

Aleksandra Perz  
Wren Lab  
Oklahoma Medical Research Foundation

# Overview

- MNEMONIC
  - Goals
  - Data acquisition and processing
  - Results and current state
- PubQC
  - Goals
  - Results so far

# There is knowledge out there: objectives

Bring in the already available knowledge to interpret a new finding

Find samples that are similar:  
learn something new about  
the finding based on the literature

Compare shifts observed  
between conditions:  
find samples that exhibit similar  
changes in taxonomic abundance

Predict characteristics  
of the finding:  
confirm the finding

Make and evaluate statements  
about global relationships  
between entities

A researcher's  
interface to database

# Data

- Batch-download count data from EBI
- Represent counts as a fraction of total count within a sample (compositional data)
- Set low-count observations to zero
- TF-IDF transform counts (term frequency - inverse document frequency)
- Calculate cosine distances

## Entities and entity hierarchy:

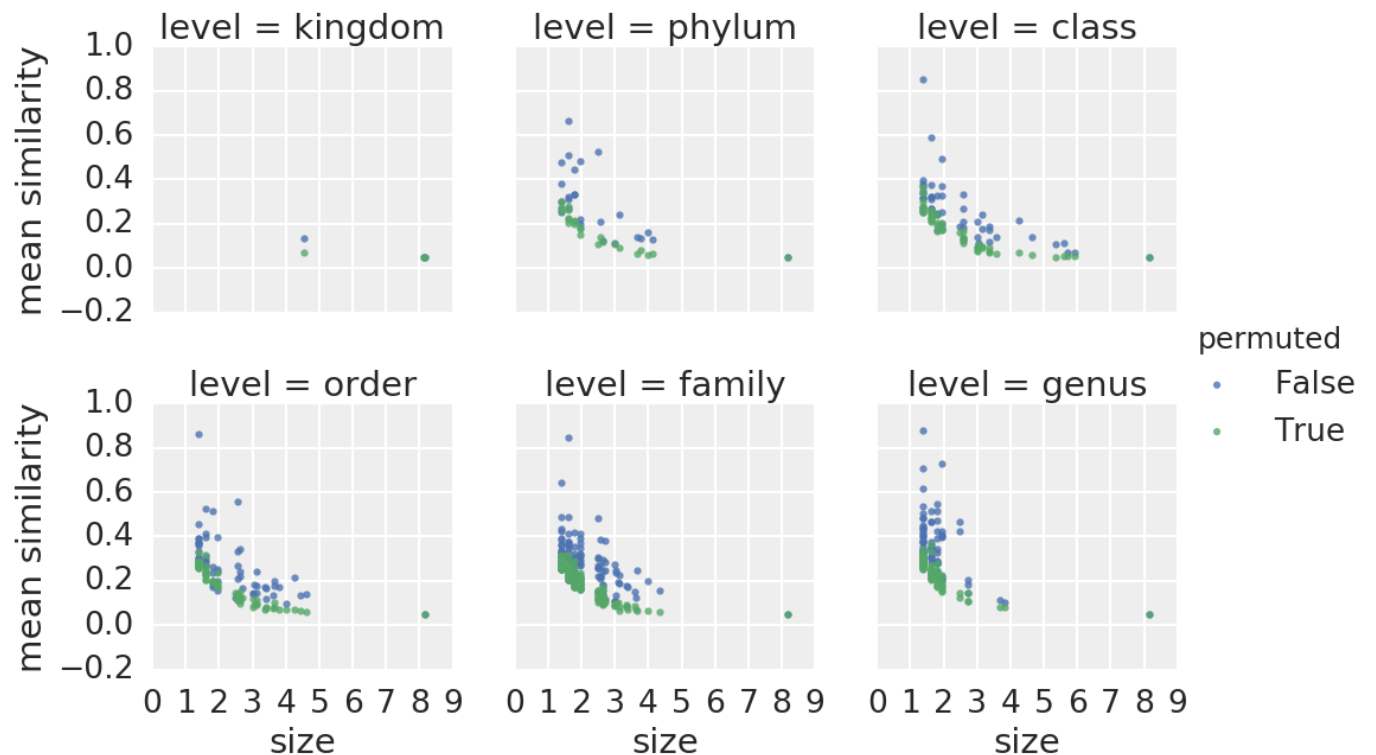
- Samples
  - Projects
  - Biomes
  - Keywords
  - Contrasts
- Taxa
  - Genera
  - Families
  - ...
- Genes
  - Functions

# Validation?

Comparison of results for sample-sample cosine distance between taxonomic data and functional data

- Mantel test: 0.28  
Permuted: ~0.00  
(10439 samples)

Comparison of mean similarity within taxonomic levels against permuted values



# Where I stand

- Metadata browsing

<http://10.84.146.16:9000/home>

- Sample-sample (also project-project, biome-biome)

<http://10.84.146.16:9000/projects/ERP010458>

<http://10.84.146.16:9000/biomes/Fecal>

- Taxon-taxon

[http://10.84.146.16:9000/taxa/k\\_\\_Bacteria;%20p\\_\\_Firmicutes;%20c\\_\\_Clostridia;%20o\\_\\_Clostridiales;%20f\\_\\_Peptococcaceae;%20g\\_\\_\[Clostridium\];%20s\\_\\_difficile](http://10.84.146.16:9000/taxa/k__Bacteria;%20p__Firmicutes;%20c__Clostridia;%20o__Clostridiales;%20f__Peptococcaceae;%20g__[Clostridium];%20s__difficile)

- Contrasts (differential abundance)

<http://10.84.146.16:9000/contrasts/soil-fecal>

- Data management, optimization: getting results for > 300 samples and 3000 taxons is very slow!

# Sample, project, biome results

- Precalculated distance matrix for all sample-sample relationships
- Collapsing and averaging for a higher-level entity (e.g. project)

## Biomes most similar to Fecal

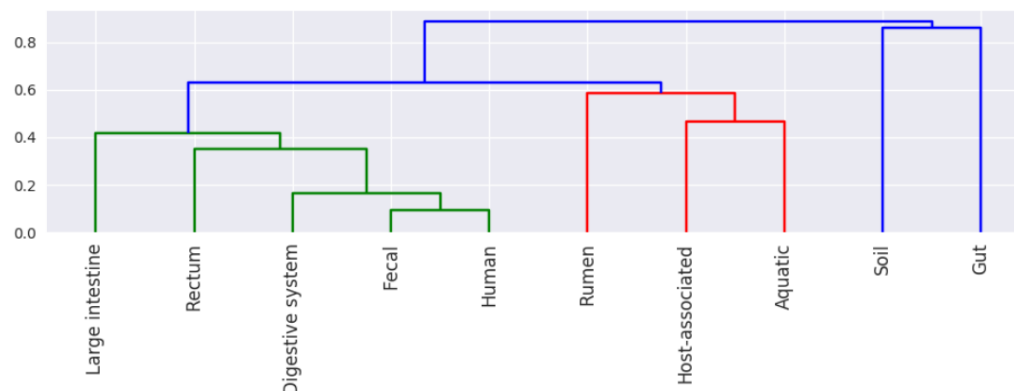
For agglomerative entities like project,

Biome 2	Metric
<a href="#">Fecal</a>	0.719689
<a href="#">Rectum</a>	0.731858
<a href="#">Human</a>	0.752949
<a href="#">Digestive system</a>	0.766736
<a href="#">Large intestine</a>	0.858444
<a href="#">Soil</a>	0.876893
<a href="#">Aquatic</a>	0.889793
<a href="#">Host-associated</a>	0.905403
<a href="#">Gut</a>	0.917661
<a href="#">Rumen</a>	0.917746

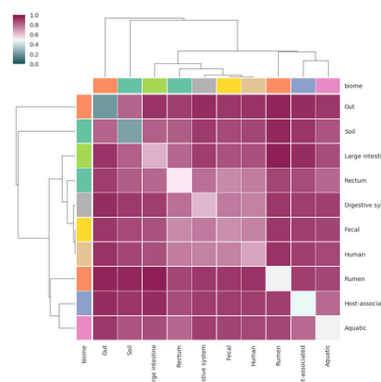
## Samples most similar to ERS940246

Sample 2	Metric
<a href="#">ERS940246</a>	0.000000
<a href="#">ERS939804</a>	0.261820
<a href="#">ERS939485</a>	0.324476
<a href="#">ERS941546</a>	0.346890
<a href="#">ERS939653</a>	0.348082
<a href="#">ERS920506</a>	0.353270
<a href="#">ERS941537</a>	0.355168
<a href="#">ERS915909</a>	0.356859
<a href="#">ERS915910</a>	0.358304
<a href="#">ERS918534</a>	0.358816
<a href="#">ERS940404</a>	0.360702

Biomes dendrogram for Fecal



Biomes heatmap for Fecal



TODO:

- Include more metrics (already implemented in taxon comparison)

# Taxon results

[HOME](#)[HELP](#)[ABOUT](#)

**K\_BACTERIA; P\_FIRMICUTES; C\_CLOSTRIDIA; O\_CLOSTRIDIALES; F\_Peptostreptococcaceae; G\_[CLOSTRIDIUM]; S\_DIFFICILE**

[DOWNLOAD TABLE](#)

Tf-idf cosine; ascending=True

Taxon 2	Tf-idf cosine	N overlapping	Fisher exact p-value	Correlation	Chisquare kernel
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Peptostreptococcaceae; g_[Clostridium]; s_difficile</a>	0.000000	2596.0	0.000007	1.000000	1.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Peptostreptococcaceae; g_ ; s_</a>	0.283319	2452.0	0.000010	0.642032	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae; g_Clostridium; s_neonatale</a>	0.297549	1176.0	0.000007	0.133426	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae; g_Clostridium; s_perfringens</a>	0.329332	1937.0	0.000009	0.139407	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae; g_Clostridium; s_butyricum</a>	0.387502	1207.0	0.000006	0.086361	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Eubacteriaceae; g_Pseudoramibacter_Eubacterium; s_</a>	0.439118	619.0	0.000006	0.158153	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Carnobacteriaceae; g_ ; s_</a>	0.466686	771.0	0.000007	0.195472	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Erysipelotrichi; o_Erysipelotrichales; f_Erysipelotrichaceae; g_Coprobacillus; s_cateniformis</a>	0.467144	657.0	0.000005	0.121383	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Enterococcaceae; g_Enterococcus; s_</a>	0.475901	2300.0	0.000009	0.031046	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Enterococcaceae; g_Enterococcus; s_casseliflavus</a>	0.484032	1258.0	0.000008	0.112064	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Erysipelotrichi; o_Erysipelotrichales; f_Erysipelotrichaceae; g_[Eubacterium]; s_dolichum</a>	0.494058	1383.0	0.000010	0.141750	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_ ; g_ ; s_</a>	0.497414	1666.0	0.000010	0.032788	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Enterococcaceae; g_Vagococcus; s_</a>	0.500240	1556.0	0.000008	0.030739	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Leuconostocaceae; g_Weissella; s_</a>	0.505225	1012.0	0.000008	0.105376	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Clostridia; o_Clostridiales; f_Clostridiaceae; g_ ; s_</a>	0.523169	2566.0	0.000007	0.137969	0.0
<a href="#">k_Bacteria; p_Actinobacteria; c_Coriobacteriia; o_Coriobacteriales; f_Coriobacteriaceae; g_Eggerthella; s_lenta</a>	0.529286	1162.0	0.000010	0.104832	0.0
<a href="#">k_Bacteria; p_Firmicutes; c_Bacilli; o_Lactobacillales; f_Leuconostocaceae; g_ ; s_</a>	0.554177	897.0	0.000008	0.023938	0.0

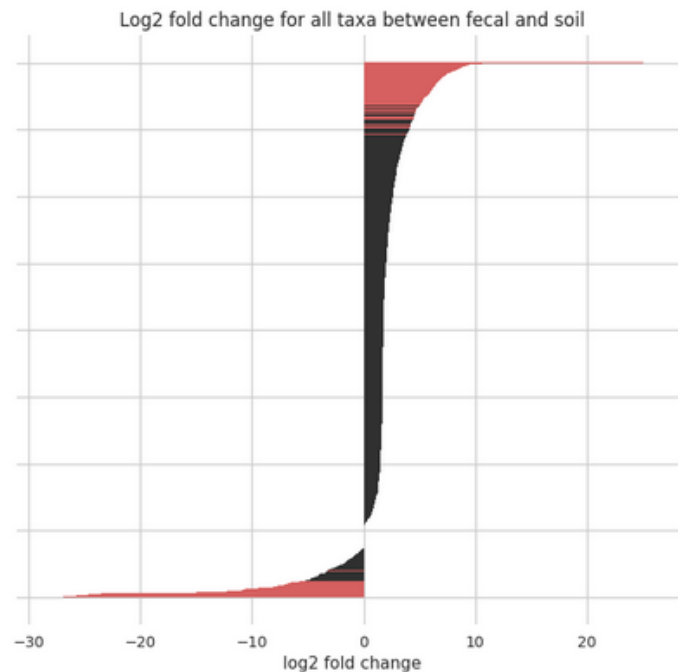
TODO:

