Workflow Designer

- 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
  - 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
- 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 by Annotation Number
        - Marking by Length
    - Data Merging
        - Find Substrings in Sequences
        - Merge Sequences and Shift Corresponding Annotations
        - Search for TFBS
    - HMMER
        - Build HMM from Alignment and test it
        - Search Sequences with Profile HMM
    - NGS

- ChIP-Seq Coverage
- ChIP-seq Analysis with Cistrome Tools
- Extract Consensus from Assembly
- Extract Coverage from Assembly
- Extract Transcript Sequences
- Quality Control by FastQC
- De novo Assemble Illumina PE Reads
- De novo Assemble Illumina PE and Nanopore Reads
- De novo Assemble Illumina SE Reads
- De Novo Assembly and Contigs Classification
- Parallel NGS Reads Classification
- Serial NGS Reads Classification
- RNA-Seq Analysis with TopHat and StringTie
- RNA-seq Analysis with Tuxedo Tools
- Variation Annotation with SnpEff
- Call Variants with SAMtools
- Variant Calling and Effect Prediction
- Raw ChIP-Seq Data Processing
- Raw DNA-Seq Data Processing
- Raw RNA-Seq Data Processing
- Get Unmappet Reads

- 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
  - Intersect Annotations
  - Filter out Short Sequences
  - Merge Sequences and Annotations
  - In Silico PCR Sample
  - Remote BLASTing
  - Get Amino Translations of a Sequence
- Transcriptomics
  - Search for Transcription Factor Binding Sites (TFBS) in Genomic Sequences