



#### On the Stability and Reproducibility of Data Science Pipelines

## **Professor Gavin Brown**University of Manchester, UK



## Nature, 2016

THI

**EDITORIALS** 

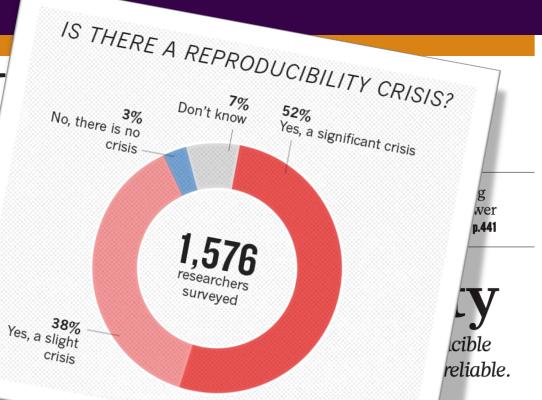
**POSTDOCS** Mo but fewer jothe way **p.4** 

# Reality che

A survey of Nature readers rev results. Researchers, funders

s there a reproducibility crisis in science? Yes, according to the readers of *Nature*. As we report on page 452, two-thirds of researchers who responded to a survey by this journal said that current levels of reproducibility are a major problem.

The ability to reproduce experiments is at the heart of science, yet failure to do so is a routine part of research. Some amount of irreproducibility is inevitable: profound insights can start as fragile signals,

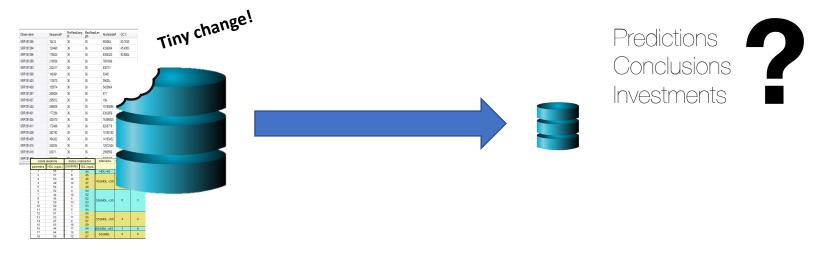


really be onature picking, conscious or ne workflows that avoid having a single research harge of preparing

images or collecting results. Dozens of respondents reported steps to make better use of statistics, randomization or blinding. One described an institution-level initiative to teach scien-

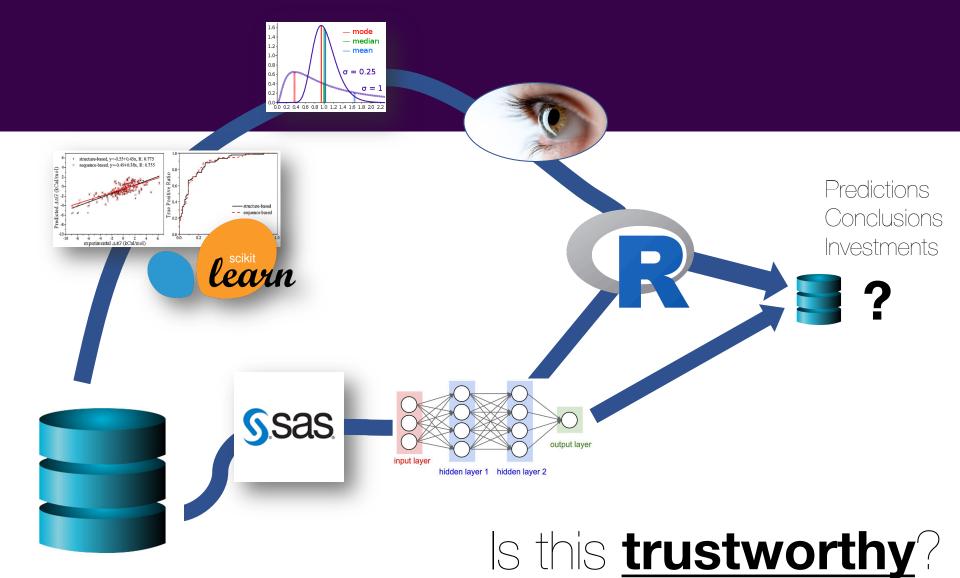
.....

