Martin Bens, Transcriptomics, 2:2
http://dx.doi.org/10.4172/2329-8936.S1.003

OMICS International
conferenceseries.com

International Conference on
Transcriptomics

July 27-29, 2015 Orlando, USA

FRAMA: From RNA-seq data to annotated mRNA assemblies

Martin Bens
Leibniz Institute for Age Research, Germany

In recent years, the introduction of second-generation sequencing of RNA (RNA-seq) has allowed the near-complete characterization of transcriptomes to become affordable. However, the short read length of RNA-seq data constitutes a problem for optimal representation of full-length mRNAs. Assembly programs designed to reconstruct mRNAs have difficulties due to the complexity of eukaryotic transcriptomes that comprise multiple alternative splice variants and highly similar paralogs for many genes. Here, we present FRAMA (from RNA-seq to annotated mRNA assemblies), a genome-independent annotation pipeline for de novo mRNA assemblies, which accomplishes several post-assembly tasks, such as assignment of orthologs, identification and correction of misassembled transcripts, scaffolding of fragmented transcripts and coding sequence identification based on a phylogenetically related well-annotated reference transcriptome. We applied FRAMA to the transcriptome of the naked mole-rat (Heterocephalus glaber), a promising long-lived model in ageing research. We demonstrate FRAMA's competitiveness with pre-existing genome-dependent transcript annotation approaches by comparing 21,943 naked mole-rat transcripts assembled by FRAMA to publicly available transcript sets. Our results indicate that FRAMA's compilation of representative transcripts provides an improved basis for multiple downstream analyses, including gene expression studies and comparative sequence analyses.

Biography

Martin Bens graduated from the Friedrich-Schiller-University, Jena, Germany in bioinformatics and is currently a PhD student under the guidance of Matthias Platzer, Leibniz Institute for Age Research - Fritz Lipmann Institute, Jena, Germany.

mbens@fli-leibniz.de