

# Workflow Designer Manual

- About the Workflow Designer
- Introduction
  - Launching Workflow Designer
  - Workflow Designer Window Components
  - Workflow Elements and Connections
  - Managing Parameters
  - UGENE Components and Workflow Designer
    - Task View, Notifications and Log View
    - Actions Menu
    - Toolbar
    - Context Menus
    - Application Settings
  - How to Create and Run Workflow
  - How to Use Sample Workflows
- Manipulating Element
  - Adding Element
  - Copying Element
  - Pasting Element
  - Cutting Element
  - Deleting Element
  - Selecting All Elements on Scene
- Manipulating Workflow
  - Creating New Workflow
  - Loading Workflow
  - Saving Workflow
  - Exporting Workflow as Image
  - Validating Workflow
  - Running Workflow
  - Dashboard
    - Dashboard Window Components
    - Using Dashboard
  - Stopping and Pausing Workflow
- Changing Appearance
- Custom Elements with Scripts
  - Functions Supported for Multiple Alignment Data
  - Functions Supported for Sequence Data
  - Functions Supported for Set of Annotations Data
  - Functions Supported for Files
  - Common Function
- Custom Elements with Command Line Tools
  - Creating Element
  - Editing Element
  - Adding Existent Element
  - Removing Element
- Using Script to Set Parameter Value
- Running Workflow from the Command Line
- Running Workflow in Debugging Mode
  - Creating Breakpoints
  - Manipulating Breakpoints
- Workflow File Format
  - Header
  - Body
    - Elements
    - Dataflow
    - Metainformation
- Workflow Elements
  - Data Readers
    - Read Alignment Element
    - Read Annotations Element
    - Read FASTQ File with SE Reads Element
    - Read FASTQ Files with PE Reads Element
    - Read File URL(s) Element
    - Read NGS Reads Assembly Element
    - Read Plain Text Element
    - Read Sequence Element
    - Read Sequence from Remote Database Element
    - Read Variants Element
  - Data Writers
    - Write Alignment Element
    - Write Annotations Element
    - Write FASTA Element
    - Write NGS Reads Assembly Element
    - Write Plain Text Element
    - Write Sequence Element
    - Write Variants Element
  - Data Flow
    - Filter Element
    - Grouper Element

- Multiplexer Element
- Sequence Marker Element
- Basic Analysis
  - Amino Translations Element
  - Annotate with UQL Element
  - CD-Search Element
  - Collocation Search Element
  - Export PHRED Qualities Element
  - Fetch Sequences by ID From Annotation Element
  - Filter Annotation by Name Element
  - Filter Annotations by Qualifier
  - Find Correct Primer Pairs Element
  - Find Pattern Element
  - Find Repeats Element
  - Gene-by-gene approach report
  - Get Sequences by Annotations Element
  - Group Primer Pairs Element
  - Import PHRED Qualities Element
  - Intersect Annotations Element
  - Local BLAST Search Element
  - Local BLAST+ Search Element
  - Merge Annotations Element
  - ORF Marker Element
  - Remote BLAST Element
  - Sequence Quality Trimmer Element
  - Smith-Waterman Search Element
- Data Converters
  - Convert bedGraph Files to bigWig Element
  - Convert Text to Sequence Element
  - File Format Conversion Element
  - Reverse Complement Element
  - Split Assembly into Sequences Element
- DNA Assembly
  - Assembly Sequences with CAP3
- HMMER2 Tools
  - HMM2 Build Element
  - HMM2 Search Element
  - Read HMM2 Profile Element
  - Write HMM2 Profile Element
- HMMER3 Tools
  - HMM3 Build Element
  - HMM3 Search Element
  - Read HMM3 Profile
  - Write HMM3 Profile
- Multiple Sequence Alignment
  - Align Profile to Profile with MUSCLE Element
  - Align with ClustalO Element
  - Align with ClustalW Element
  - Align with Kalign Element
  - Align with MAFFT Element
  - Align with MUSCLE Element
  - Align with T-Coffee Element
  - Extract Consensus from Alignment as Sequence
  - Extract Consensus from Alignment as Text
  - In Silico PCR Element
  - Join Sequences into Alignment Element
  - Map to Reference Element
  - Split Alignment into Sequences Element
- NGS: Basic Functions
  - CASAVA FASTQ Filter Element
  - Cut Adapter Element
  - Extract Consensus from Assembly Element
  - Extract Coverage from Assembly Element
  - FASTQ Merger Element
  - FASTQ Quality Trimmer Element
  - FastQC Quality Control Element
  - Filter BAM/SAM Files Element
  - Genome Coverage Element
  - Improve Reads with Trimmomatic Element
  - Merge BAM Files Element
  - Remove Duplicates in BAM Files Element
  - Slopbed Element
  - Sort BAM Files Element
- NGS: ChIP-Seq Analysis
  - Annotate Peaks with peak2gene Element
  - Build Conservation Plot Element
  - Collect Motifs with SeqPos Element
  - Conduct GO Element
  - Create CEAS Report Element

