

# 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

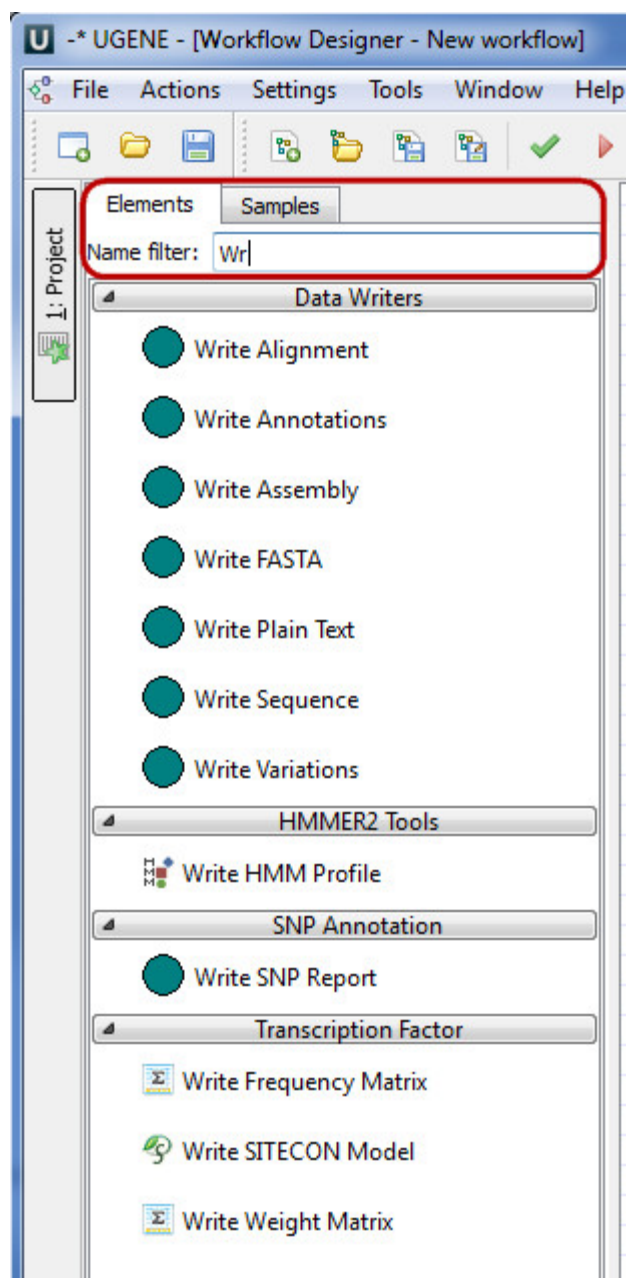
## **assembly**

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
  - 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
  - Intersect Annotations 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
- In Silico PCR Element
- 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 Analysis
  - Call Variants with SAMtools Element
  - Change Chromosome Notation for VCF 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