

Methods

Acquiring yeast transcriptomes

A custom python script was used to extract the coding DNA sequence (CDS) for each of the 5,474 Scer protein coding genes. A BED file produced by Scannell et al. (2011) [CITE] provided coordinates for the 5,474 orthologous genes in Spar. The CDS for Spar genes was extracted with the same python script.

The script produced a FASTA file for each species, Scer and Spar, with a sequence for each CDS labelled with the gene name. These FASTA files formed the respective transcriptomes for the yeast species.

Custom python scripts were also used to ensure that the chromosome and gene names were formatted identically for both Scer and Spar for downstream analysis.

Quantifying transcript abundance

The raw RNA-seq reads (50bp in length) for Scer and Spar were mapped against their respective transcriptomes using kallisto [CITE]. The resulting output provides metrics required for differential expression analysis (gene length, abundance estimates, and transcripts per kilobase-millions).

Quantifying translation abundance (Ribosomal profiling)

The raw Ribo-seq reads (50bp in length) for Scer and Spar were mapped against their respective transcriptomes using kallisto [CITE]. The resulting output provides metrics required for differential ribosome occupancy analysis (gene length, abundance estimates, and transcripts per kilobase-millions).

Analyzing differential expression, translation, and translational efficiency

DESeq2 [CITE]

Gene ontology analysis

Gene lists were made for each category of evolution (i.e., coordinated evolution - expression/translational efficiency both up/down, compensatory evolution – expression up/down, translational efficiency down/up). These lists were run through the Gene Ontology (GO) Slim Mapper on the Saccharomyces Genome Database [CITE], using the Process GO set with both manually curated and high-throughput annotation methods.

Results