

Opening Report of Crispr/Cas9-based Screening Data Analysis

Y.Q. Yang

ABSTRACT

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Background

In the first week of starting this project, I think it necessary for understanding what Crispr/Cas9-based genetic screening is, and what should be considered in analyzing the screening data. The idea of Crispr/Cas9-based genetic screening was to use a pool of sgRNA-expressing lentivirus to generate a library of knockout cells that could be screened under both positive and negative selection.¹ In addition to transfection, Pooled screening can avoid experimental errors caused by high expression of sgRNA. However, the data generated by these screens pose several challenges to computational analysis. First, variance and statistical significance of comparisons between sample and control should be calculated under a extremely small sample size. Second, different sgRNAs target the same gene might have different specificities and knockout efficiencies, which should be taken into account in the algorithm. Third,²

Results

Up to three levels of **subheading** are permitted. Subheadings should not be numbered.

Subsection

Example text under a subsection. Bulleted lists may be used where appropriate, e.g.

- First item
- Second item

Third-level section

Topical subheadings are allowed.

Discussion

The Discussion should be succinct and must not contain subheadings.

Methods

Topical subheadings are allowed. Authors must ensure that their Methods section includes adequate experimental and characterization data necessary for others in the field to reproduce their work.

References

1. Wang, T., Wei, J. J., Sabatini, D. M. & Lander, E. S. Genetic screens in human cells using the crispr-cas9 system. *Science* **343**, 80–84 (2014).
2. Li, W. *et al.* Mageck enables robust identification of essential genes from genome-scale crispr/cas9 knockout screens. *Genome biology* **15**, 554 (2014).

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For data citations of datasets uploaded to e.g. *figshare*, please use the `howpublished` option in the bib entry to specify the platform and the link, as in the `Hao:gidmaps:2014` example in the sample bibliography file.

Acknowledgements (not compulsory)

Acknowledgements should be brief, and should not include thanks to anonymous referees and editors, or effusive comments. Grant or contribution numbers may be acknowledged.

Author contributions statement

Must include all authors, identified by initials, for example: A.A. conceived the experiment(s), A.A. and B.A. conducted the experiment(s), C.A. and D.A. analysed the results. All authors reviewed the manuscript.

Additional information

To include, in this order: **Accession codes** (where applicable); **Competing interests** (mandatory statement).
The corresponding author is responsible for submitting a [competing interests statement](#) on behalf of all authors of the paper. This statement must be included in the submitted article file.



Figure 1. Legend (350 words max). Example legend text.

Condition	n	p
A	5	0.1
B	10	0.01

Table 1. Legend (350 words max). Example legend text.

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