Bioinformatics at geneXplain GmbH

Introducing IMC

geneXplain GmbH

Products

▸ Bioinformatics and systems biology: geneXplain platform

▸ Bioinformatics and NGS: IMC and GenomeTraveler

▸ Cheminformatics: PASS, PharmaExpert, GUSAR

Cheminformatics and Systems Biology

▸ geneXplain platform

  ◦ Collection, storage and analysis of experimental data

  ◦ Network clustering and search for master regulators

  ◦ Graphical programming of workflows

  ◦ Possibility to write new scripts and add-ons

▸ PASS and PharmaExpert

  ◦ Qualitative biological activity prediction for libraries of chemical compounds

  ◦ Drug-drug interactions and identification of most promising candidates

▸ GUSAR

  ◦ Quantitative biological activity prediction for libraries of chemical compounds

  ◦ (Q)SAR model building

geneXplain GmbH

Products

▸ Bioinformatics and systems biology: geneXplain platform

▸ **Bioinformatics and NGS: IMC** and GenomeTraveler

▸ Cheminformatics: PASS, PharmaExpert, GUSAR

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- Why you should try IMC

in silico
Molecular Biology

» Major functions of IMC

General Information

IMC comes in three different editions and features three major *in silico* experiment areas:

▸ Cloning (Standard, Genomics and Array Edition)

▸ Genome analysis (Genomics and Array Edition)

▸ Array analysis (Array Edition)

The software accepts a range of sequence files:

▸ GenBank, EMBL, GPFF formats

▸ FastA format

▸ Amino acid files

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Cloning

The "Cloning" menu lists a number of possible actions for *in silico* molecular cloning experiments. Included are all necessary functions for:

- PCR (including gel electrophoresis of results)

- Ligation and sequence editing

- Restriction enzymes and digestion (example below)

Genome Analysis

The "Genome Analysis" menu is filled with functions from statistics to visualization to working with sequences:

- ◦ Translation
- ◦ Annotation
- ◦ EST and trace mapping
- ◦ Homology searches
- ◦ Dot plot, Venn diagram (examples below), KEGG pathways

Genome Analysis | Array Analysis | Help

- Show Codon Usage...
- Statistics...
- Reverse Complement...
- ORF Extraction...
- Translation
- EST Mapping...
- Trace Mapping...
- A.A. Sequence Mapping...
- EST Mapping by DB...
- Homology Search by input sequence
- Homology Search by all Feature
- Homology Search by all Sequence
- Operon Extraction...
- Repeat Search...
- Search Unique Regions...
- Dot Plot...
- Genome Rearrangement Map...
- Venn Diagram...
- Multiple Alignment by selected sequence
- KEGG PATHWAY...
- Feature Fusion...
- Auto Annotation...
- Local Genome Rearrangement Map
- List EC-Number between Genomes...
- 16S rRNA Metagenome Analysis...

Genome Analysis

A special feature of the genome analysis functionality is the genome rearrangement map. With it, you can compare the positions of loci in different genomes as seen in the example below.

Genome Analysis menu:

- Show Codon Usage...
- Statistics...
- Reverse Complement...
- ORF Extraction...
- Translation
- EST Mapping...
- Trace Mapping...
- A.A. Sequence Mapping...
- EST Mapping by DB...
- Homology Search by input sequence
- Homology Search by all Feature
- Homology Search by all Sequence
- Operon Extraction...
- Repeat Search...
- Search Unique Regions...
- Dot Plot...
- Genome Rearrangement Map... ←
- Venn Diagram...
- Multiple Alignment by selected sequence
- KEGG PATHWAY...
- Feature Fusion...
- Auto Annotation...
- Local Genome Rearrangement Map
- List EC-Number between Genomes...
- 16S rRNA Metagenome Analysis...

