Universität Münster

DE NOVO DISCOVERIES:
INNOVATIVE TOOLS FOR DE NOVO GENE RESEARCH

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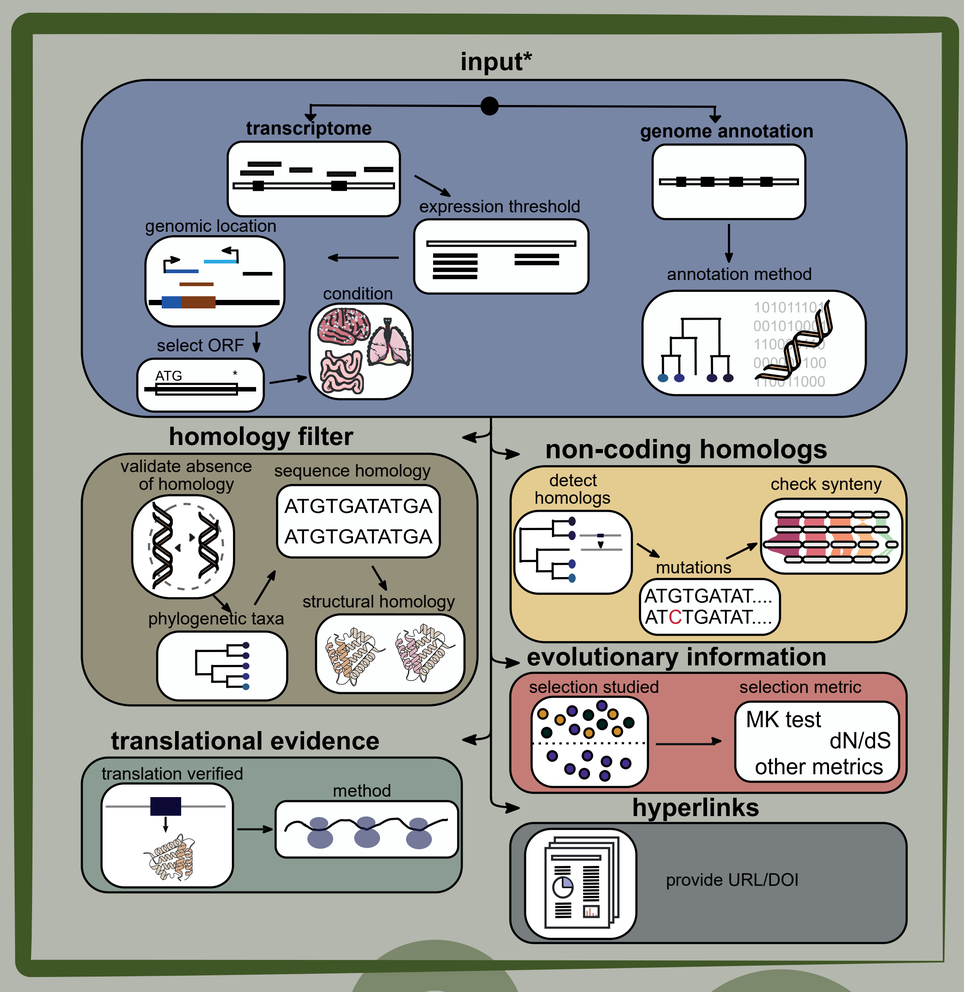
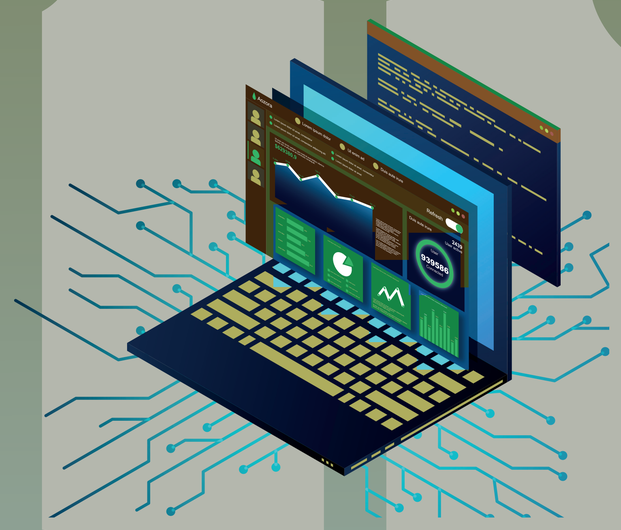
DENOFO

De novo genes are a young and fast-moving area of research with a high degree of variation in methods and terminology. We developed a standardised annotation format to make de novo studies reproducible and comparable to accelerate advancements in this field.



DeNoFo is a toolkit that provides easy access to this de novo gene annotation format. Any researcher can use the tools without prior knowledge to annotate their de novo gene discovery methodology and save it in a separate file or annotate fasta and gff files with it. Additional tools allow easy comparison between studies and conversion of file types.

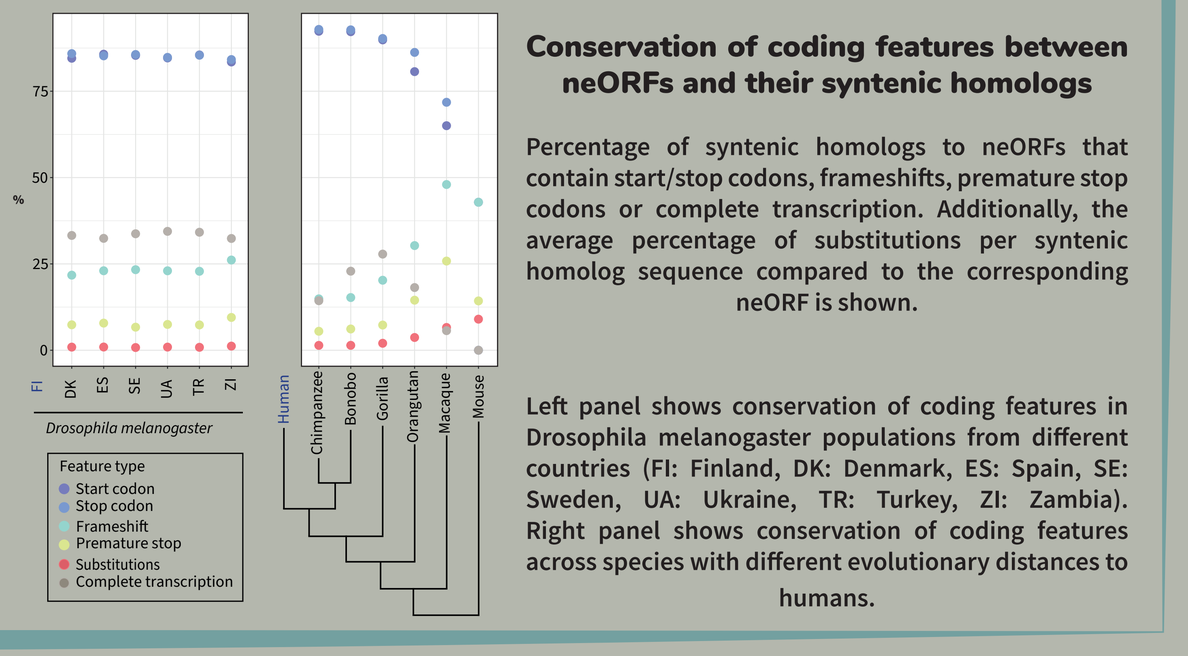


GitHub

DESwoMAN

DESwoMAN is a tool that automates the detection of precursors of de novo genes - newly expressed Open Reading Frames (neORFs) - based on transcriptome data. With this tool it is possible to study mutations of neORFs within populations and/or across species.

GitHub



Conservation of coding features between neORFs and their syntenic homologs

Percentage of syntenic homologs to neORFs that contain start/stop codons, frameshifts, premature stop codons or complete transcription. Additionally, the average percentage of substitutions per syntenic homolog sequence compared to the corresponding neORF is shown.

Left panel shows conservation of coding features in Drosophila melanogaster populations from different countries (FI: Finland, DK: Denmark, ES: Spain, SE: Sweden, UA: Ukraine, TR: Turkey, ZI: Zambia). Right panel shows conservation of coding features across species with different evolutionary distances to humans.

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