

1                   **Github Readme File to:**  
2           Searching for best lower dimensional  
3   visualization angles for high dimensional  
4                   data

5                   Wanli Zhang<sup>1¶</sup> and Yanming Di<sup>1¶</sup>

6                   <sup>1</sup>Department of Statistics, Oregon State University,  
7                   Corvallis, Oregon, United States of America

8                   ¶ These authors contributed equally to this work.

9       The folder **Code** contains the R code used by the authors to produce the results  
10 presented in the article.

11   (1) **data generation.R**: Produces the relative expression levels from raw read  
12       counts

13   (2) **figure\_ code.R**: Generate all figures in the article

14   (3) **functions.R**: Contains all functions necessary for simulation and data analysis

15   (4) **PCA cross\_ validation.R**: Generate results for PCA cross-validation

16   (5) **plot functions.R**: Contains functions necessary for generating graphs

17   (6) **run simulations.R**: Wrapper functions for generating simulation results

18   (7) **summarize simulation results.R**: Code for integrating simulation results into  
19       single files

20       Folder **Data** contains the raw read counts as well as expression levels for genes  
21 involved in the study. See **data generation.R** for more details.

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23       Folder **Graphs** contain all figures used in this article.

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25       Folder **Output** contain the analysis output from the data generation process.

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27       Folder **Results** contain cross-validation results for 2-, 3-, and 4-dimensional feature  
28 subsets.