

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
 - File List Element
 - Read Alignment Element
 - Read Annotations Element
 - Read Assembly Element
 - Read from DAS Element
 - Read from Remote Database Element
 - Read Plain Text Element
 - Read Sequence Element
 - Read Variations Element
 - Data Writers
 - Write Alignment Element
 - Write Annotations Element
 - Write Assembly Element
 - Write FASTA Element
 - Write Plain Text Element
 - Write Sequence Element
 - Write Variations Element
 - Data Flow
 - Filter Element
 - Grouper Element
 - Multiplexer Element

- Sequence Marker Element
- Basic Analysis
 - Amino Translations Element
 - Annotate with DAS 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
 - Local BLAST Search Element
 - Local BLAST+ Search Element
 - Merge Annotations Element
 - ORF Marker Element
 - Remote BLAST 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
 - HMM Build Element
 - HMM Search Element
 - Read HMM Profile Element
 - Write HMM Profile Element
- HMMER3 Tools
 - HMM3 Build Element
 - HMM3 Search Element
 - Read HMM3 Profile
 - Write HMM3 Profile
- Includes
 - Script-Get the First Half of Sequence Element
 - Script-Get the Second Half of Sequence Element
- Multiple Sequence Alignment
 - Align Profile to Profile with MUSCLE Element
 - Align to Reference 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
 - Join Sequences into Alignment Element
 - Split Alignment into Sequences Element
- NGS: Align Short Reads
 - Align Reads with Bowtie Element
 - Align Reads with Bowtie2 Element
 - Align Reads with BWA Element
 - Align Reads with BWA-MEM Element
 - Align Reads with UGENE Genime Aligner Element
- NGS Basic
 - Assemble Genomes with SPAdes Element
 - 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
 - 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: RNA-Seq Analysis
 - Assembly Transcripts with Cufflinks Element
 - Extract Transcript Sequences with gffread Element
 - Find Splice Junction with TopHat Element
 - Merge Assemblies with Cuffmerge Element
 - Test for Diff. Expression with Cuffdiff Element
- NGS: Variant Calling
 - Call Variants with SAMtools Element
 - Create VCF consensus
 - SnpEff Annotation and Filtration Element
- SNP Annotation
 - Annotate variations with SNPToolbox Element
 - Detect Transcription Factors with rSNP-Tools Element
 - Determine SNP effect on TATA-boxes Element
 - ProtStability1D Element
 - ProtStability3D Element
 - SNP Chip Tools Element
 - SNP Effect on PDB sites Element
 - Write SNP Report 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
- Custom Elements With Script
 - CASAVA FASTQ Filter Script Element
 - Dump Sequence Info Element
 - FASTQ Trimmer Element
 - Get the First Half of Sequence Element
 - Get the Second Half of Sequence Element
 - LinkData Fetch Element
 - Quality Filter Element
 - Read One Sequence 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 Sequences by Annotation Number
 - Marking Sequences by Length
 - Data Merging
 - Find Substrings at Sequences
 - Merge Sequences and Shift Corresponding Annotations
 - Search for TFBS
 - HMMER
 - Build HMM from Alignment and Test It
 - Search Sequences with Profile HMM
 - NGS
 - Assembly with Spades

- Call Variants with SAMtools
- ChIP-Seq Coverage
- ChIP-seq Analysis with Cistrome Tools
- Extract Consensus from Assembly
- Extract Coverage from Assembly
- Extract Transcript Sequences
- Quality Control by FastQC
- Raw ChIP-Seq Processing
- Raw DNA-Seq Processing
- Raw RNA-Seq Processing
- RNA-seq Analysis with Tuxedo Tools
- Variation Annotation with SnpEff
- 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
 - Merge Sequences and Annotations
 - Remote BLASTing
 - Get Amino Translations of a Sequence
- Transcriptomics
 - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences