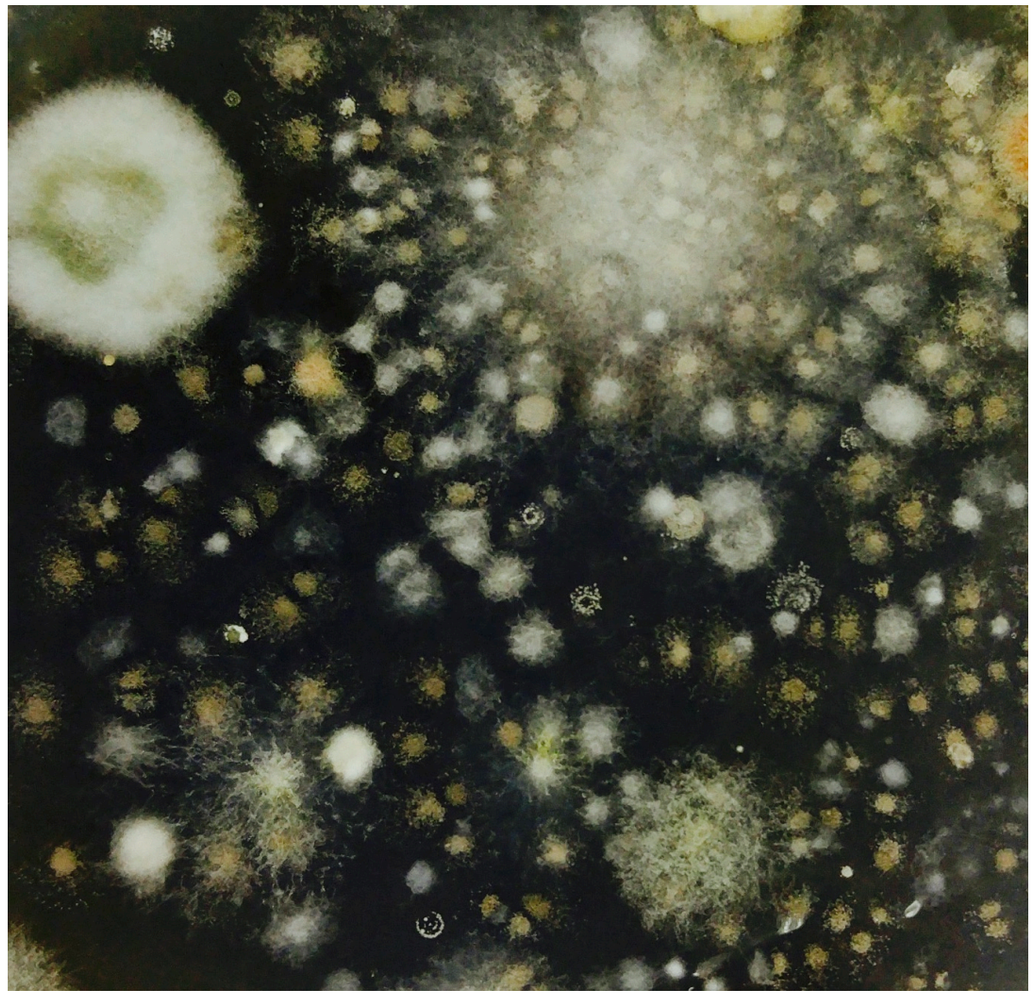
doi: https://doi.org/10.1101/2022.08.19.504330

Ben Callahan (NCSU)

R packages: radEmu from github.com/statdivlab

A rigorous & rational approach to

Microbial differential abundance



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Slides: github.com/statdivlab/presentations

Non-linear, fully non-parametric (potentially causal) generalization

Want: $\Psi_j = \log\left(\frac{\mathbb{E}\left[\mathbb{E}\left[Y_{\cdot j}|A=1,X\right]\right]}{\mathbb{E}\left[\mathbb{E}\left[Y_{\cdot j}|A=0,X\right]\right]}\right)$

i.e., log fold-difference in covariate-weighted conditional mean abundance of category j

Grant Hopkins

Have: distorted data $W_{ij} \approx S_i \times E_j \times Y_{ij}$

Results: Nonparametric identifiability; consistent & efficient estimation

Implications: Meaningful estimand on "true" scale without structural/distribution assumptions

Sarah Teichman

arXiv > stat > arXiv:2510.23920

Statistics > Methodology

[Submitted on 27 Oct 2025]

Nonparametric Identification and Estimation of Ratios of Multi-Category Means under Preferential Sampling

