

Problems with Correlations in Relative Data and a Proposed Alternative

Dominic LaRoche

November 3, 2015

The Papers

Proportionality: A Valid Alternative to Correlation for Relative Data

David Lovell, Vera Pawlowsky-Glahn, Juan Jos Egozcue, Samuel Marguerat, and Jrg Bhler
PLoS Computational Biology 11(3) (2015)

Proportions, Percentages, PPM: Do the Molecular Biosciences Treat Compositional Data Right?

Lovell DR, Muller W, Taylor JM, Zwart AB, Helliwell CA
Compositional data analysis: Theory and applications p193-207 (2011)



Section 1

Introduction to the Problem

What is Relative Data? –Also called “Compositional Data”

- Compositional data are vectors of non-negative components showing the *relative* weight or importance of a set of *parts in a total*
- The total sum of a compositional vector is considered irrelevant, or an artifact of the sampling procedure.
- No individual component can be interpreted isolated from the other. A composition carries no absolute information on increment/decrement of mass.

Is *my* data relative??

Relative data arises naturally in many biological measurements:

- Is your sample a fixed size?
 - 1 gram of tissue
 - 1 μg of total RNA
 - 1 μg of meta-genomic DNA
 - 1 mL of blood, etc.

Is *my* data relative??

Relative data arises naturally in many biological measurements:

- Is your sample a fixed size?
 - 1 gram of tissue
 - 1 μg of total RNA
 - 1 μg of meta-genomic DNA
 - 1 mL of blood, etc.
- Is your data a constrained count?
 - How many total reads can your favorite platform handle?
 - Counts of codons or bases in a fixed length of DNA

Is *my* data relative??

Relative data arises naturally in many biological measurements:

- Is your sample a fixed size?
 - 1 gram of tissue
 - 1 μg of total RNA
 - 1 μg of meta-genomic DNA
 - 1 mL of blood, etc.
- Is your data a constrained count?
 - How many total reads can your favorite platform handle?
 - Counts of codons or bases in a fixed length of DNA
- Is your data based on proportions?
 - Different k-mers in genomes
 - GO terms in samples
 - different reads in NGS sequencing runs

Is *my* data relative??

Relative data arises naturally in many biological measurements:

- Is your sample a fixed size?
 - 1 gram of tissue
 - 1 μg of total RNA
 - 1 μg of meta-genomic DNA
 - 1 mL of blood, etc.
- Is your data a constrained count?
 - How many total reads can your favorite platform handle?
 - Counts of codons or bases in a fixed length of DNA
- Is your data based on proportions?
 - Different k-mers in genomes
 - GO terms in samples
 - different reads in NGS sequencing runs

Then your data might be relative!



Should I *care* if my data is relative??



Should I *care* if my data is relative??

Yes

Should I *care* if my data is relative??

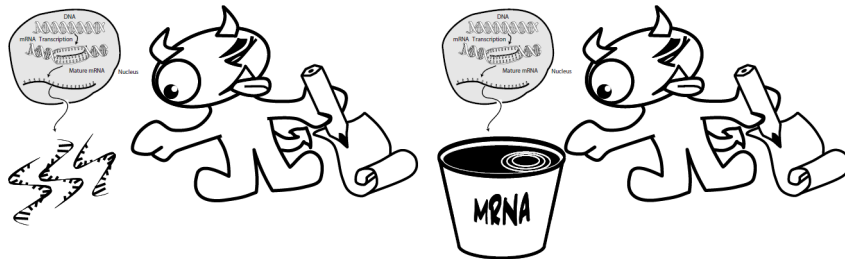
Yes

Long answer: It depends...

In certain cases it doesn't matter much but in others it matters a lot.

The 'Omics Imp'

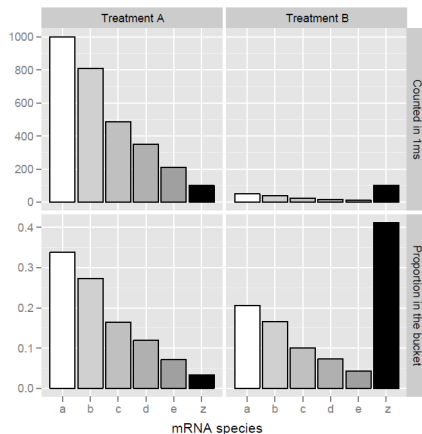
Lovell et al.



