Gene set analysis of correlated, paired-sample transcriptome data to enable precision medicine

A. Grant Schissler, PhD
Department of Mathematics & Statistics
University of Nevada, Reno

✉aschissler@unr.edu
🌐www.grantschissler.com

Motivating data & background
Correlation-adjusted analytics
Motivating data
Interdisciplinary work products

Example paired RNA-seq[1] quantified mRNA (normalized) expression data in a gene set[2]

Gene	Case expression	Baseline expression	Difference
CYP4A11	0.00	3.71	-3.71
AGTR1	6.13	7.86	-1.73
OR51E2	2.90	1.54	1.36
CYP11B2	0.00	0.00	0.00
PTPRO	3.72	6.22	-2.50
CYP4F2	0.00	0.40	-0.40
AGT	8.40	7.89	0.52
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SERPINF2	6.38	9.57	-3.19

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[1]Wang, Z., Gerstein, M., et al. 2009.
[2]Ashburner, M., Ball, C. A., et al. 2000.

A statistician's nightmare

Interdisciplinary focus: Biomedical questions of interest and work products

- Can you provide a meaningful effect size[3]?
- Can you provide a measure of uncertainty (e.g., P-value[4]?)

[3]Schissler, A. G., Gardeux, V., et al. 2015, *Bioinformatics*.
[4]Schissler, A. G., Piegorsch, W. W., et al. 2017, *Stat. Methods Med. Res.*

Interdisciplinary focus: Biomedical questions of interest and work products

- Can you provide a meaningful effect size[3]?
- Can you provide a measure of uncertainty (e.g., P-value[4]?)
- How can these statistics be used in research and practice?
  - Single-subject inferences: breast cancer patients[3,4], HIV[5].
  - single-cell data[6].
  - R package[7].

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[3]Schissler, A. G., Gardeux, V., et al. 2015, *Bioinformatics*.
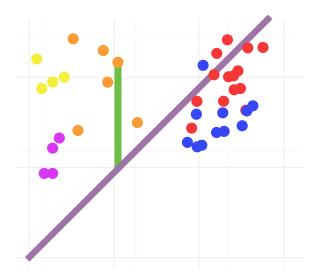[4]Schissler, A. G., Piegorsch, W. W., et al. 2017, *Stat. Methods Med. Res.*
[5]Li, Q., Schissler, A. G., et al. 2016, *J. Biomed. Inform.*
[6]Schissler, A. G., Li, Q., et al. 2016, *Bioinformatics*.
[7]http://www.lussiergroup.org/publications/N-of-1-pathways

Illustrative representation of methods

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Illustrative summary