## This is your data science pipeline.



"How much do you **trust** your data pipeline?"

"How reproducible is your result?"



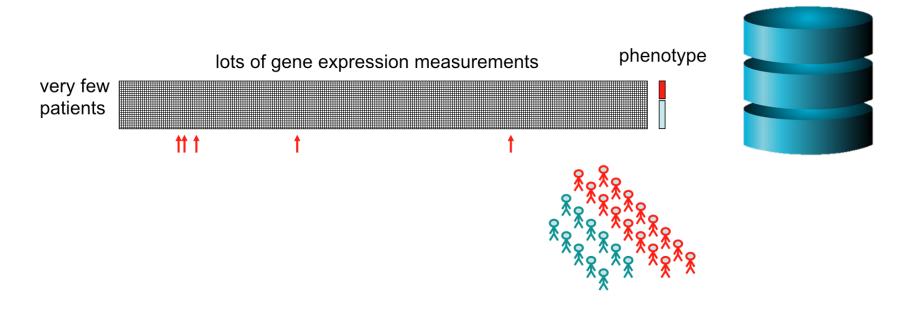
## Reproducibility = <u>Trust</u>

Reproducibility is not a "yes/no" question.

Conjecture: We can measure reproducibility.

### Let's take something specific.

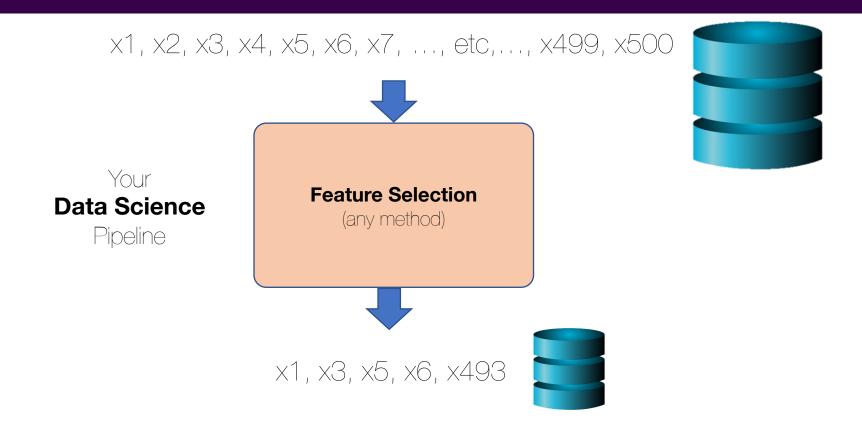
#### Data-driven biomarker selection



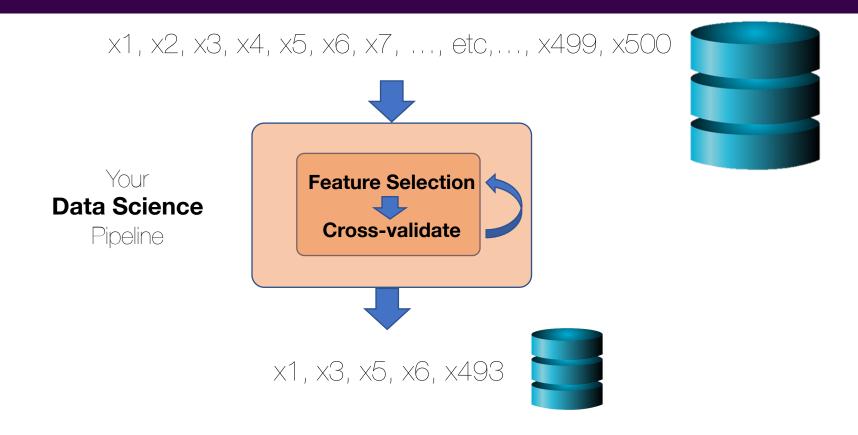
Only a subset of features actually influence the phenotype.



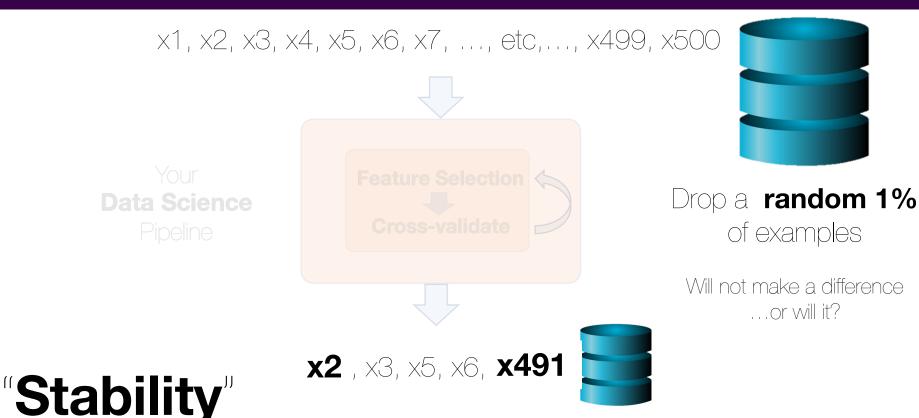
#### How much do you trust your choices?



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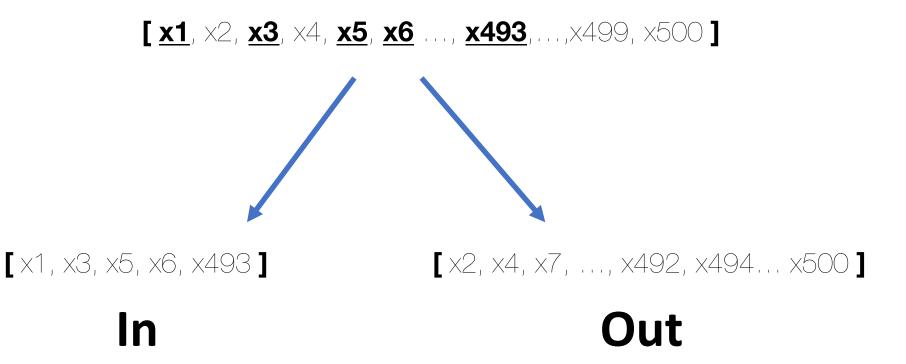
# "Stability"

A specific instance of **reproducibility.** 

For the task of data-driven biomarker selection.

But... how to measure it?

## Estimating **Stability**



## Estimating **Stability**

Set intersection? (i.e. features in common)

$$\phi(s_i, s_j) = 3$$

My selected biomarkers. When using **ALL** data.

[x1, x3, x5, x6, x493]

[x2, x3, x5, x6, x491]

Small change if I drop a random 1% of data

## Estimating Stability... which set measure?

Dunne et al. (2002)	Hamming	$1 - \frac{ s_i \setminus s_j  +  s_i \setminus s_j }{d}$	
Kalousis et al. (2005)	Jaccard	$\frac{ s_i {\cap} s_j }{ s_i {\cup} s_j }$	
Yu et al. (2008)	Dice-Sørenson	$\frac{2 s_i\cap s_j }{ s_i + s_j }$	
Goh and Wong (2016)	Ochiai	$\frac{ s_i \cap s_j }{\sqrt{ s_i  s_j }}$	
Shi et al (2006)	POG	$rac{ s_i \cap s_j }{ s_i }$	
Kuncheva (2007)	Consistency	$\frac{r_{i,j} - \frac{k^2}{d}}{k - \frac{k^2}{d}}$	
Lustgarten et al. (2009)	Lustgarten	$\frac{r_{i,j} - \frac{k_i k_j}{d}}{\min(k_i, k_j) - \max(0, k_i + k_j - d)}$	
Wald et al. (2013)	Wald	$\frac{r_{i,j} - \frac{k_i k_j}{d}}{\min(k_i, k_j) - \frac{k_i k_j}{d}}$	

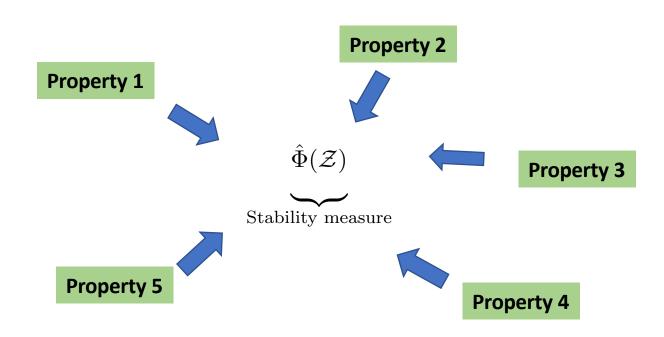
Set theoretic measures 1957-2017.

Many definitions (about 20)

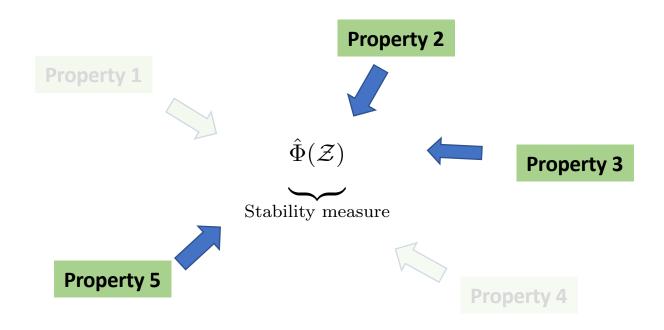
Mostly heuristic.
Conflicting opinions.

No principled way to choose between them.

## What properties do we want?



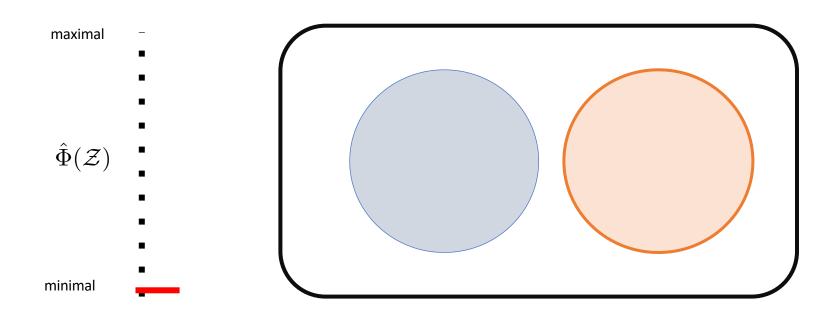
### What properties do we want?



## Desirable property 2: Strict Monotonicity

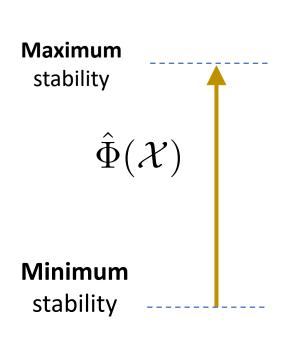
**Property 2** 

...as the sets overlap more, the measure should increase.



## **Desirable property 3:** Known upper/lower Bounds

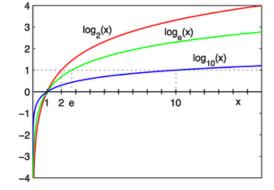
**Property 3** 



For **interpretability** and **comparison** across problems/algorithms,

... it should have

known, finite upper/lower bounds,



No logarithms!

## Desirable property 5: Correction for chance

**Property 5** 

Selecting 2 features from 200...

Is very different to selecting 2 from 5...

 High chance of intersection, even if random!

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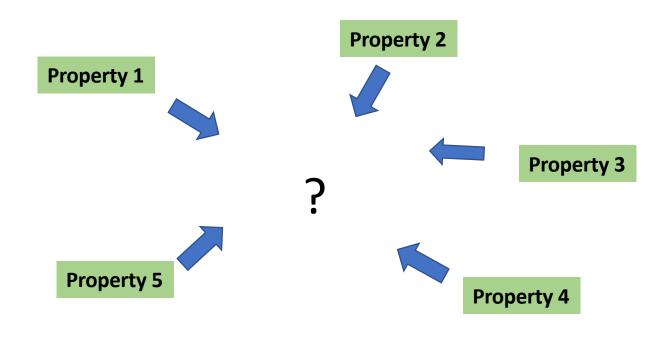
## Remember this?

#### Results...

5 2 4 3 Fully defined | Monotonicity | Bounds | Maximum | Name Correction Hamming Jaccard Dice Ochiai POG Kuncheva Lustgarten Wald nPOG Goh Davis Krízek Guzmán  $CW_{rel}$ Lausser

See paper for the 75 proofs!