- Add genus, family, ... collapsing
- Draw plots for taxon results similar to sample results

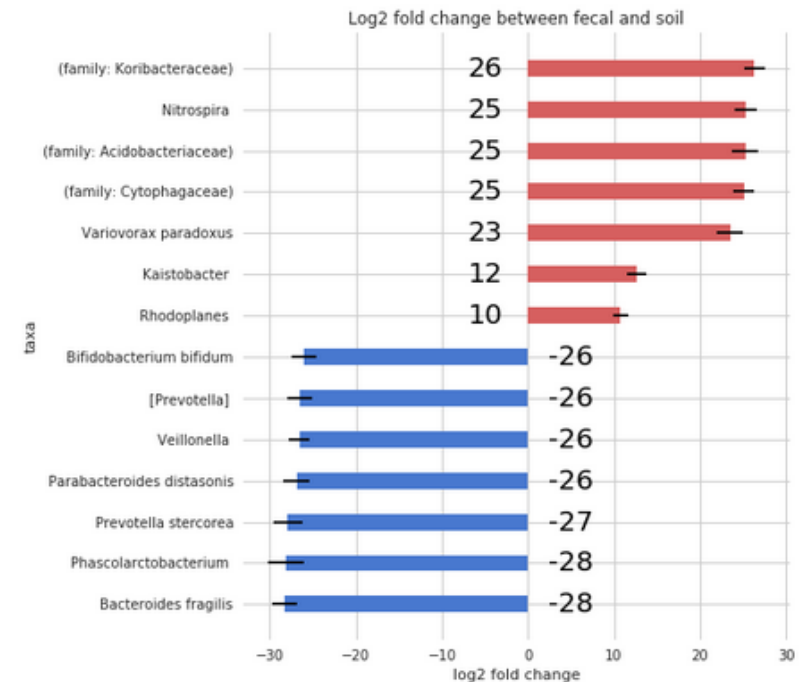


# Contrasts

## SOIL-FECAL



Comparison of fecal to soil (reference).

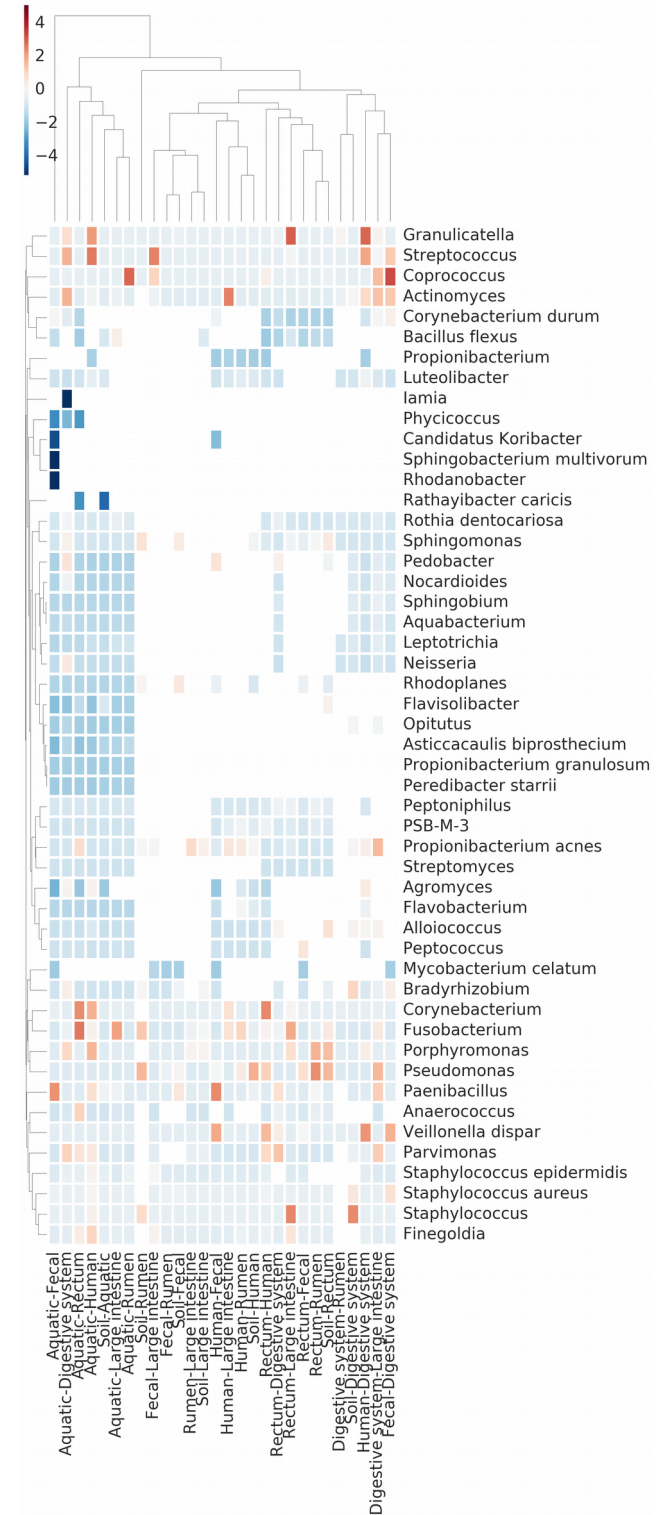


Comparison of fecal to soil (reference).  
Showing 14 out of 282 taxa for which adjusted p-value < 0.01.  
Standard errors are shown.

