Various Compiled TODOs and Notes

July 28, 2017

Contents

1 Resources

1.1 Gilchrist Lab Materials

- Style guide: https://github.com/clandere/RibModelDev/blob/master/desc/ribModel_specs.pdf
- RFP Model pdf: https://github.com/clandere/RibModelDev/blob/master/desc/rfp.model.pdf
- Ensure these are the up-to-date PDFs: run "pdflatex" on the .tex files in the same repo.
- Gilchrist and Wagner paper (2006):
  - http://www.sciencedirect.com/science/article/pii/S0022519305003395
- Gilchrist, Chen, Shah, Landerer, Zaretzki paper (2015):
  - https://academic.oup.com/gbe/article-lookup/doi/10.1093/gbe/evv087
  - http://biorxiv.org/content/early/2015/04/17/009670

1.2 External Sources

- General info about Yeast gene nomenclature:
  - http://www.yeastgenome.org/help/community/nomenclature-conventions
- Weinberg Data paper link: http://biorxiv.org/content/early/2015/07/06/021501.
- Lareau Data paper link: https://elifesciences.org/content/3/e01257.
- Pop Data paper link: http://www.ncbi.nlm.nih.gov/pmc/articles/PMC4300493/.

2 Short-Term Requirements

3 Maintenance-based Requirements (do as needed)

3.1 Unit Testing

- In general, each new function added to the framework should have unit testing done on it (as most new functions are likely to be simple).
  - In particular, new functions to Utility.h, SequenceSummary.cpp, Gene.cpp, or Genome.cpp will likely belong here.

3.2 Commenting

- There should be a documentation block above each function in C++. This still needs to be done for many functions in C++. Focus especially on the arguments, the outputs, and how each function connects to each other. Note if it is exposed to RCPP, and what function "wraps" each other as they are progressively called.
- Similarly, some details need to be filled out in the R code. Ensure that the document() command is run so that "roxygen2" can properly fill out the documents.

4 Long-Term Suggestions

5 R Code

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