

# Problems with Correlations in Relative Data and a Proposed Alternative

Dominic LaRoche

November 2, 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.



Relative data arises naturally in many biological measurements:

- Is your sample oa fixed size?
  - 1 gram of tissue
  - 1  $\mu$ g of total RNA
  - 1  $\mu$ g of metagenomic DNA
  - 1 mL of blood, etc.



Relative data arises naturally in many biological measurements:

- Is your sample oa fixed size?
  - 1 gram of tissue
  - 1  $\mu$ g of total RNA
  - 1  $\mu$ g of metagenomic 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



Relative data arises naturally in many biological measurements:

- Is your sample oa fixed size?
  - 1 gram of tissue
  - 1  $\mu$ g of total RNA
  - 1  $\mu$ g of metagenomic 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



Relative data arises naturally in many biological measurements:

- Is your sample oa fixed size?
  - 1 gram of tissue
  - 1  $\mu$ g of total RNA
  - 1  $\mu$ g of metagenomic 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'

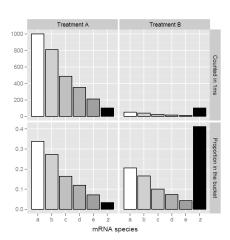
Lovell et al.



- 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



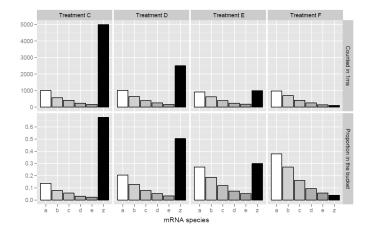
# Relative data can be misleading Example 1.





# 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  $var(c_3) \uparrow$



#### Correlations on Relative Data

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

David Lovell scaring you about correlating proportions



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