## TODO:

- Add a possibility to specify arbitrary groups of samples
- Log fold change plots for higher taxonomy levels

# One step higher: cluster contrasts



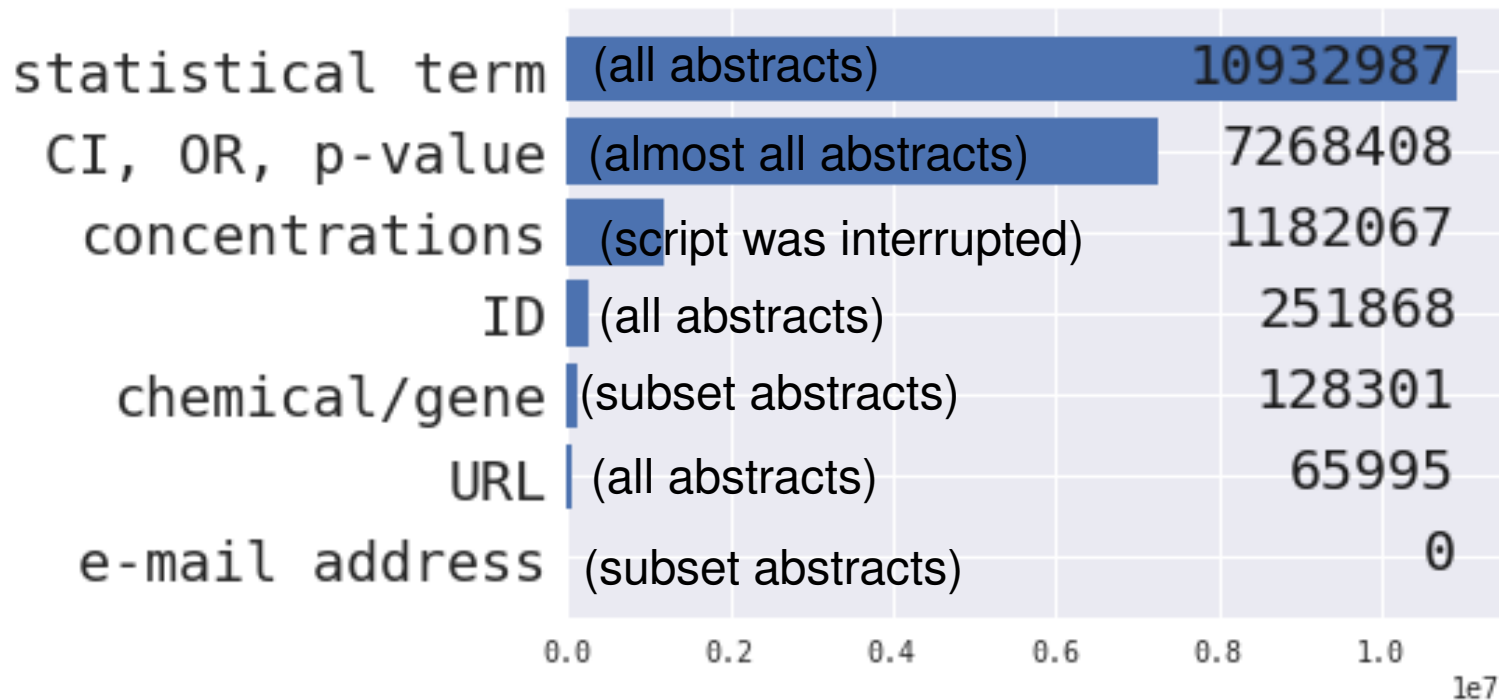
# PubQC

Correct errors in scientific publications submitted to journals (“Reviewer n+1” scheme)

