Permutation

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Idea: Permute labels to “break relationship”

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PLOS MEDICINE

An Erythroid Differentiation Signature Predicts Response to Lenalidomide in Myelodysplastic Syndrome

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Response	R	R	•••	NR	NR

	Patient 1	Patient 2	•••	Patient n-1	Patient n
Gene 1	-1.64	-0.42	•••	-1.39	-0.38
Gene 2	-3.12	-3.60	•••	-3.80	-2.82
⋮	⋮	⋮	•••	⋮	⋮
⋮	⋮	⋮		⋮	⋮
⋮	⋮	⋮	•••	⋮	⋮
⋮	⋮	⋮		⋮	⋮

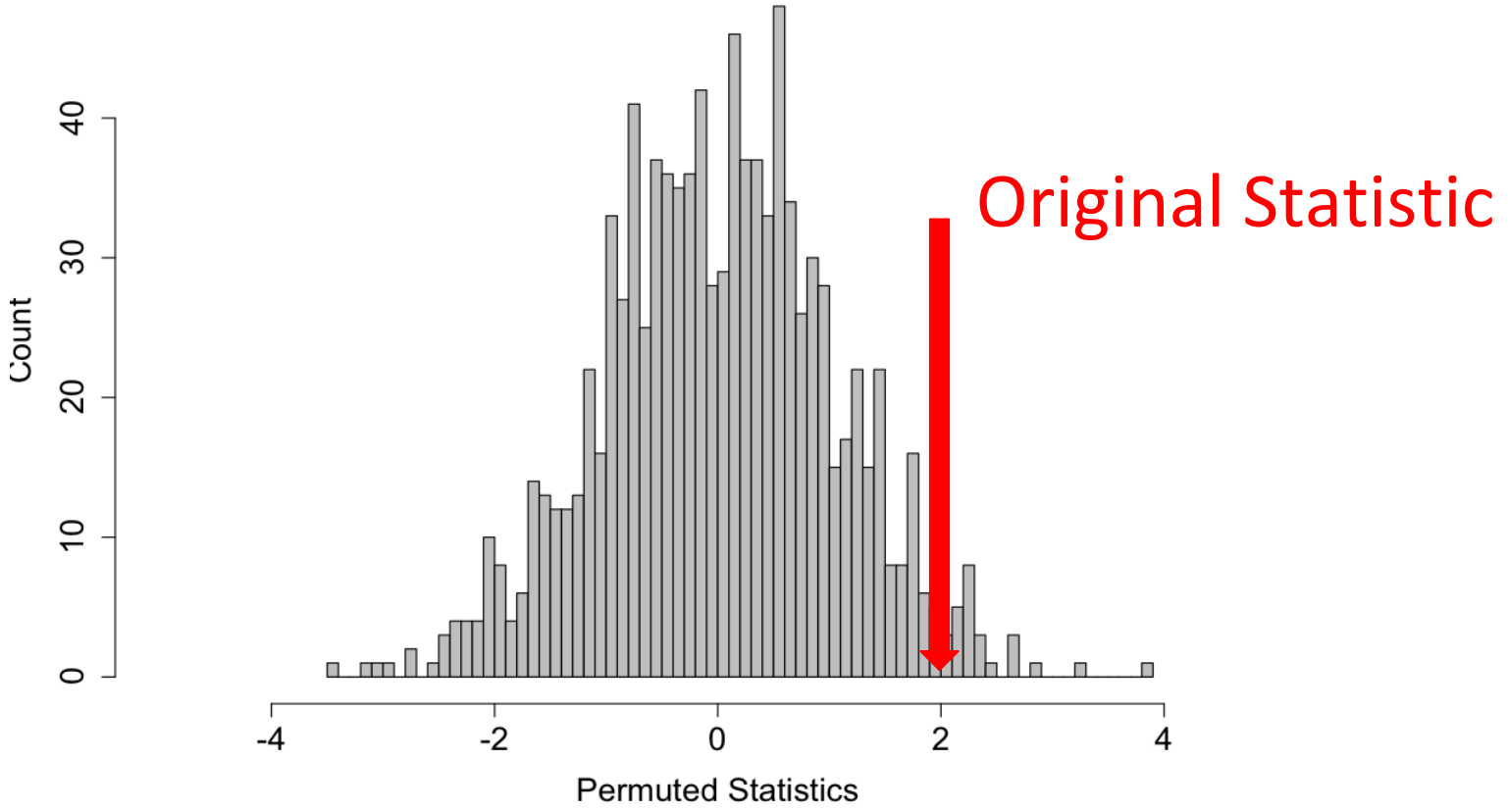
https://en.wikipedia.org/wiki/T-statistic

$$\frac{\overline{Y} - \overline{X}}{\sqrt{\frac{s_Y^2}{N} + \frac{s_X^2}{M}}}$$

Response	R	R	•••	NR	NR
	Patient 1	Patient 2	•••	Patient n-1	Patient n
Gene 1	-1.64	-0.42	•••	-1.39	-0.38
Gene 2	-3.12	-3.60	•••	-3.80	-2.82
:	:	:	•••	:	:
:	:	:		:	:
:	:	:	•••	:	:
:	:	:		:	:
Gene m-1	-2.34	-0.22	•••	-1.22	-2.76
Gene m	4.53	3.23	•••	0.29	3.11

Response	NR	R	•••	NR	R
	Patient 1	Patient 2	•••	Patient n-1	Patient n
Gene 1	-1.64	-0.42	•••	-1.39	-0.38
Gene 2	-3.12	-3.60	•••	-3.80	-2.82
:	:	:	•••	:	:
:	:	:		:	:
:	:	:	•••	:	:
:	:	:		:	:
Gene m-1	-2.34	-0.22	•••	-1.22	-2.76
Gene m	4.53	3.23	•••	0.29	3.11

Leaves the relationship between genes unchanged.


Original Statistic
Count
0
10
20
30
40
-4
-2
0
2
4
Permuted Statistics

Notes and further reading

- Permutation is used all the time!
- Assumes that if you switch the labels the data come from the exact same distribution - *not a comparison of means!*
- More information:
  - https://www.edx.org/course/statistics-r-life-sciences-harvardx-ph525-1x