Array Analysis

The "Array Analysis" menu contains all functions necessary for the creation and analysis of array data:

- ◦ Probe design (example below)
- ◦ Import of probe and array data
- ◦ Statistics and peak detection
- ◦ Two expression graphs and clustering

Summary

in silico molecular cloning options include PCR, restriction and ligation of sequences.

Genome analysis features translation, annotation, homology searches and more.

IMC offers a range of functions for *in silico* molecular biology.

Array analysis offers probe design, data import, peak detection and more.

IMC comes in three different editions: standard, genomics and array.

Search and Customization
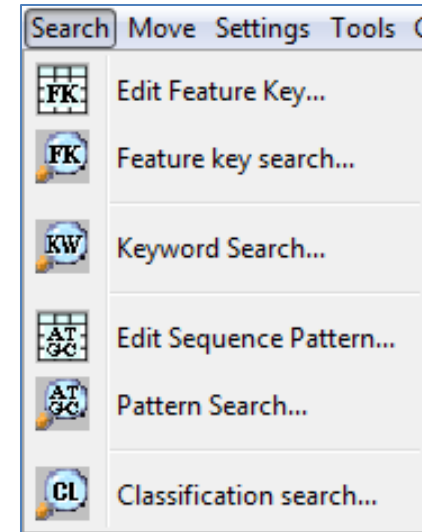
>> Additional features of all IMC editions

General Information

In addition to the previously introduced major functions, IMC also stands out from the crowd for its:

▸ search,

▸ customizability and

▸ visualization options.
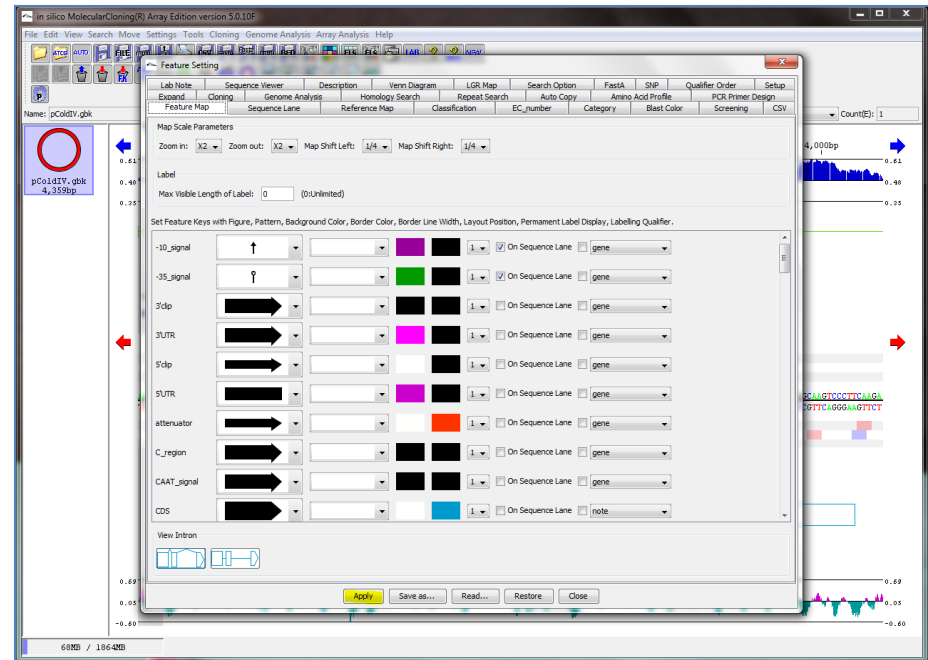
Search Functions