Analyze the errors in scientific literature in the wild

# PubQC

Total accessible  
abstracts: 27,444,507

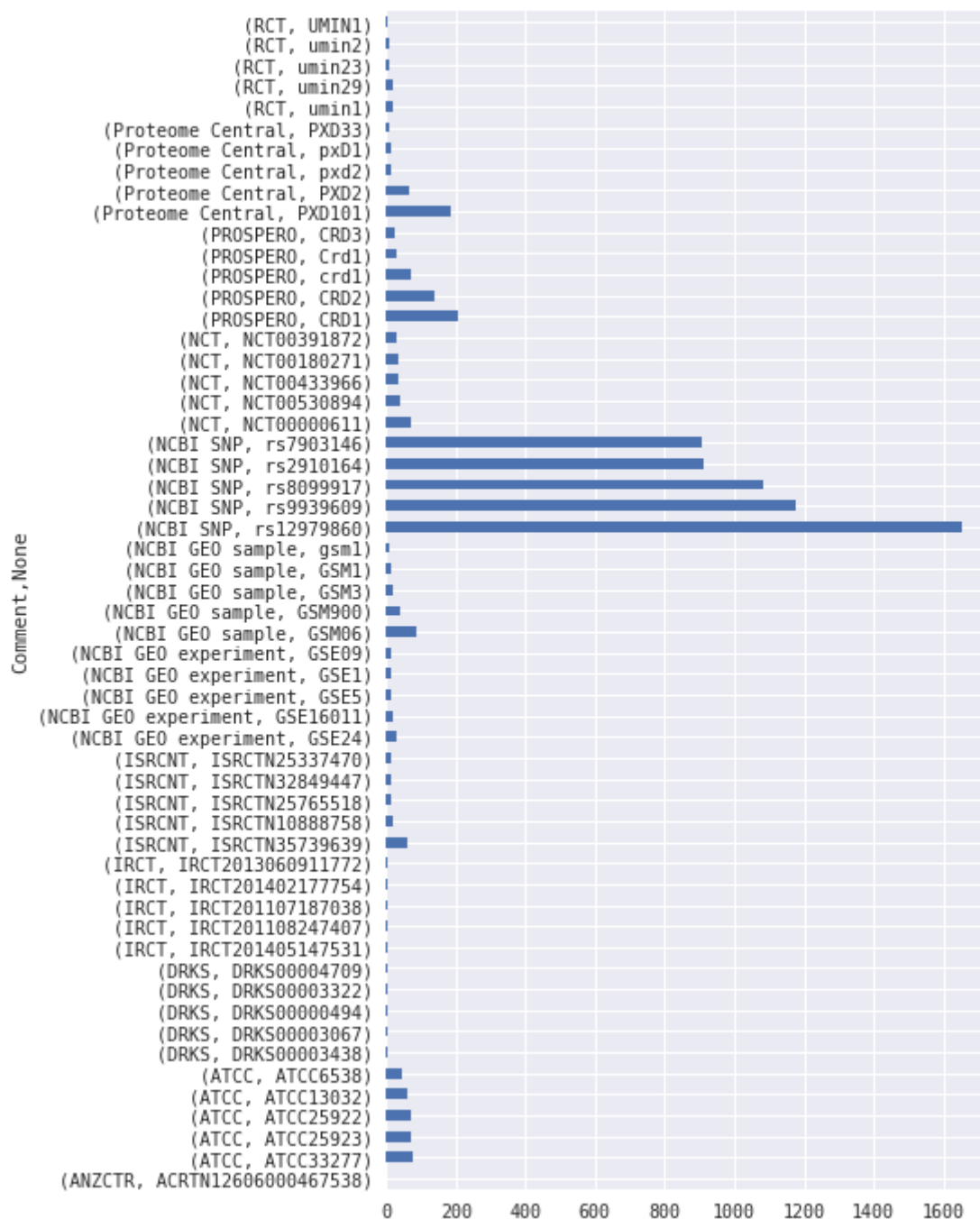


<http://10.84.146.16:9001/home>

[http://10.84.146.16:2460/notebooks/pubqc\\_test\\_results.ipynb](http://10.84.146.16:2460/notebooks/pubqc_test_results.ipynb)

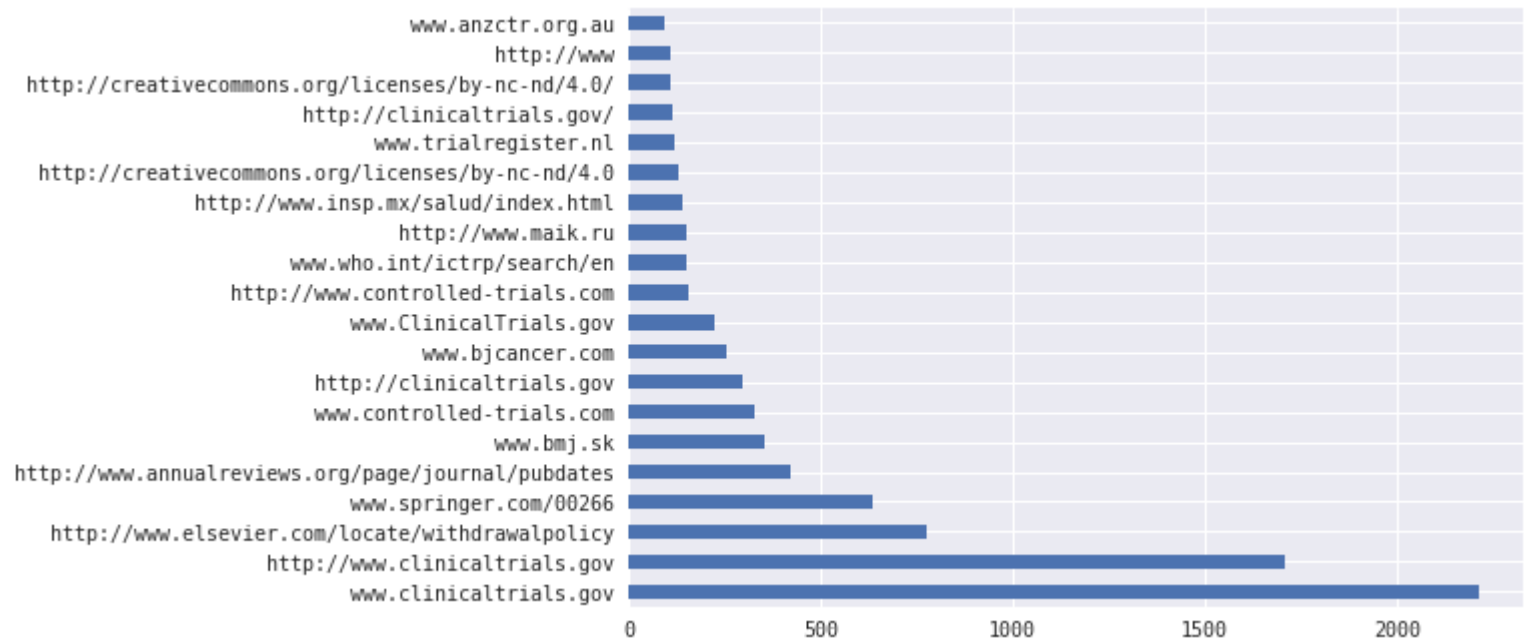
# PubQC – IDs (regex)

- 251,868 found
- Belinostat (**PXD101**) is a novel HDAC inhibitor with IC50 of 27 nM in a cell-free assay, with activity demonstrated in cisplatin-resistant tumors
- **rs12979860** is a SNP near the IL28B gene, encoding interferon-lambda-3 (IFN-lambda-3)
- **rs9939609** is a SNP in the fat mass and obesity associated FTO gene, aka the "Fat Gene"
- **ATCC 33277** Porphyromonas gingivalis genome - human pathogen
- **rs8099917** is related to hepatitis C treatment response
- **GSE16011** is a glioma cohort
- (TODO) **GSM1** is a protein, **GSM06** is a cell line, **CRD1** a protein domain, etc.