- Find Peaks with MACS Element
- NGS: Map/Assemble Reads
  - Assemble Reads with SPAdes Element
  - Map Reads with Bowtie Element
  - Map Reads with Bowtie2 Element
  - Map Reads with BWA Element
  - Map Reads with BWA-MEM Element
  - Map Reads with UGENE Genome Aligner Element
  - Map RNA-Seq Reads with TopHat Element
- NGS: Metagenomics Classification
  - Build CLARK Database
  - Build DIAMOND Database
  - Build Kraken Database
  - Classification Report Element
  - Classify Sequences with CLARK
  - Classify Sequences with DIAMOND
  - Classify Sequences with Kraken
  - Classify Sequences with MetaPhlan2
  - Ensemble Classification Data
  - Filter by Classification
  - Improve Classification with WEVOTE
- NGS: RNA-Seq Analysis
  - Assemble Transcripts with StringTie Element
  - Assembly Transcripts with Cufflinks Element
  - Extract Transcript Sequences with gffread Element
  - Merge Assemblies with Cuffmerge Element
  - StringTie Gene Abundance Report Element
  - Test for Diff. Expression with Cuffdiff Element
- NGS: Variant Analysis
  - Call Variants with SAMtools Element
  - Change Chromosome Notation for VCF Element
  - Convert SnpEff Variations to Annotations Element
  - Create VCF Consensus Element
  - SnpEff Annotation and Filtration Element
- Transcription Factor
  - Build Frequency Matrix Element
  - Build SITECON Model Element
  - Build Weight Matrix Element
  - Convert Frequency Matrix Element
  - Read Frequency Matrix Element
  - Read SITECON Model Element
  - Read Weight Matrix Element
  - Search for TFBS with SITECON Element
  - Search for TFBS with Weight Matrix Element
  - Write Frequency Matrix Element
  - Write SITECON Model Element
  - Write Weight Matrix Element
- Utils
  - DNA Statistics Element
  - Generate DNA Element
- Workflow Samples
  - Alignment
    - Align Sequences with MUSCLE
    - Extract Consensus as Sequence
    - Extract Consensus as Text
  - Conversions
    - Convert "seq/qual" Pair to FASTQ
    - Convert Alignments to ClustalW
    - Convert UQL Schema Results to Alignment
    - Convert Sequence to Genbank
  - Custom Elements
    - CASAVA FASTQ Filter
    - FASTQ Trimmer
    - Dump Sequence Info
    - LinkData Fetch
    - Quality Filter
  - Data Marking
    - Marking by Annotation Number
    - Marking by Length
  - Data Merging
    - Find Substrings in Sequences
    - Merge Sequences and Shift Corresponding Annotations
    - Search for TFBS
  - HMMER
    - Build HMM from Alignment and test it
    - Search Sequences with Profile HMM
  - NGS
    - ChIP-Seq Coverage
    - ChIP-seq Analysis with Cistrome Tools

- Extract Consensus from Assembly
- 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 Unmappet 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
  - Remote BLASTing
  - Get Amino Translations of a Sequence
- Transcriptomics
  - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences