

# 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

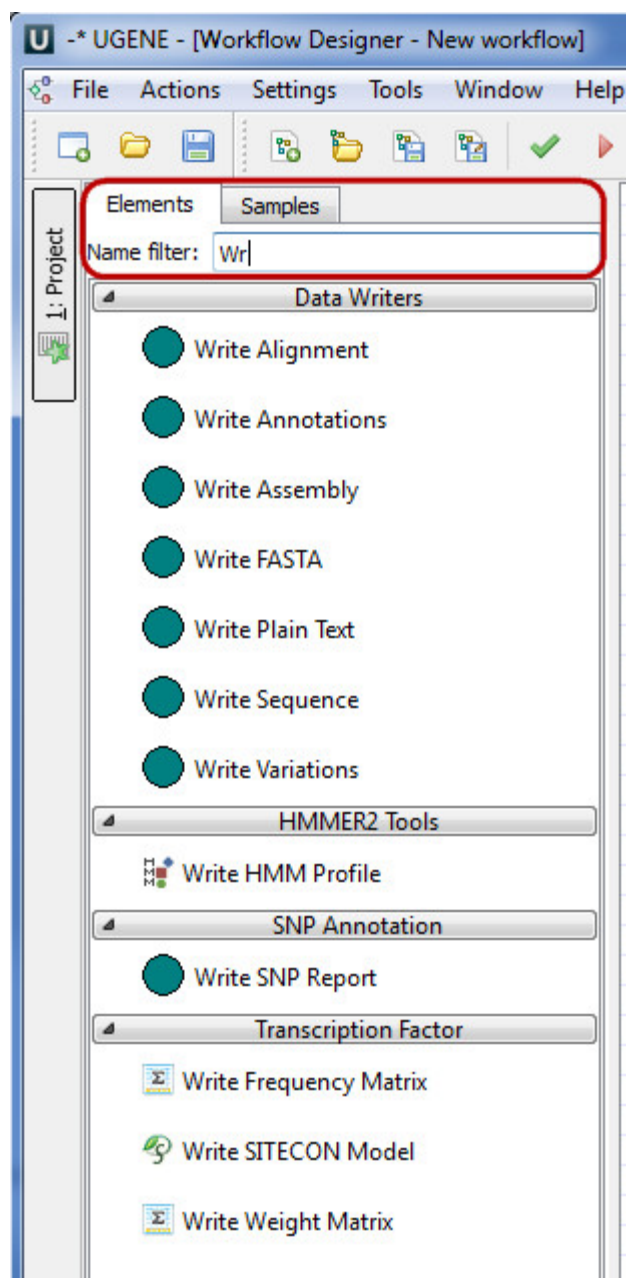
## **assembly**

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 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