

Robust Probabilistic Averaging (RPA)

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1 Introduction

RPA (Robust Probabilistic Averaging)¹ provides tools for fully scalable preprocessing of arbitrarily large short oligonucleotide microarray atlases. It outperforms the standard RMA algorithm [1] on moderately sized data sets [2, 3] and in contrast to the another scalable alternative, fRMA [4], Online-RPA is applicable to all short oligonucleotide platforms. In addition, RPA can be used for probe reliability analysis, and more generally to summarize normally distributed multivariate observations that target the same object with varying degrees of reliability.

2 Usage examples

For usage examples on-line, see <https://github.com/antagomir/RPA/wiki>

3 Methodology and Citations

For details, see [2, 3]. Kindly cite these documents if you find the method useful.

4 Details

This document was written using:

```
> sessionInfo()
```

*<http://www.iki.fi/Leo.Lahti>

¹<http://bioconductor.org/packages/release/bioc/html/RPA.html>

R version 2.15.3 (2013-03-01)
Platform: x86_64-pc-linux-gnu (64-bit)

locale:
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8 LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=C LC_NAME=C
[9] LC_ADDRESS=C LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C

attached base packages:
[1] parallel stats graphics grDevices utils datasets methods
[8] base

other attached packages:
[1] RPA_1.15.35 affydata_1.11.17 affy_1.36.1 Biobase_2.18.0
[5] BiocGenerics_0.4.0

loaded via a namespace (and not attached):
[1] affyio_1.26.0 BiocInstaller_1.8.3 preprocessCore_1.20.0
[4] tools_2.15.3 zlibbioc_1.4.0

References

- [1] R. A. Irizarry, B. M. Bolstad, F. Collin, L. M. Cope, B. Hobbs, and T. P. Speed. Summaries of Affymetrix GeneChip probe level data. *Nucl. Acids Res.*, 31(4):e15, 2003.
- [2] L. Lahti, L. L. Elo, T. Aittokallio, and S. Kaski. Probabilistic analysis of probe reliability in differential gene expression studies with short oligonucleotide arrays. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1):217–225, 2011.
- [3] L. Lahti, A. Torrente, L. L. Elo, A. Brazma, J. Rung. A fully scalable online-preprocessing algorithm for short oligonucleotide microarray atlases In review. arXiv preprint available at: <http://arxiv.org/abs/1212.5932>
- [4] MN McCall and RA Irizarry. Thawing Frozen Robust Multi-array Analysis (fRMA) *BMC Bioinformatics* 12:369, 2011.