The "Search" menu offers the possibility to search for keywords, patterns (short sequences, see example below) and classifications.
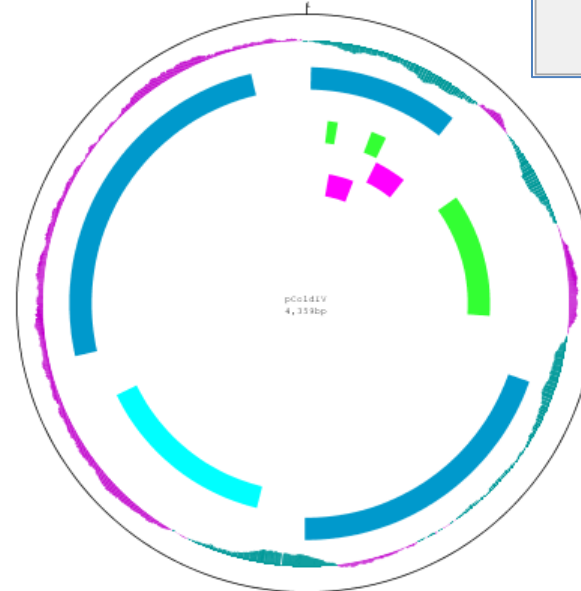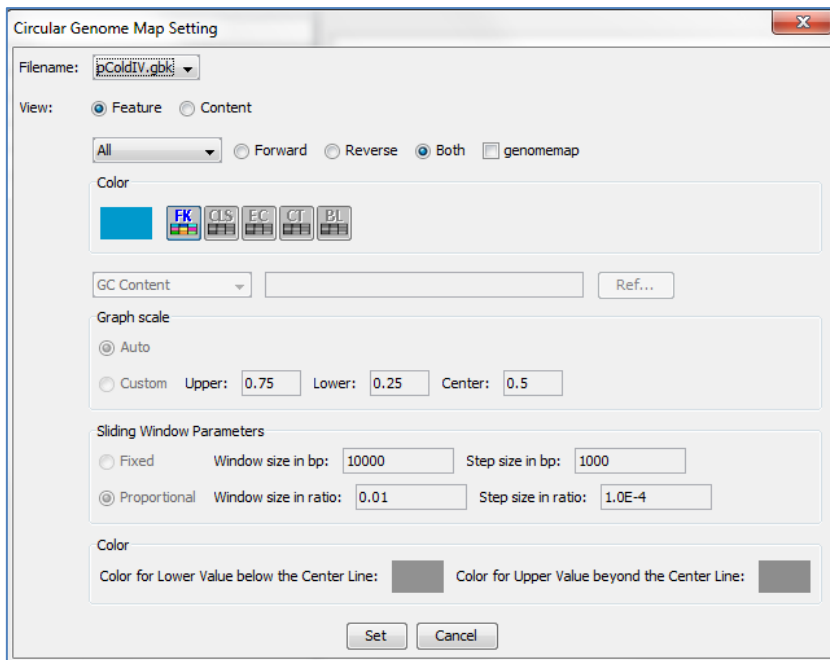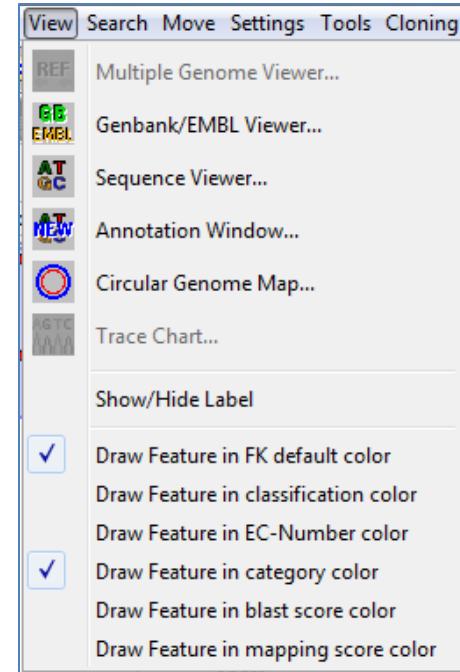
Visualization

