

Internship report

# Alternative PCA algorithms analysis with missing values

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Abstract



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DE BRUXELLES

## 1 Introduction

Start with generic context – Then zoom in: why is your approach necessary and relevant within this context? – Finish with a brief description of your method and what you found out – Read background information! – Brief, 1 page (font size 11, normal margins)

- Presenting what is Single -Cell RNA seq.
- Explain why it is important to use SCR-NAseq in some case
- Explain the difficulty of the modelisation part
- Present some models?
- Description on the content of the work

## 2 Methods

- Describe the datasets you are using • Both their content and where you got them – Describe the methods you implemented to get your results • Describe separate steps required (reproducibility!) • Overview figures can help.
- 2-3 pages

## 3 Results

- Describe your results • This can be in relation to: – Different input/validation data – Different method parameterisations, ... – Explain what the results mean – Use tables for numbers (do not list in the text) – Figures for distributions, relationships, ... (easier to understand than text) – 2-3 pages

## 4 Discussion

Which issues did you identify, and which problems did you encounter? – What is different about your approach (and the results you get) in comparison to the original method? Why? – What are advantages/disadvantage of each method? – 1 page

## 5 Conclusion

## References

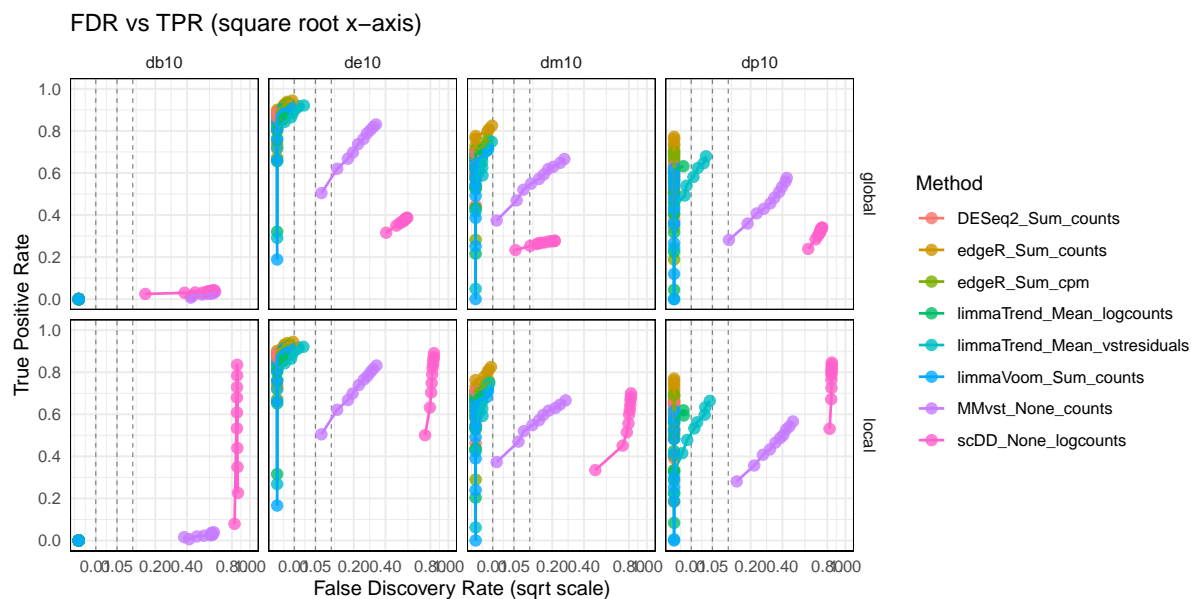


Figure 1:

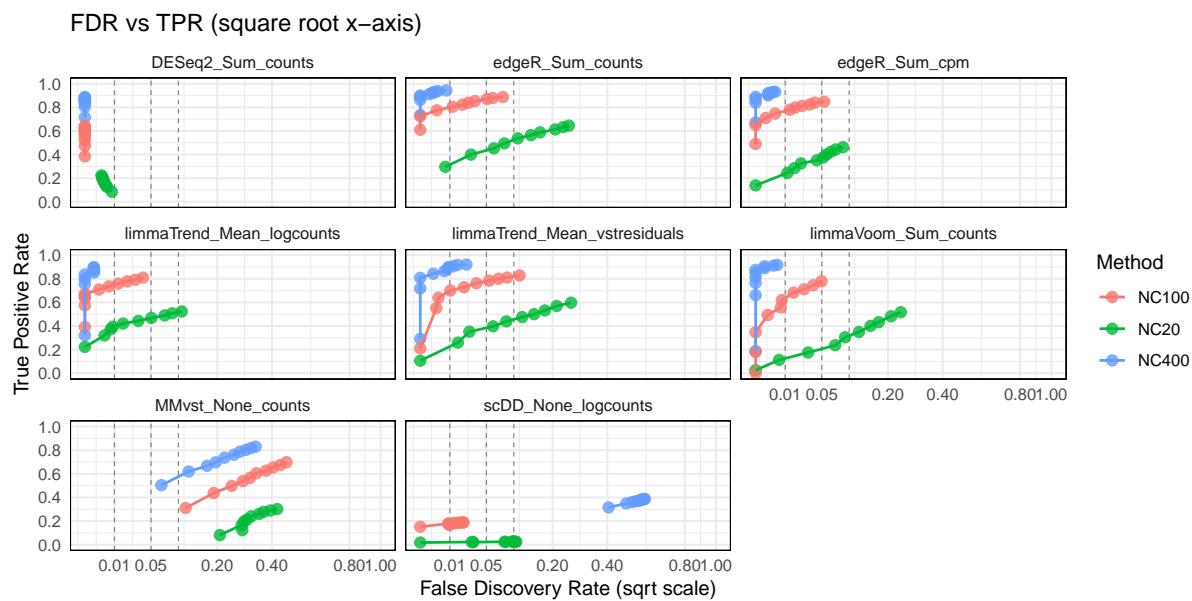


Figure 2: