Integration of Random Barcode Transposon Sequencing Applications into KBase

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http://kbase.us/

Project Goals:

In order to accelerate the pace of gene annotation for the numerous novel genes found in recently sequenced organisms, there need to exist widely-available methods that allow us to probe multiple gene functions at once. RB-TnSeq (Random Barcode Transposon Sequencing), a protocol created by the Arkin Lab, allows us to do this by knocking out thousands of genes at random and testing mutant growth under dozens of conditions simultaneously[1]. Our objective is to allow others to easily use and understand RB-TnSeq by making its software available on KBase[2].

Next-generation sequencing has provided biologists with millions of gene sequences with no known function. An ongoing challenge is to find ways to test the functions of multiple genes at once. A proven method to approach this challenge is RB-TnSeq, which uses barcoded transposon insertions to get a library of organisms with different genes knocked out and barcodes to represent the abundance of those organisms. With the recent addition of the RB-TnSeq data-analysis applications to KBase, scientists have a large part of the process simplified (with included data visualizations). Additionally, having the application included in KBase means that the results can be used downstream in applications such as Cello (MIT), which together have the potential to streamline production of high-performing inducible biofuel strains.

The RB-TnSeq applications are divided into three components, each of which returns a statistical summary of the results, a visualization to interpret the results, and all the newly generated files. The statistical summary and visualization make quality assessment simple, and the other files returned to the user allow for custom analysis.

References

1. Wetmore, K.M. *et al*. Rapid quantification of mutant fitness in diverse bacteria by sequencing randomly bar-coded transposons. *MBio* **6**, e00306–e00315 (2015).
2. Arkin, A., Cottingham, R., Henry, C. *et al.* KBase: The United States Department of Energy Systems Biology Knowledgebase. *Nat Biotechnol* 36, 566–569 (2018). https://doi.org/10.1038/nbt.4163

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