Bioinformatics and Computational
Genomics Laboratory

Reproducible research, algorithms, and data

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2 open postdoc positions:
Re radiomics and single-cell RNA-seq

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Replicability, reproducibility and reusability

- Implement and document your functions
  → **Replicability**

- Adapt your functions to similar datasets
  → **Reproducibility**

- Extend your functions to datasets generated in different settings (samples, platforms, normalization, ...)
  → **Reusability**

Building upon previous work

If you can do it with your own functions, you can do it with published algorithms

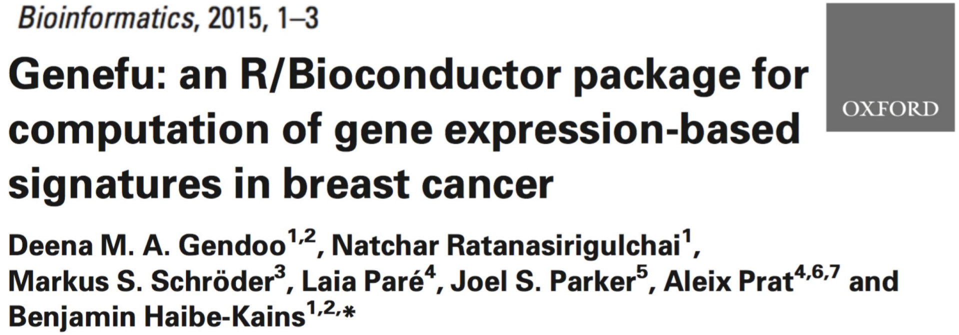
→ ***genefu*** R package reproducing published molecular subtyping classifiers and gene “signatures” with common interface

+ my own models

This holds true for dataset

→ ***MetaGxData*** data pack

and ovarian (*n*=3,752) cancers

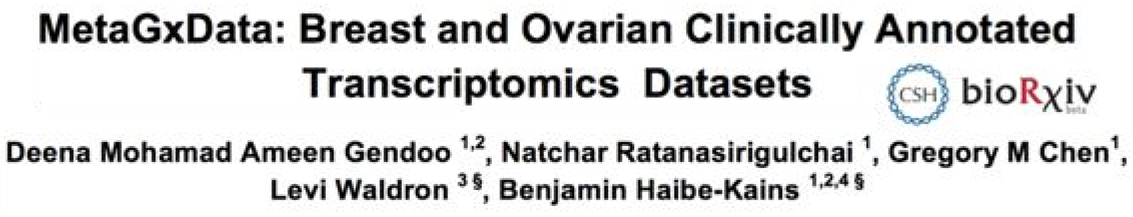


Bioinformatics, 2015, 1–3

Genefu: an R/Bioconductor package for computation of gene expression-based signatures in breast cancer

OXFORD

Deena M. A. Gendoo[1,2], Natchar Ratanasirigulchai[1], Markus S. Schröder[3], Laia Paré[4], Joel S. Parker[5], Aleix Prat[4,6,7] and Benjamin Haibe-Kains[1,2,*]



MetaGxData: Breast and Ovarian Clinically Annotated Transcriptomics Datasets

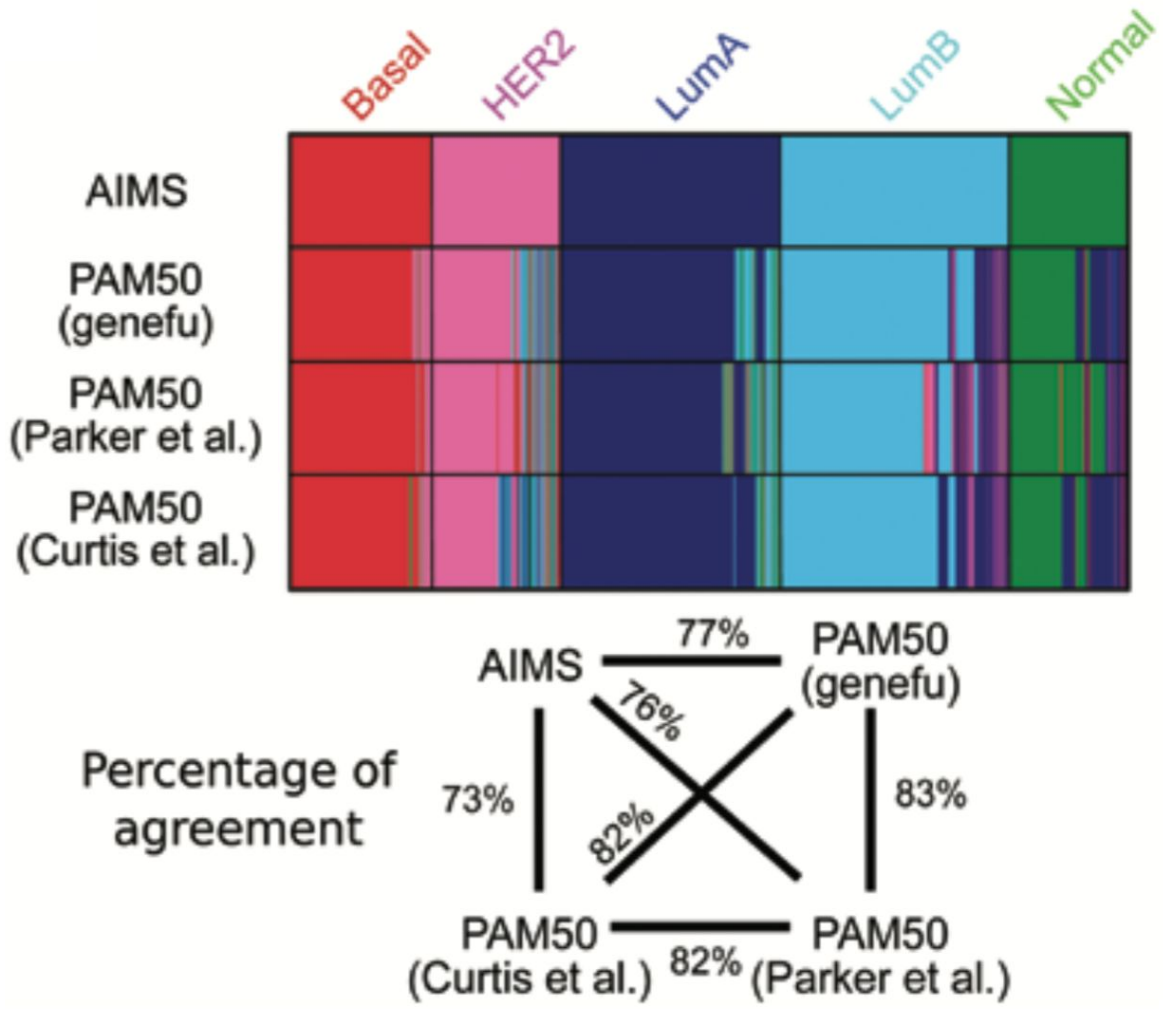
CSH bioRχiv

Deena Mohamad Ameen Gendoo [1,2], Natchar Ratanasirigulchai [1], Gregory M Chen[1], Levi Waldron [3 §], Benjamin Haibe-Kains [1,2,4 §]

Hard to fully replicate results!

- ▷ Devil is in the details
- ▷ Try to reproduce the figures of the main paper
  - ○ Exact same results ~10%
  - ○ Approximately the same ~50%
  - ○ The remaining 40%, well… I guess we are not smart enough to understand the methods section...
- ▷ Start communicating with the authors early on, most are willing to help
- ▷ Tons of unit testing and documentation
- ▷ Make your code and documentation publicly available to get the community to scrutinize your work

Same algorithm, different implementations, different results



JNCI J Natl Cancer Inst, 2015, 1–9

OXFORD

Absolute Assignment of Breast Cancer Intrinsic Molecular Subtype

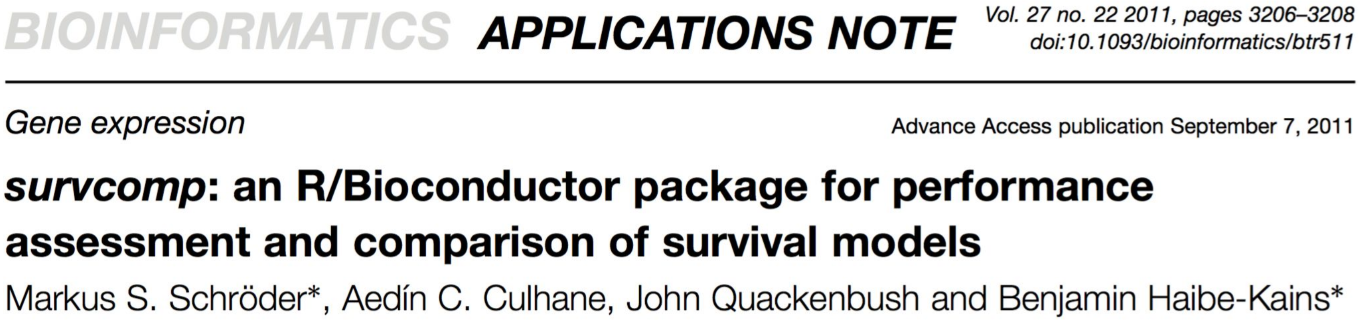
Eric R. Paquet, Michael T. Hallett

Meta-analysis and comparative studies

With functions and data in hand, hard to resist the temptation to further challenge your model:

- Is my model robust?
- Is my model's performance reproducible in multiple independent datasets?
- How does my model compare to competitors?

→ ***survcomp*** R package to compare the prognostic value of published and new gene signatures



BIOINFORMATICS **APPLICATIONS NOTE**

Vol. 27 no. 22 2011, pages 3206–3208
doi:10.1093/bioinformatics/btr511

Gene expression

Advance Access publication September 7, 2011

***survcomp*: an R/Bioconductor package for performance assessment and comparison of survival models**

Markus S. Schröder*, Aedín C. Culhane, John Quackenbush and Benjamin Haibe-Kains*

Conclusion

Prototyping, implementing, documenting, testing, sharing, fixing, testing, extending, sharing, …

This cycle is vital in my lab where code is scrutinized and tested by multiple members before public release

This helped me improve my Science and truly value the benefits of data and code sharing

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OICR

NSERC CRSNG

CIHR IRSC

The Cancer Research Society

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Thank you
for your attention!

Questions?