

Robust Probabilistic Averaging (RPA)

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1 Introduction

RPA (Robust Probabilistic Averaging)¹ is a fully scalable preprocessing method for arbitrarily large short oligonucleotide microarray atlases. It outperforms the standard RMA model [1] on moderately sized data sets [2, 3] and unlike the another scalable alternative, *fRMA* [4], it is applicable to all short oligonucleotide platforms. *RPA* can be additionally used for probe reliability analysis, and for general summarization of normally distributed multivariate observations that target the same object with varying degrees of noise and bias.

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:

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

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

R version 3.1.1 (2014-07-10)

Platform: x86_64-apple-darwin10.8.0 (64-bit)

locale:

[1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8

attached base packages:

[1] stats graphics grDevices utils datasets methods base

loaded via a namespace (and not attached):

[1] tools_3.1.1

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 *Nucl. Acids Res.* 2013. In press. 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.