Grant Hopkins, Sarah Teichman, Ellen Graham, Amy D Willis

Ellen Graham

Consistency of efficiencies

Strain	Genome size (Mbp)	Copy number	Estimated efficiency
L. crispatus	2.04	4	**2.03**
L. iners	1.30	1	**6.83**

Data from Brooks *et al* (2015) BMC Microbiology

Comparing radEmu to other methods

- Make W_{ij}'s realistic lots of zeroes, high-variance

- Ask

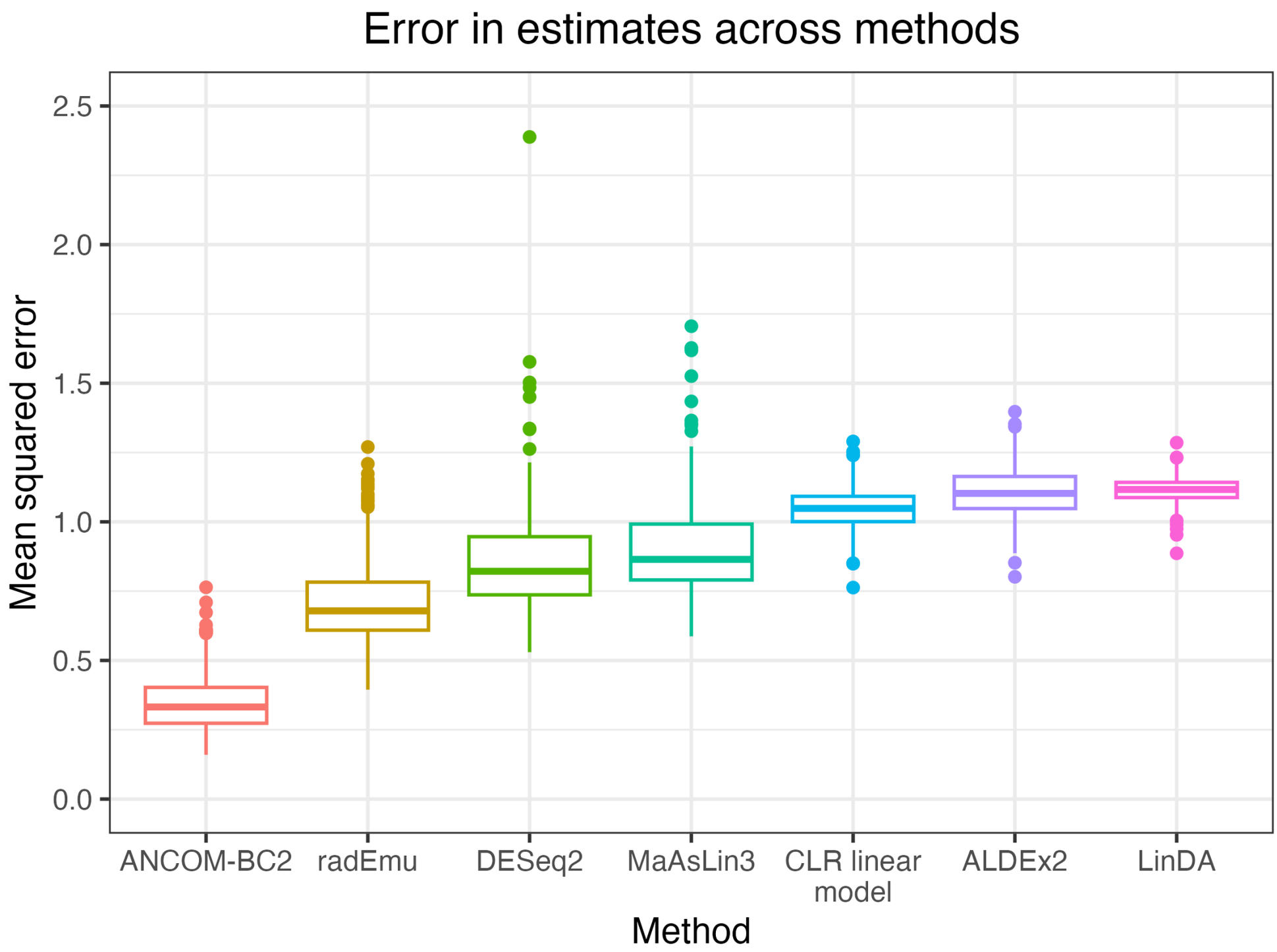
1. "How good are our estimates?"

2. "Do we have error rate control?"

