

Workflow Elements

This section contains detailed description of all workflow elements presented in the Workflow Designer.

For each element you can find:

- Description of the parameters used in the GUI
- Corresponding parameters names used in a workflow file
- Information about input and output ports

The type of a parameter can be one of the following:

string

A string.

numeric

A number.

boolean

A boolean data type. Available values are: true / false, 0 / 1 and yes / no.

A port's slot type can be one of the following:

sequence

Biological sequence

msa

Multiple sequence alignment

text

A text

annotation-table

Table of annotations

annotation-table-list

A list of different tables of annotations

ebwt-index

Bowtie index

hmm2-profile

A HMM profile of HMMER2 package

fmatrix

Frequency matrix

wmatrix

Weight matrix

sitecon-model

SITECON model

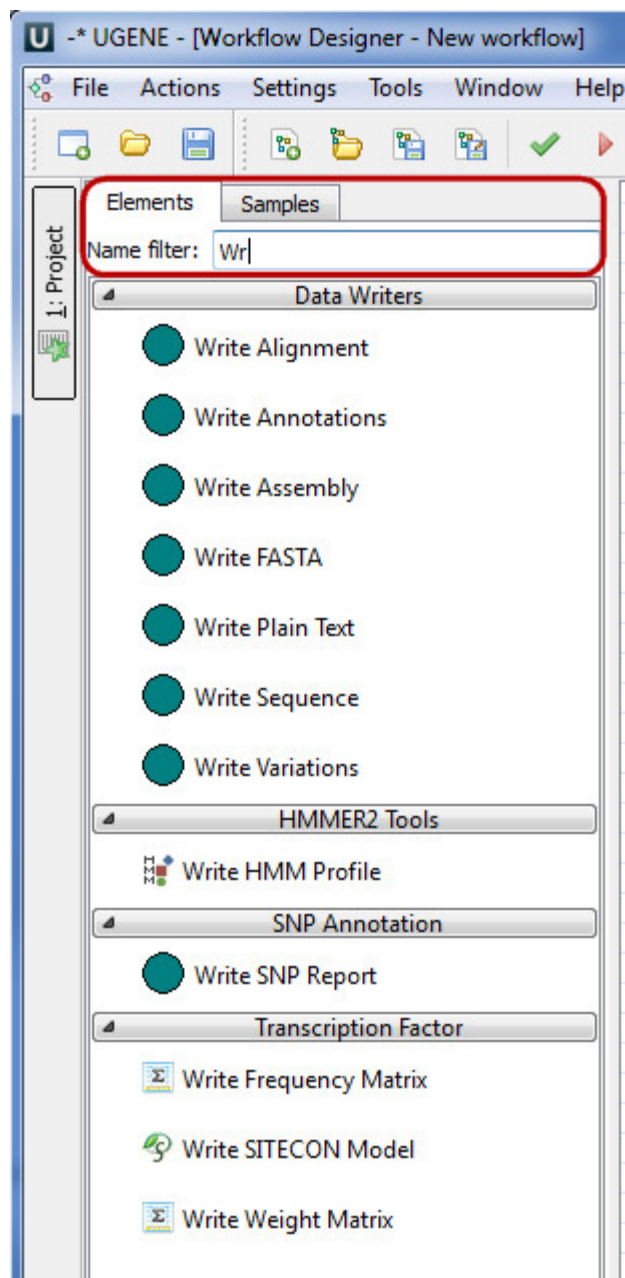
assembly

Assembly

variation

Variation track

To search an element use the name filter or press the *Ctrl+F* shortcut that moves you to the name filter also:



- 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 Acid Translation 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
 - 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: Mapping 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 Element
 - Build Kraken Database Element
 - Classification Report Element
 - Classify Sequences with CLARK Element
 - Classify Sequences with DIAMOND Element
 - Classify Sequences with Kraken Element
 - Classify Sequences with MetaPhlAn2 Element
 - Ensemble Classification Data Element
 - Filter by Classification Element
 - Improve Classification with WEVOTE Element
- 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