PIMA: An inferential framework for multiverse analysis

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A leading example

In real data analysis, researchers face many choices:

- variable transformation (log, sqrt, splines, etc.)
- inclusion of covariates and interactions
- outlier deletion
- ...

Example

- one over 4 possible predictors X_1, X_2, X_3, X_4
- gender + (a subset of) other covariates/mediators
- possible interaction between X₁ or X₂ and gender

 \longrightarrow We easily get lost in the forest of possible models!

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p-hacking (data snooping or data dredging)

Performing many statistical tests on the same data and only reporting those that give significant results

Consequences

Dramatically increases and understates the risk of false positives

This is a main reason of the replicability crisis in psychology, neuroscience, biology, economics, etc.¹

¹Ioannidis. Why most published research findings are false. *PLoS Med.*, 2005.

'Don't hide what you tried, report all the p-values and discuss'

A philosophy of reporting the outcomes of many different analyses to explore:

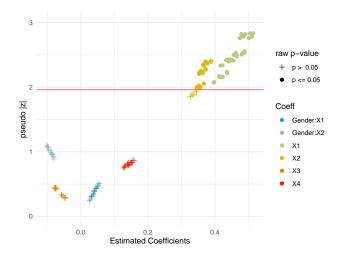
- robustness of results
- key choices that are most consequential in their fluctuation

Main tool: histogram of p-values

 \longrightarrow discussed in terms of % of significant p-values

¹Steegen et al. Increasing transparency through a multiverse analysis. *Perspect. Psychol. Sci.*, 2016.

Results: p-values in the example



pseudo |z| = qnorm(1 - p/2)

Ok, let's go multiverse! 43% of the tested coefficients have $p \le 0.05$. Quite a strong evidence, isn't it?

No! We don't get any inferential clue from it.

Multiverse analysis is important to make data analysis transparent, but a formal inferential approach is missing.

p-hacking is an informal selective inference problem. Make it formal and get p-values that account for this multiplicity!

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Valid p-hacking via PIMA²

PIMA constructs permutation-based test statistics/p-values, combining information from all plausible models

- ? Is there any non-null effect among the tested models?
- I Global p-value (weak FWER control) Like Specification Curve¹, but done right
- ? Which models are significant?
- ! Adjusted p-values for each model (strong FWER control) using the maxT algorithm → choose the model you like best!

¹(not valid in GLM) Simonsohn, U., Simmons, J. P., & Nelson, L. D. (2020). Specification curve analysis. *Nature Human Behaviour*, 4(11), 1208-1214. ²Girardi et al. Post-selection Inference in Multiverse Analysis (PIMA): An inferential framework based on the sign flipping score test. *Psychometrika*, 2024.

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PIMA

Consider K plausible general linear models (GLM):

$$g_k(\mathbb{E}(y_{ki})) = \beta_k x_{ki} + \gamma_k z_{ki} \qquad (i = 1, \dots, n)$$

- y_{ki}: response —> outlier deletion or leverage point removal
- *x_{ki}* and *z_{ki}*: transformed predictors → selection, combination and transformation

Hypothesis testing

Model $k: H_{0k}: \beta_k = 0,$ Global null: H_{0k}

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Sign flip score test (univariate)¹

Single model: *n* independent observations with density $f_{\beta,\gamma,x_i,z_i}(y_i)$

Score test:
$$T^1 = T^{\text{obs}} = \sum_{i=1}^n \nu_i, \qquad \nu_i = \frac{\partial}{\partial \beta} \log f_{\beta,\gamma,x_i,z_i}(y_i) \mid_{\hat{\gamma},\beta=0}$$

Random sign flips: $T^b = \sum_{i=1}^n \pm \nu_i \qquad (b = 2, \dots, B)$

Under $H_0: \beta = 0: T^{obs} \stackrel{d}{=} T^b$ asymptotically

$$\mathsf{p-value} = \frac{\#_b(\mathcal{T}^b \geq \mathcal{T}^{\mathsf{obs}})}{B}$$

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K models:

K score test statistics: $(T_1^{obs}, \ldots, T_K^{obs})$ Random sign flips: (T_1^b, \ldots, T_K^b) $(b = 2, \ldots, B)$ obtained by jointly flipping the signs of $\pm (\nu_{1i}, \ldots, \nu_{Ki})$

Under
$$H_0: \beta_1 = \ldots = \beta_K = 0$$
:
 $(T_1^{obs}, \ldots, T_K^{obs}) \stackrel{d}{=} (T_1^b, \ldots, T_K^b)$ asymptotically

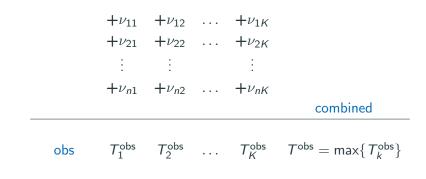
A multiverse p-value is obtained combining the single tests (e.g., $T^b = max\{T_1^b, \dots, T_K^b\}$)

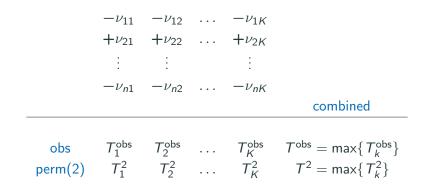
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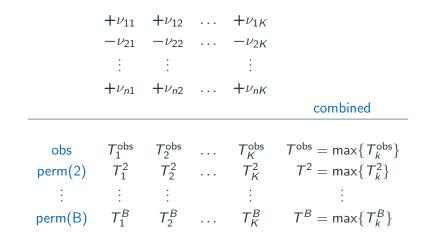
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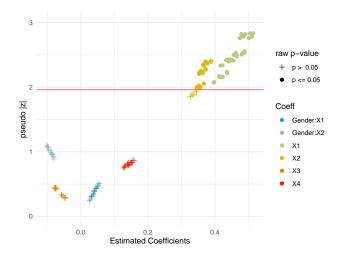
		$-\nu_{21}$	$+\nu_{12}$ $-\nu_{22}$ \vdots		$ + \nu_{1K} \\ - \nu_{2K} \\ \vdots$	
		$+\nu_{n1}$	+ <i>v</i> _{n2}		$+\nu_{nK}$	combined
perr	n(2)	T_1^2	:	•••	T_K^2	$T^{obs} = \max\{T_k^{obs}\}$ $T^2 = \max\{T_k^2\}$ \vdots
pern	n(B)	T_1^D	T_2^B			$T^{B} = \max\{T^{B}_{k}\}$ $= \frac{\#_{b}(\max\{T^{b}\} \ge \max\{T^{obs}\})}{B}$

- Can be used whenever we can write a score test (GLMs and much more)
- Asymptotically exact (exact, in practice¹)
- Very robust to variance misspecification, if the link function is correctly specified
- Can be extended to the case of multiple parameters of interest

¹De Santis et al. Inference in generalized linear models with robustness to misspecified variances. *ArXiv*, 2022.

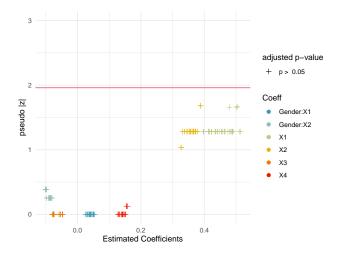
Results

Raw (unadjusted) p-values



Data are generated with no effects at all, these are ALL False Positives!

Adjusted p-values, strong FWER control

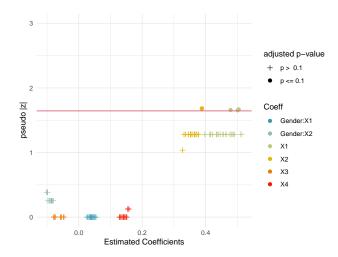


Global Null: p-value=0.089992 \longrightarrow all null effects!

Conclusion

TakeHome Message

Assuming significance level 10% (instead of 5%)



Accounting for Selective Inference (i.e. Multiple Testing, adjusted p-values) is crucial

- ? Is there any non-null effect among the tested models?
- ! Take the Global (i.e. max T) p-value: 0.089992 Yes, there is an overall effect (= at least one model)
- ? Which models are significant?
- ! There are 4 possible models: Choose the model/story you like most!!

PIMA allows:

- any transformation of variables (predictors, responses)
- any GLM
- any outlier deletion method

BUT all the above models must be

- planned in advance
- valid (at least the right link)

There is no free lunch

Sign flip score test

github.com/livioivil/flipscores and CRAN

- control of the type I error even for small sample size
- GLMs and any other model with score test
- robust to some model misspecifications

PIMA

github.com/livioivil/jointest

- inference framework for multiverse analysis
- model picking with adjusted p-values