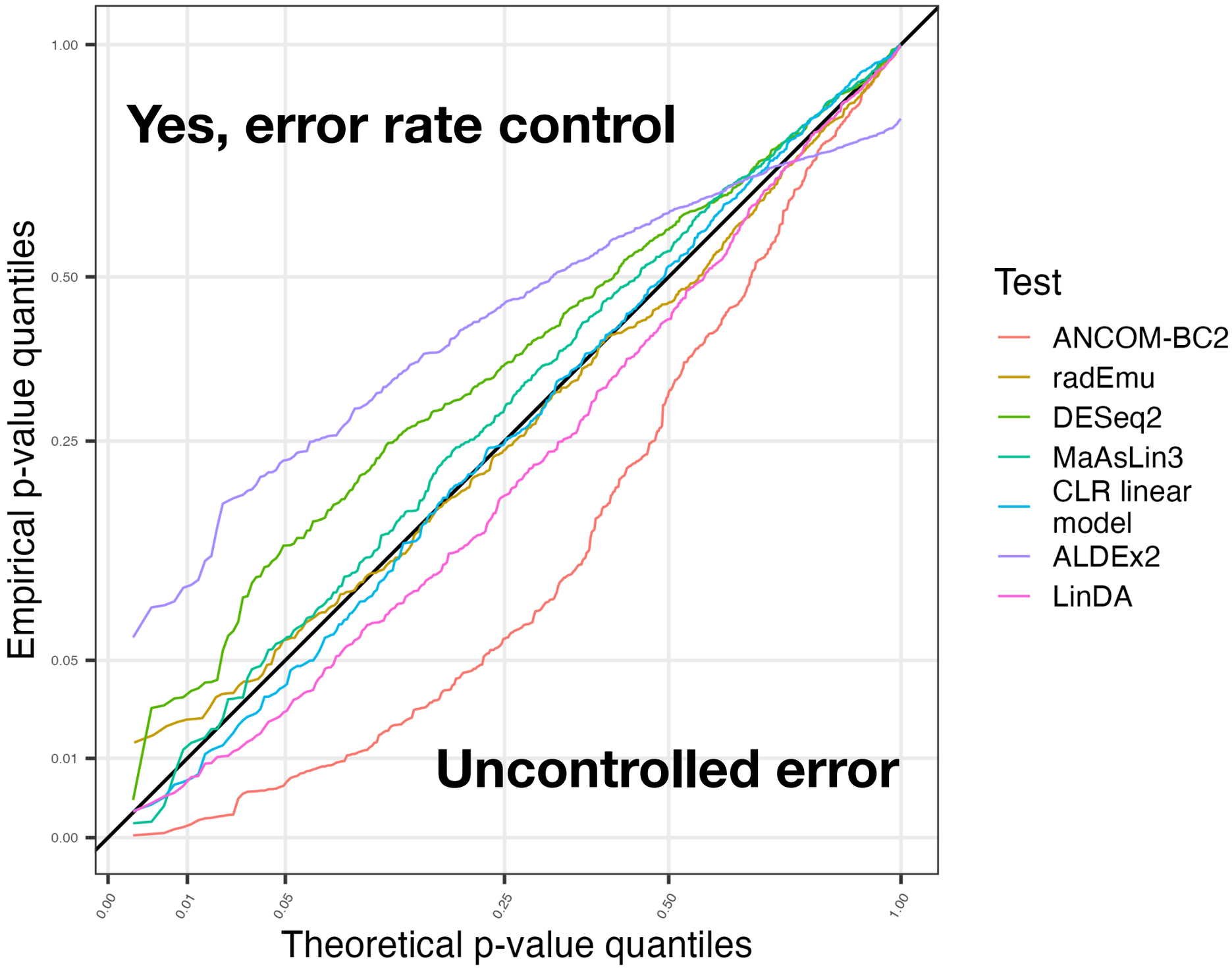
    - Null hypothesis: "Fold difference (cases vs. controls) in *F. praus* is equal to typical fold difference across taxa"

Many, many thanks to Sarah! 😻

“How good are our estimates?”



“Do we have error rate control?”



Type I error rate control results

Method	1% Type 1 error	5% Type 1 error rate
ALDEx2	0%	0%
ANCOM-BC2	9%	22%
CLR t-test	1%	7%
DESeq2	0%	2%
radEmu	0%	4%
MaAsLin3	0%	4%
LinDA	2%	8%

Simulation takeaways

- TL;DR In a realistically pathological setting,
    - radEmu has the lowest error in estimation out of all methods that control error Type 1 error rate

Using spike-ins to estimate total abundances gives biased estimates

in an unknown, taxon-dependent direction.

Furthermore…

Why do spike-ins?

- Recall: radEmu can estimate

$$\log\left(\frac{\mathbb{E}Y_{\text{group 1},j}}{\mathbb{E}Y_{\text{group 2},j}}\right) - \log\left(\frac{\mathbb{E}Y_{\text{group 1},j'}}{\mathbb{E}Y_{\text{group 2},j'}}\right)$$

- If j' is your spike-in, you know that

$$\log\left(\frac{\mathbb{E}Y_{\text{group 1},j'}}{\mathbb{E}Y_{\text{group 2},j'}}\right) = 0$$

Why do spike-ins?

- So radEmu + spike-ins can estimate

$$\log\left(\frac{\mathbb{E}Y_{\text{group 1},j}}{\mathbb{E}Y_{\text{group 2},j}}\right)$$

- "We estimate that the average abundance of *O intestinalis* in metagenomes is 11 times greater (95% CI 4x-30x, q = 0.12) after commencing dairy work**~~, when compared to the typical fold-differences in the average abundance of taxa across these visits~~**…"

- i.e. with spike-ins, you can cut "when compared to typical…"

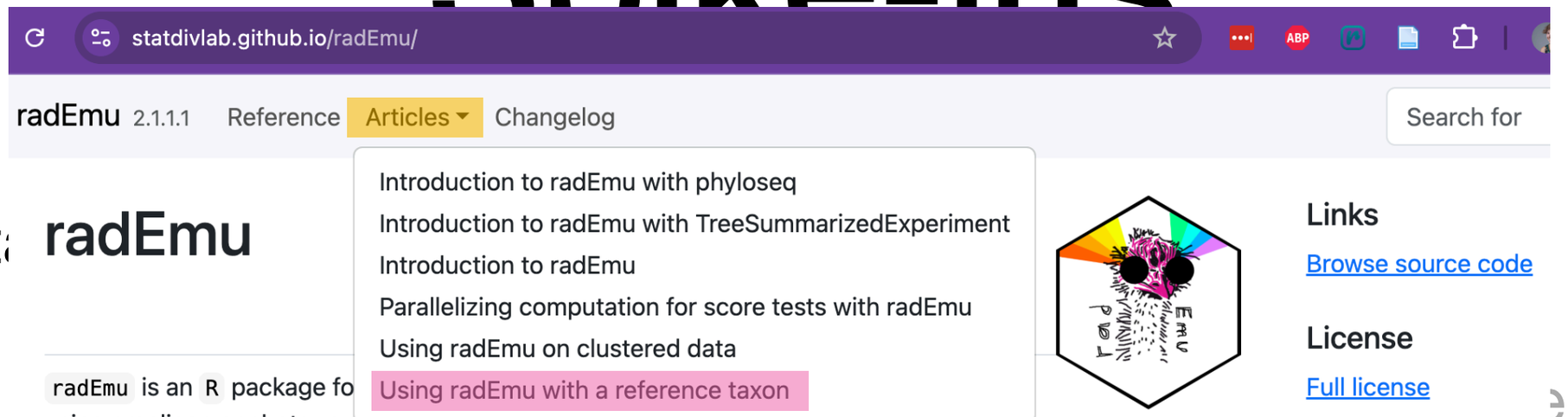
Why wouldn’t you do spike-ins?

- More steps in experimental protocol
- You risk losing all of your samples?
- You can learn this without them:

$$\log \frac{\mathbb{E}Y_{\text{group 1},j}}{\mathbb{E}Y_{\text{group 2},j}} - \text{average}_{j'} \log \left(\frac{\mathbb{E}Y_{\text{group 1},j'}}{\mathbb{E}Y_{\text{group 2},j'}} \right)$$

  - All log fold differences will go up/down by the same value
    - e.g., with spike-ins $\hat{\beta}_1 = 0.8$ and $\hat{\beta}_1 = -0.4$
    - without spike-ins $\hat{\beta}_1 = 0.81$ and $\hat{\beta}_1 = -0.39$
- My intuition — **not supported by data** — results will change by <0.01
- “Relative to typical” is less tricky (objectively) and just as good (my opinion)

Spike-ins



- If t
  - …
  - ab
- If y

… then you can use spike-ins to estimate $\log\left(\frac{\text{group 1},j}{\mathbb{E}Y_{\text{group 2},j}}\right)$

Spike-ins: Why?!

- What do people do when they have absolute abundances?

- THEY DO DIFFERENTIAL ABUNDANCE!!!! 🤯

- All that fuss and no benefit **over just using radEmu**

Summary: Spike-ins

- So why are there all these papers about how they work?
  - If the changes in absolute abundance are LARGE…
    - …relative to the differences in detectability…
      - …the *direction* of change will be correctly estimated
        - No guarantees for the magnitude!

Summary of the summary

- Spike-ins are in my view, based on data
  - **Not plausible** for absolute quantification
  - **Useful** for differential abundance…
    - …but not worth the effort…