RiboGalaxy: a platform for the alignment, analysis and visualization of ribo-seq data.

http://ribogalaxy.ucc.ie

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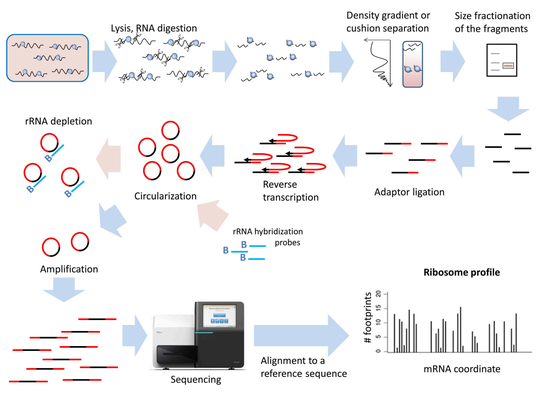
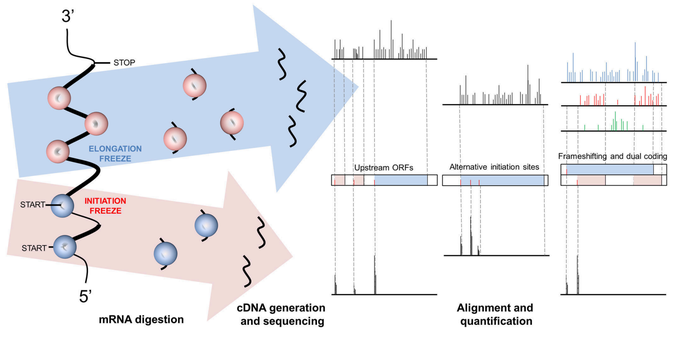
Ribosome profiling (ribo-seq) is a technique that uses high-throughput sequencing technology to reveal the exact locations and densities of translating ribosomes at the transcriptome level. However experimentalists who generate ribo-seq data often have to rely on bioinformaticians to process and analyse their data. We have developed RiboGalaxy (http://ribogalaxy.ucc.ie/), a freely available Galaxy-based web server specifically tailored for pre-processing, aligning and analysing ribo-seq data with the visualization functionality provided by GWIPS-viz (http://gwips.ucc.ie).

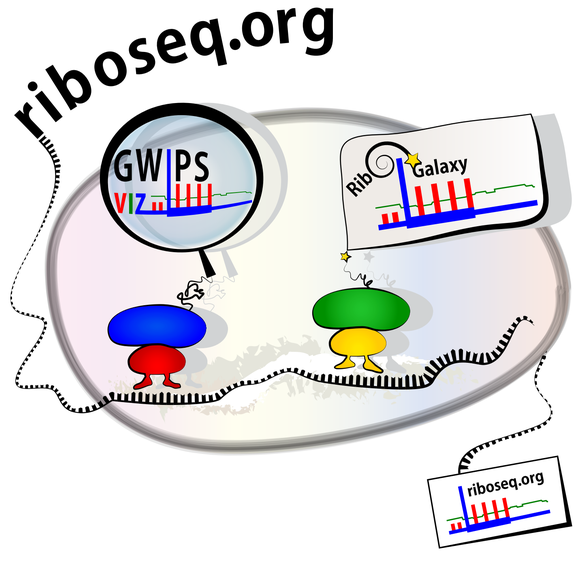
Ribosome profiling



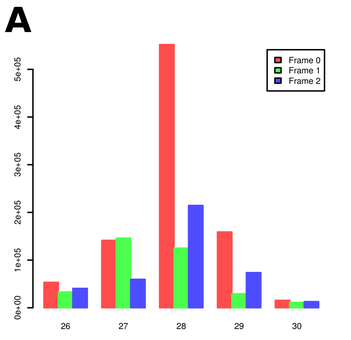
Ribosome profiling strategies



riboseq.org

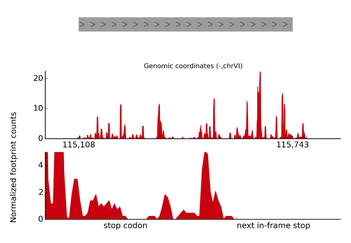


RiboSeq.org hosts tools for the alignment and analysis (RiboGalaxy) and visualization (GWIPS-viz) of ribo-seq and corresponding mRNA-seq data. You only have to remember this url to access these tools.