- On the left the imp tallies sequences as they are produced in a fixed time period
- On the right the imp counts the sequences in some fixed size bucket
 - Data on the right are parts of a total

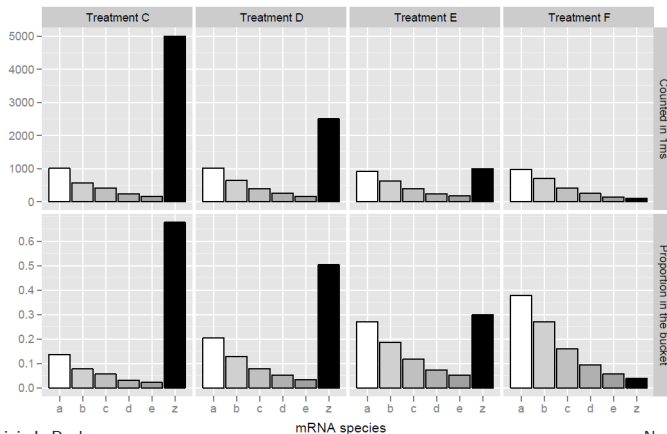
Relative data can be misleading

Example 1.



Relative data can be misleading

Example 2.



When is relative data likely to be misleading?

Take a 3 component example: $Total = c_1 + c_2 + c_3$

When is relative data likely to be misleading?

Take a 3 component example: $Total = c_1 + c_2 + c_3$

- $c_1, c_2 \gg c_3$
 - As $c_1 \uparrow$ then $c_2 \downarrow$
 - Correlation is attenuated

When is relative data likely to be misleading?

Take a 3 component example: $Total = c_1 + c_2 + c_3$

- $c_1, c_2 \gg c_3$
 - As $c_1 \uparrow$ then $c_2 \downarrow$
 - Correlation is attenuated
- $c_3 \gg c_1, c_2$
 - Here $var(c_3)$ dominates the composition
 - Correlation is biased high as $var(c_3) \uparrow$



David Lovell's Take

Yes, I am going to show a slide show during a slide show.

David Lovell scaring you about correlating relative data

A little background before the proposed alternative: Model 2 regression

Also known as Standardized Major Axis (SMA) Regression

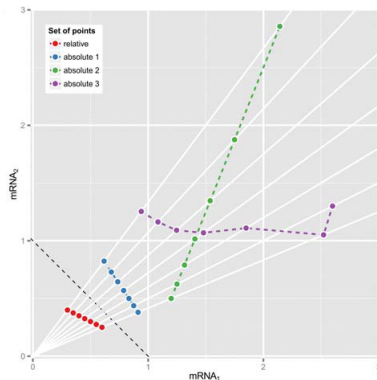
- Traditional regression has 1 random variable: $Y = \beta_0 + \beta X + \epsilon$
 - X is considered “fixed” so has no random error (ϵ)

A little background before the proposed alternative: Model 2 regression

Also known as Standardized Major Axis (SMA) Regression

- Traditional regression has 1 random variable: $Y = \beta_0 + \beta X + \epsilon$
 - X is considered “fixed” so has no random error (ϵ)
- SMA regression gives the relationship between two random variables
 - Accounts for the random error in both variables
 - Slope estimate: $\beta = \frac{sd(Y_1)}{sd(Y_2)}$

Correlations on Relative Data



Correlations on relative data tell us absolutely nothing about the relationship between the absolute abundances.

The proposed alternative to correlation

The authors propose “proportionality”, ϕ , as a substitute for correlation.

- They start with Aitchison’s log-ratio variance:

$$\text{var}(\log(x/y)) = \text{var}(\log x - \log y)$$

The proposed alternative to correlation

The authors propose “proportionality”, ϕ , as a substitute for correlation.

- They start with Aitchison’s log-ratio variance:

$$\text{var}(\log(x/y)) = \text{var}(\log x - \log y)$$

- They factor log-ratio variance using the properties of variance:

$$= \text{var}(\log(x)) \left(1 + \frac{\text{var}(\log(y))}{\text{var}(\log(x))} - 2 \sqrt{\frac{\text{var}(\log(y))}{\text{var}(\log(x))} \frac{\text{cov}(\log(x), \log(y))}{\sqrt{\text{var}(\log(x))\text{var}(\log(y))}}} \right)$$

The proposed alternative to correlation

The authors propose “proportionality”, ϕ , as a substitute for correlation.

- They start with Aitchison’s log-ratio variance:

$$\text{var}(\log(x/y)) = \text{var}(\log x - \log y)$$

- They factor log-ratio variance using the properties of variance:

$$= \text{var}(\log(x)) \left(1 + \frac{\text{var}(\log(y))}{\text{var}(\log(x))} - 2 \sqrt{\frac{\text{var}(\log(y))}{\text{var}(\log(x))} \frac{\text{cov}(\log(x), \log(y))}{\sqrt{\text{var}(\log(x))\text{var}(\log(y))}}} \right)$$

- They identify the SMA slope estimate β and the correlation:

$$= \text{var}(\log(x))(1 + \beta^2 - 2\beta|r|)$$

The proposed alternative to correlation

The authors propose “proportionality”, ϕ , as a substitute for correlation.