It is possible to access different views of your sequence files via the "View" menu, including circular genome maps (example below). These are, of course, also fully customizable.
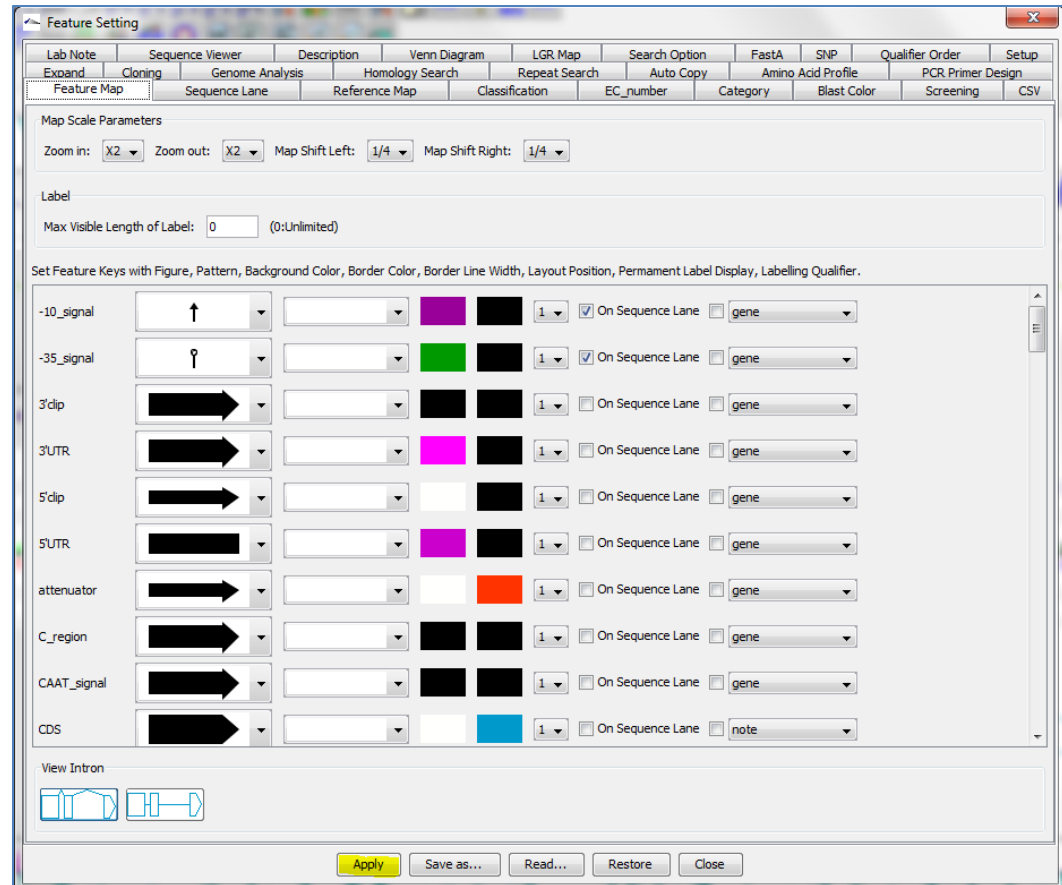
Feature Customization

It is possible to change form and color of every kind of feature, adjust their position on the feature map and activate or deactivate labels.

Additionally, the layout of the main feature map is also fully adaptable.

Interface Customization

The toolbox of IMC is customizable as well. Remove the buttons you don't need to focus on your favorite functions!

Summary

Customization of features and the feature map.

Search for keywords and sequence patterns.

Thanks to all the little things, IMC is a very flexible tool.

Visualize your sequence in different formats.

Flexible selection of function buttons.

Why You Should Try IMC

» Advantages of the Software

Advantages of IMC

▸ IMC offers a wide range of functions to work with whole genome data, from *in silico* cloning to genome and array analysis.

▸ The program can read a number of sequence file formats.

▸ There are three different editions of IMC: you only pay for the functions you need!

▸ Layouts in IMC are fully customizable.

▸ The software is already well-established on the Japanese market and is updated regularly.

▸ You can download a free two-week trial version of IMC at http://www.genexplain.com/imc