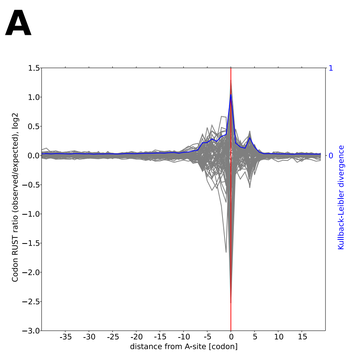
The riboSeqR suite

A. A triplet periodicity plot showing the sub-codon positions of ribo-seq alignments of read lengths 26-30nt to the protein coding regions (CDS) of the Zebrafish transcriptome. **B.** A metagene profile of ribo-seq alignments to the annotated start and stop codons in Zebrafish. **C.** A sub-codon ribosome profile showing the ribo-seq alignments to the CDS open reading frame (blue) for the Zebrafish *krt5* gene. The background grey alignments represent mRNA-seq data for the corresponding transcript. The plots were generated using the riboSeqR suite (Hardcastle TJ 2014) on RiboGalaxy using ribo-seq data from the Bazzini AA, *et al*., (2014) study.



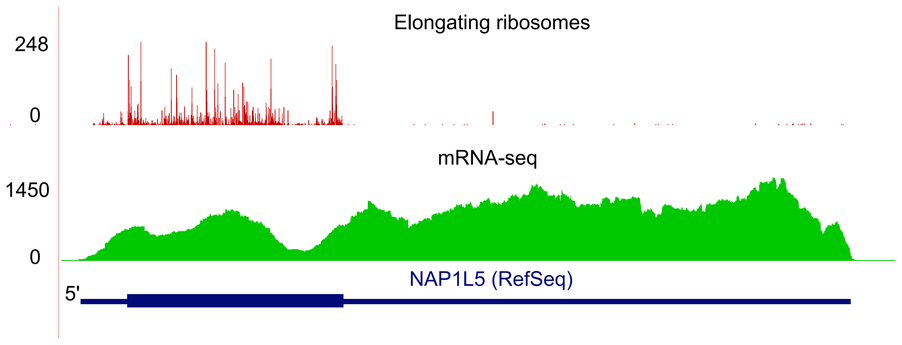
The RiboTools suite

A. A ribo-seq profile for the yeast *WWM1* gene (YFL010C) showing the alignment of ribosome footprints downstream of the annotated stop codon **B.** A sub-codon ribosome profile for the yeast *ABP140* gene (YOR239W). The bottom panel shows the open reading frame (ORF) architecture for this gene's mRNA sequene. The transition in footprint alignments from sub-codon positon 1 (blue) to sub-codon postion 2 (red) corresponds to the location of the known programmed ribosomal frameshift. **C.** Comparison of the ribosome occupancy across amino acids for two yeast ribo-seq datasets. The plots were generated using the RiboTools suite (Legendre R, *et al*., 2015) on RiboGalaxy using ribo-seq data from the Baudin-Baillieu A, *et al*., (2014) study.



The RUST suite

A. A RUST metafootprint profile that reveals the influence of mRNA codons on the relative read density across the entire ribosome and nascent peptide region. The Kullback-Leibler divergence across these sites is also provided. **B.** The RUST ratio for the predicted A-site for individual codons grouped by amino acid. **C.** With just a few parameters, RUST can recapitulate the ribosome density profile as shown here for the observed and and expected profiles for the human NM_001030 transcript. The profiles show 120 nucleotides after the start codon and 60 nucleotides before the stop codon. The plots were generated using the RUST suite (O'Connor PBF, *et al*., 2015) on RiboGalaxy using data from the Andreev DE, *et al*., (2015) study.



The GWIPS-viz Mapping suite

Visualization of ribo-seq (red) and mRNA-seq (green) data for the human *NAP1L5* gene in GWIPS-viz (Michel AM, *et al*. 2014). With the GWIPS-viz mapping suite of tools in RiboGalaxy, users can explore their own ribo-seq data alignment results as a custom track in GWIPS-viz (http://gwips.ucc.ie). This allows the researcher to compare their own ribo-seq data with the published ribo-seq tracks in GWIPS-viz. The custom track is visible only to the researcher and not to other public users of GWIPS-viz. All of the alignments, ribosome coverage and profile information can be downloaded from RiboGalaxy while snapshot images of the ribosome profiles can be generated in GWIPS-viz.

All of the resources on RiboSeq.Org are supported by

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If you have any queries regarding the resources on RiboSeq.Org please go to our Forum http://gwips.ucc.ie/Forum/