### So where do these properties point?



Definition 2 (Effective Stability for Pairwise Feature Redundancy). Given a matrix  $\mathbb{C}$  specifying feature relationships, the effective stability is

$$\widehat{\Phi}_{\mathbb{C}}(\mathcal{Z}) = 1 - \frac{\sum_{f=1}^{d} \sum_{f'=1}^{d} c_{f,f'}\widehat{\operatorname{cov}}(Z_{f}, Z_{f'})}{\sum_{f=1}^{d} \sum_{f'=1}^{d} c_{f,f'}\widehat{\operatorname{cov}}(Z_{f}, Z_{f'}|H_{0})} = 1 - \frac{\operatorname{tr}(\mathbb{C}\mathbf{S})}{\operatorname{tr}(\mathbb{C}\mathbf{\Sigma}^{0})}, \quad (5)$$

there  $\mathbf{S}$  is the set of the set

where  $\mathbf{S}$  is an unbiased estimator of the variance-covariance matrix of  $\mathbf{Z}$ , i.e.  $\mathbf{S}_{f,f'} = \widehat{\mathrm{Cov}}(Z_f, Z_{f'}) = \frac{M}{M-1}(\hat{p}_{f,f'} - \hat{p}_f\hat{p}_{f'}), \ \forall \ f, f' \in \{1...d\}, \ \text{while } \mathbf{\Sigma}^0 \text{ is the } \mathbf{\Sigma}^0 \text{ is the$ 

- 1. All 5 desirable properties, as discussed.
- 2. Clean **statistical** interpretation

....Confidence intervals and hypothesis tests come for free

3. Computable in **closed form**, as opposed to quadratic

#### Journal off Machine Machine Learning Research, 2018

Journal of Machine Learning Research 18 (2018) 1-54

Submitted 9/17; Revised 2/18; Published 4/18

#### On the Stability of Feature Selection Algorithms

Sarah Nogueira Konstantinos Sechidis Gavin Brown

School of Computer Science University of Manchester Manchester M13 9PL, UK

Editor: Isabelle Guyon

SARAH.NOGUEIRA@MANCHESTER.AC.UK KONSTANTINOS.SECHIDIS@MANCHESTER.AC.UK GAVIN.BROWN@MANCHESTER.AC.UK

#### Abstract

Feature Selection is central to modern data science, from exploratory data analysis to predictive model-building. The "stability" of a feature selection algorithm refers to the robustness of its feature preferences, with respect to data sampling and to its stochastic nature. An algorithm is 'unstable' if a small change in data leads to large changes in the chosen feature subset. Whilst the idea is simple, quantifying this has proven more challenging—we note numerous proposals in the literature, each with different motivation

## Case Study: Non-Small Cell Lung Cancer

Efficacy of **gefitinib** vs **chemotherapy** for lung cancer.

#### 2 competing biomarker sets. Which do we trust?

Rank	GBM	CMIM
1	EGFR expression $(X_4)$	$\mid$ EGFR mutation $(X_2)$
2	Disease stage $(X_{10})$	Serum $ALP(X_{13})$
3	WHO perform. status $(X_1)$	Blood leukocytes $(X_{21})$
$4 \mid$	Serum $ALT(X_{12})$	Serum ALT $(X_{12})$

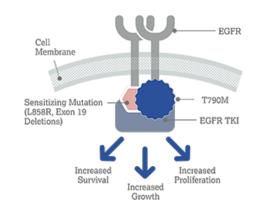


## Case Study: Non-Small Cell Lung Cancer

	GBM		CMIM
Stability $\widehat{\Phi}(\mathcal{Z})$	0.87	>	0.68
- within <b>Group A</b>	0.96		0.45
- within ${f Group}\ {f B}$	0.82		0.80
- within <b>Group C</b>	0.14		0.43
Effective stability $\widehat{\Phi}_{\mathbb{C}}(\mathcal{Z})$	0.87	<	0.91

All EGFR gene mutations

(known to play a role in NSCLC)



#### Measure within-group stability

to see what's happening...

#### Changes our view

of the "best" algorithm to invest in.



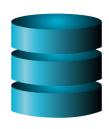


#### On the Reproducibility of Data Science Pipelines

#### The Take-Home Message

Reproducibility is not a yes /no question.

Reproducibility = <u>Trust</u>



The industry needs methods to **quantify reproducibility.** 





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