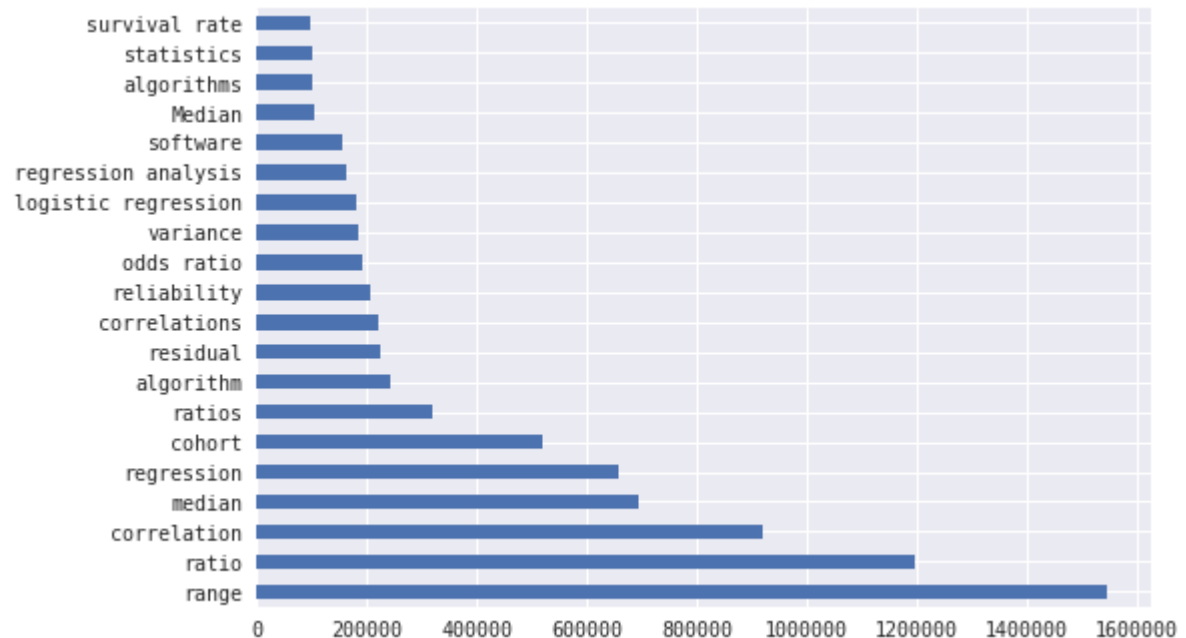
# PubQC – URLs (regex)

- 65,995 found
- **www.springer.com/00266** - aesthetic plastic surgery (??)
- (TODO) '**http://www**' is almost always matched when there's a space after the 'www.'
- (TODO) spaCy results were rubbish – why?
- (TODO) programatically get response from the server



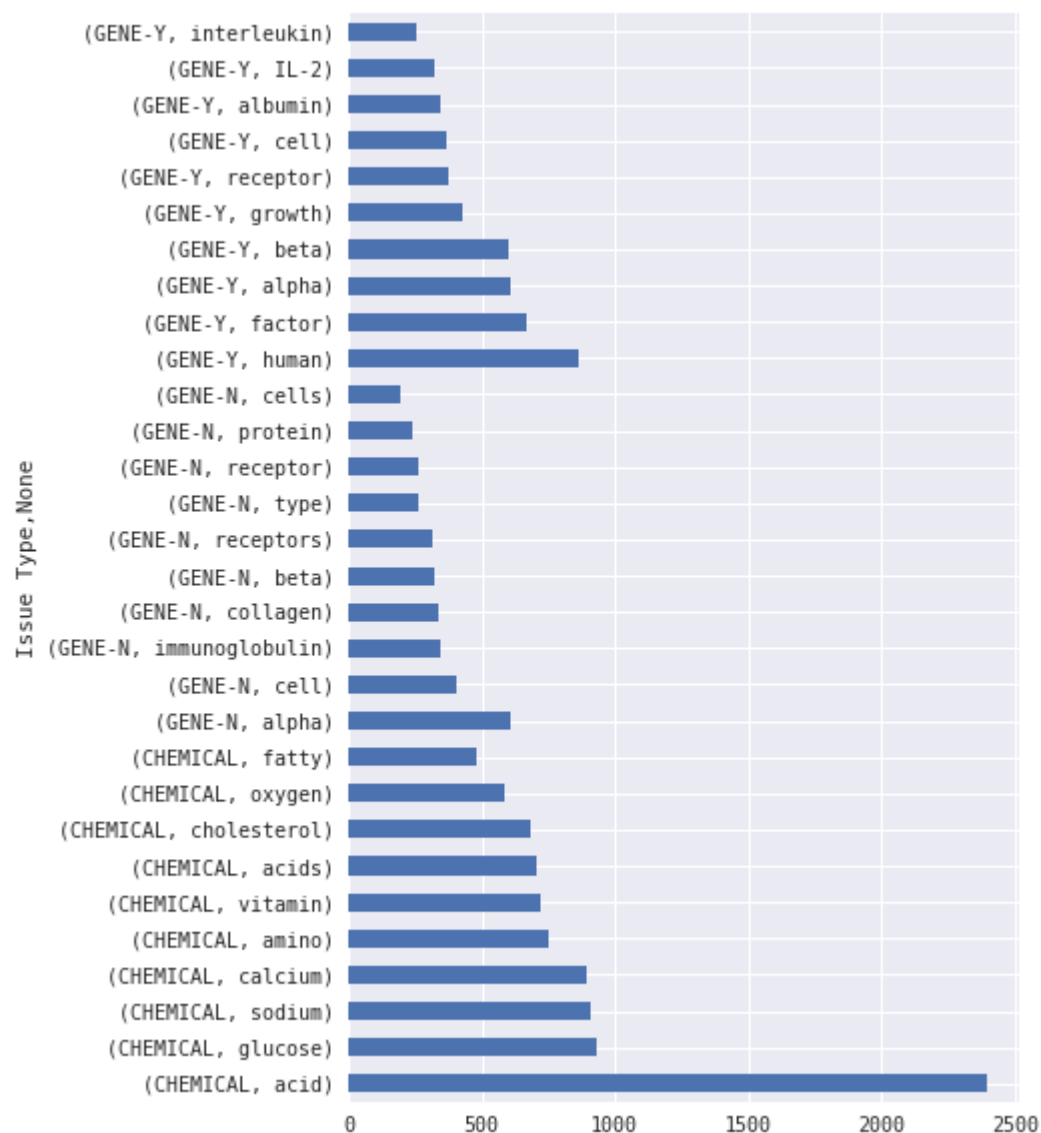
# PubQC – terms (simple pattern match)

- 10,932,987 found
- (TODO) ignore case



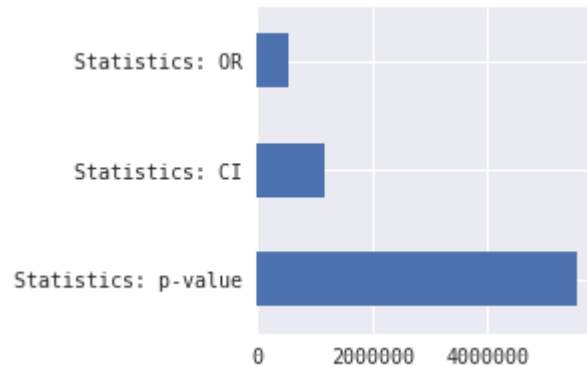
# PubQC – chemicals, genes (spaCy)

- 128,301 found, but...





# PubQC – CI, OR, p-value



- Number of values associated with each

Statistics: CI	3	12043
	4	545
	2	12
	5	5
	6	4
Statistics: OR	1	6208
	2	1
Statistics: p-value	1	63403

- (TODO) scientific notation
- (TODO) recalculate statistics

- Extracted p-values

0.050000	13836
0.001000	11933
0.010000	8188
0.000100	3201
0.020000	1857
0.000000	1543
...	
1.000000	184
...	
648.000000	1
6.540000	1

PMI D	Pattern	Location	value	Lower	Upper	Rec alcu late d OR	Pattern	Location	Context
3384 186	95% CI (CI)=(0.93, 3.17	(762, 785)	[95.0, 0.93, 3.17]	0.93	3.17		OR)=1.7 1	(752, 760)	ve to the NHWs [odds ratio (OR)=1.71; 95% CI (CI)=(0.93, 3.17)]. The risk of severe retinopathy (pr
3387 899	95% CI, 1.5-3.5	(943, 958)	[95.0, 1.5, 3.5]	1.5	3.5		OR=2.3	(935, 941)	eir place of residence indicated (OR=2.3; 95% CI, 1.5-3.5). There was a trend for patients to repor
3387 899	95% CI, 0.9-6.7	(1032, 1047)	[95.0, 0.9, 6.7]	0.9	6.7		OR=2.4	(1024, 1030)	s to report an unhappy childhood (OR=2.4; 95% CI, 0.9-6.7). Being unmarried, undergoing parental se
3389 360	3.94, CI=1.52- 10.20	(849, 868)	[3.94, 1.52, 10.2]	1.52	10.2		OR=3.94	(846, 853)	d an elevated risk for brain cancer (OR=3.94, CI=1.52-10.20). In addition, there was a linear relat
3389 361	1.72, CI 1.09-2.97	(750, 768)	[1.72, 1.09, 2.97]	1.09	2.97		OR 1.72	(747, 754)	the reduction division of the plant (OR 1.72, CI 1.09-2.97) including, in particular, Soderberg (OR
3389 361	1.71, CI 1.07-2.72	(810, 828)	[1.71, 1.07, 2.72]	1.07	2.72		OR 1.71	(807, 814)	including, in particular, Soderberg (OR 1.71, CI 1.07-2.72) and prebake (OR 2.26, CI. 1.27-4.02) po
3389 361	2.26, CI. 1.27-4.02	(846, 865)	[2.26, 1.27, 4.02]	1.27	4.02		OR 2.26	(843, 850)	(OR 1.71, CI 1.07-2.72) and prebake (OR 2.26, CI. 1.27-4.02) potroom workers. The risk of IHD did n
3394 698	95% CI=1.6-4.9	(877, 891)	[95.0, 1.6, 4.9]	1.6	4.9		OR)=2.8	(868, 875)	eral cancer (adjusted odds ratio (OR)=2.8, 95% CI=1.6-4.9). Further, this relation was modified by t
3394 698	95% CI=1.2-3.0	(1003, 1017)	[95.0, 1.2, 3.0]	1.2	3		OR=1.9	(995, 1001)	initial cancer diagnosis (ratio of OR=1.9, 95% CI=1.2-3.0 for a five-year differential in time since
3394 698	95% CI=0.3-1.2	(1191, 1205)	[95.0, 0.3, 1.2]	0.3	1.2		OR=0.6	(1183, 1189)	h a 36% decrease in risk (adjusted OR=0.6, 95% CI=0.3-1.2); this estimate excluded the magnitude of
3394 707	95% CI=1.1-2.2	(520, 534)	[95.0, 1.1, 2.2]	1.1	2.2		OR)=1.6	(511, 518)	showed that male sex (odds ratio (OR)=1.6, 95% CI=1.1-2.2), maternal five-year age increase (OR=1.3,
3394 707	95% CI=1.1-1.5	(578, 592)	[95.0, 1.1, 1.5]	1.1	1.5		OR=1.3	(570, 576)	, maternal five-year age increase (OR=1.3, 95% CI=1.1-1.5), plural birth (OR=3.0, 95% CI=1.2-7.1) an
3394 707	95% CI=1.2-7.1	(617, 631)	[95.0, 1.2, 7.1]	1.2	7.1		OR=3.0	(609, 615)	.3, 95% CI=1.1-1.5), plural birth (OR=3.0, 95% CI=1.2-7.1) and black maternal race (OR=0.0, 95 perce
3395 581	95% CI=1.0-2.6	(634, 648)	[95.0, 1.0, 2.6]	1	2.6		OR)=1.6	(625, 632)	icultural production (odds ratio (OR)=1.6, 95% CI=1.0-2.6). A concomitant increase was detected for
3395	95%	(708, 722)	[95.0, 1.0, 2.5]	1	2.5		OR=1.6	(700, 706)	increase was detected for farmers (OR=1.6, 95% CI=1.0-

# PubQC – concentrations, percentages

- (TODO) Get chemicals in the proximity (extract noun?)

1:1	385
2:1	178
18:2	143
18:1	121
16:0	106
...	
100mg/kg)	8
50mg/kg)	8
12:0	8
200mg/kg)	7
5mg/kg)	7
19:00	7

95%	10130
50%	3683
10%	2510
20%	2378
100%	2207
5%	2033
30%	1892
90%	1857
80%	1794
40%	1744
25%	1550
60%	1487
70%	1465
1%	1369

2.2%

Percent

(838, 842)

xed meat or chicken or pork or beef contributes 2.2%), the GH  
emission is estimated to be 0.28 or 0  
meat (CHEMICAL); chicken (CHEMICAL); pork (CHEMICAL)

0.5%

Percent (178, 182)

sound biomicroscopy. To determine the effect of 0.5%  
tropicamide and the resultant mydriasis on the  
tropicamide (CHEMICAL)

84%

percent

(635, 638)

c SBR became fully granulated and finished with 84% and 99  
of nitrogen and phosphorus removal, res  
nitrogen (CHEMICAL)

19.73ng/ml

concentration

(556, 567)