- They start with Aitchison’s log-ratio variance:

$$\text{var}(\log(x/y)) = \text{var}(\log x - \log y)$$

- They factor log-ratio variance using the properties of variance:

$$= \text{var}(\log(x)) \left(1 + \frac{\text{var}(\log(y))}{\text{var}(\log(x))} - 2 \sqrt{\frac{\text{var}(\log(y))}{\text{var}(\log(x))}} \frac{\text{cov}(\log(x), \log(y))}{\sqrt{\text{var}(\log(x))\text{var}(\log(y))}} \right)$$

- They identify the SMA slope estimate β and the correlation:

$$= \text{var}(\log(x))(1 + \beta^2 - 2\beta|r|)$$

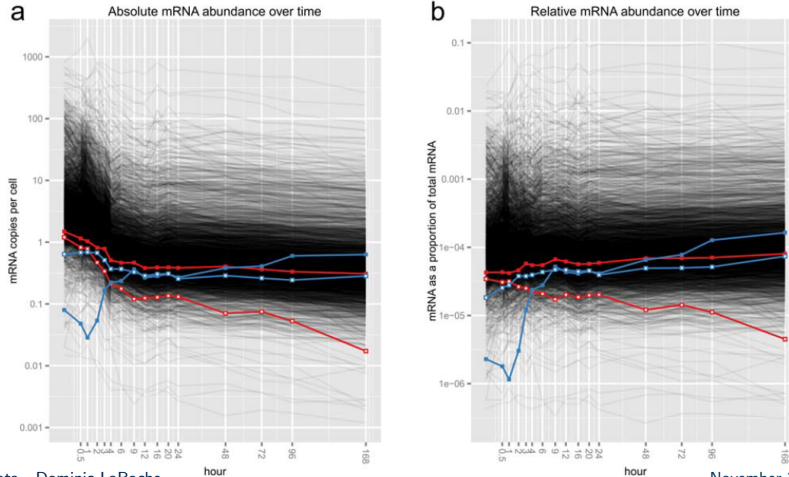
- They drop the unnecessary term to get ϕ :

$$\phi(\log(x), \log(y)) = (1 + \beta^2 - 2\beta|r|)$$

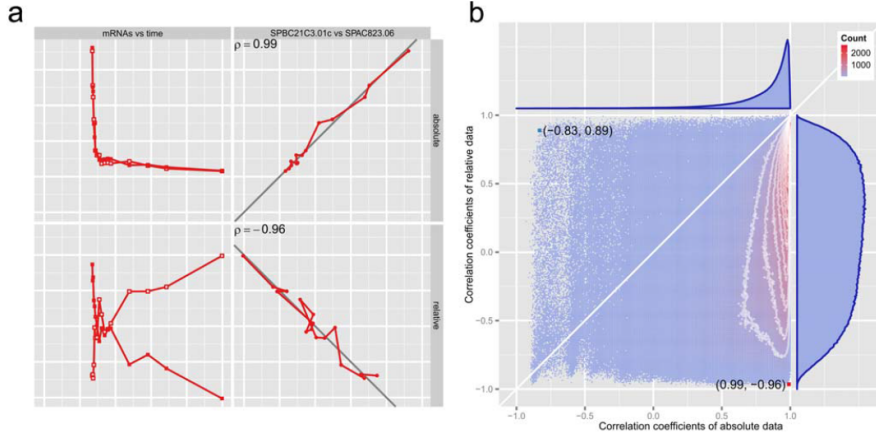
Benefits of proportionality

- Derived from Aitchison's log-ratio variance
- Composed of two established metrics of association
- However, ϕ is not symmetric like ρ

Yeast Example



Yeast Example



When can I mostly ignore the relative nature of my data?

Relative data aren't always a problem:

- Components of interest are relatively small parts of mixture samples that remain constant in size
- Only using univariate statistics (e.g. variance)
- log-transformation can *help* (due to the properties of the log)

When can I mostly ignore the relative nature of my data?

Relative data aren't always a problem:

- Components of interest are relatively small parts of mixture samples that remain constant in size
- Only using univariate statistics (e.g. variance)
- log-transformation can *help* (due to the properties of the log)

Do you feel lucky? -*Dirty Harry*

Questions?

