

Workflow Designer

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 - LinkData Fetch
 - Quality Filter
 - Data Marking
 - Marking by Annotation Number
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 - Merge Sequences and Shift Corresponding Annotations
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 - Build HMM from Alignment and test it
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- ChIP-Seq Coverage
- ChIP-seq Analysis with Cistrome Tools
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- Extract Coverage from Assembly
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- Quality Control by FastQC
- De novo Assemble Illumina PE Reads
- De novo Assemble Illumina PE and Nanopore Reads
- De novo Assemble Illumina SE Reads
- De Novo Assembly and Contigs Classification
- Parallel NGS Reads Classification
- Serial NGS Reads Classification
- RNA-Seq Analysis with TopHat and StringTie
- RNA-seq Analysis with Tuxedo Tools
- Variation Annotation with SnpEff
- Call Variants with SAMtools
- Variant Calling and Effect Prediction
- Raw ChIP-Seq Data Processing
- Raw DNA-Seq Data Processing
- Raw RNA-Seq Data Processing
- Get Unmapped Reads
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 - Trim and Align Sanger Reads
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 - Search for Inverted Repeats
 - Find Patterns
 - Gene-by-gene Approach for Characterization of Genomes
 - Group Primer Pairs
 - Intersect Annotations
 - Filter out Short Sequences
 - Merge Sequences and Annotations
 - In Silico PCR Sample
 - Remote BLASTing
 - Get Amino Translations of a Sequence
- Transcriptomics
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