. Cutoff value for detecting stage B HF was 19.73ng/ml for  
catestatin with 90% sensitivity and 50.9  
catestatin (CHEMICAL)

cat0

Column information

Column name: cat0

Column type: object

Table: Summary by cat0

cat0	logistic								lognormal								normal		
	count	mean	std	min	25%	50%	75%	max	count	mean	std	min	25%	50%	75%	max	count	mean	std
a	189.0	0.253651	1.711486	-4.02	-0.880	0.10	1.2000	6.53	189.0	1.778730	2.267438	0.07	0.600	1.05	2.1100	18.72	189.0	-0.030159	1.032
b	160.0	-0.015062	1.716513	-5.16	-0.910	-0.21	0.9675	6.50	160.0	1.607500	1.690542	0.07	0.580	1.05	1.9625	10.46	160.0	0.009625	0.968
c	151.0	0.419073	2.052203	-8.76	-0.815	0.37	1.5350	5.83	151.0	1.766556	2.838467	0.09	0.515	1.09	1.9750	30.58	151.0	-0.012517	1.002

Titles: MANOVA results for all variables

-	Df	Pillai	approx F	num_Df	den Df	Pr(>F)
cat0	2	0.014649	0.91312	8	990	0.5046
Residuals	497	-	-	-	-	-

Titles: MANOVA results for response lognormal

-	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cat0	2	3.0	1.5021	0.2839	0.753
Residuals	497	2629.5	5.2908	-	-

Titles: MANOVA results for response logistic

-	Df	Sum Sq	Mean Sq	F value	Pr(>F)
cat0	2	15.04	7.5180	2.2633	0.1051
Residuals	497	1650.90	3.3217	-	-

lognormal

Column information

Column name: lognormal

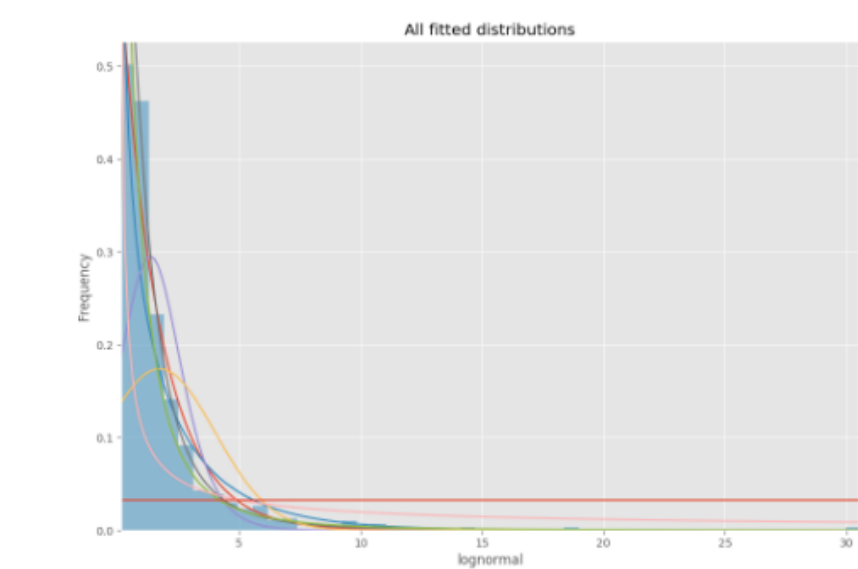
Column type: float64

Table: Column summary

count	mean	std	min	25%	50%	75%	max
500.0	1.72026	2.296861	0.07	0.58	1.065	2.0025	30.58

Table: Fitted distributions with best parameters and residual sum of squares

distribution	parameters	SSE
<a href="#">beta</a>	a=0.98, b=113.42, loc=0.07, scale=192.26	0.185949
<a href="#">chi2</a>	df=1.32, loc=0.07, scale=1.54	0.471846
<a href="#">logistic</a>	loc=1.34, scale=0.85	0.626428
<a href="#">lognorm</a>	s=0.97, loc=0.01, scale=1.06	0.0629841
<a href="#">norm</a>	loc=1.72, scale=2.29	1.05756
<a href="#">pareto</a>	b=2.02, loc=-1.83, scale=1.90	0.510913
<a href="#">powerlaw</a>	a=0.27, loc=0.07, scale=33.09	1.124
<a href="#">uniform</a>	loc=0.07, scale=30.51	2.09939



# Who Cares?

Maria K. E. Lahman<sup>1</sup>

## Keywords

methodology, poetry, research poetry

I fantasize saying,  
"Who CARES if  
YOU think poetry  
can be research?",  
with a negligent  
shrug of  
shoulders.

Research IS poetry.

We are having a  
methodological  
ARGUMENT.

Tug  
of  
War,

Over  
our DEAD fetuses' bodies,<sup>1</sup>  
a girl's ANOREXIA,<sup>2</sup>  
my postpartum DEPRESSION<sup>3</sup>  
their HIV,<sup>4</sup>  
her MURDER,<sup>5</sup>  
his SUICIDE,<sup>6</sup>  
a daughter's racial IDENTITY,<sup>7</sup>  
their COMING OUT.<sup>8</sup>

Experience,  
story,  
research,  
poetry,  
inquiry,  
explorations,  
should  
fluster,  
perplex,  
unsettle  
method...  
METHODOLATRY.<sup>9</sup>

But I'd be lying.

I  
know  
I  
care...

## Declaration of Conflicting Interests

The author(s) declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

## Funding

The author(s) received no financial support for the research, authorship, and/or publication of this article.

## Notes

1. Lahman (2013).
2. Chan (2003).
3. Lahman (2008).
4. Poindexter (2002).
5. Lahman (2011).
6. Teman (2010).
7. Davis (2007).
8. Teman (2011).
9. Janesick (1994).

## References

- Chan, Z. C. (2003). A poem: Anorexia. *Qualitative Inquiry*, 9, 956-957.
- Davis, A. M. (2007). SIP (School Induced Psychosis) poem for my daughter. *Qualitative Inquiry*, 13, 919-924.
- Janesick, V. J. (1994). The dance of qualitative research design – metaphor, methodolatry and meaning. In N. K. Denzin & Y. S. Lincoln (Eds.), *Handbook of qualitative research*. pp.209-219. Thousand Oaks, CA: Sage.

<sup>1</sup>University of Northern Colorado, Greeley, USA

## Corresponding Author:

Maria K. E. Lahman, University of Northern Colorado, McKee Hall, Box 124, Greeley, CO 80631, USA.  
Email: maria.lahman@unco.edu