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

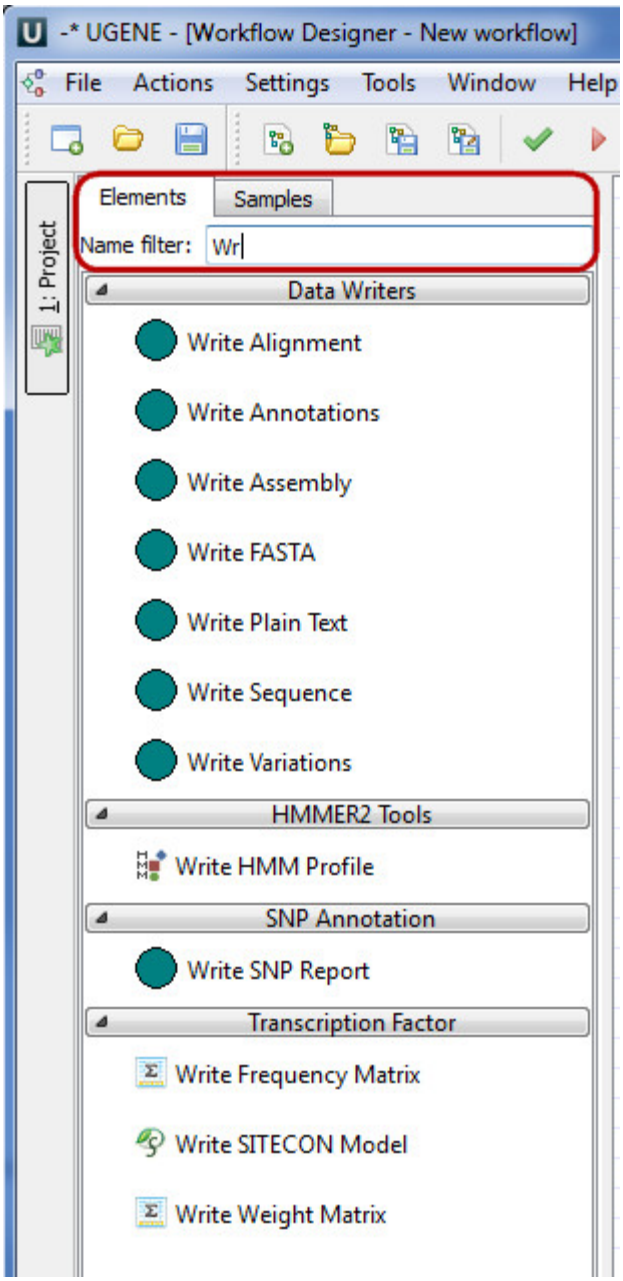
assembly

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: 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 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 Abudance 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