

Workflow Designer

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 - Map Reads with Bowtie Element
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- NGS: Metagenomics Classification
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 - CASAVA FASTQ Filter
 - FASTQ Trimmer
 - Dump Sequence Info
 - LinkData Fetch
 - Quality Filter
 - Data Marking
 - Marking by Annotation Number
 - Marking by Length
 - Data Merging
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 - Merge Sequences and Shift Corresponding Annotations
 - Search for TFBS
 - HMMER
 - Build HMM from Alignment and test it
 - Search Sequences with Profile HMM
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- ChIP-Seq Coverage
- ChIP-seq Analysis with Cistrome Tools
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- Extract Coverage from Assembly
- Extract Transcript Sequences
- 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
- Sanger Sequencing
 - Trim and Align Sanger Reads
- Scenarios
 - Filter Sequence That Match a Pattern
 - 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
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