



KODON 3.5: LIST OF NEW FEATURES

Version 3.50 Release – 16 April 2007

Annotation

- Incorporation of "zoom scroller"
- More advanced settings for frame search algorithm (e.g. more accurate filtering of overlapping genes)
- Editing of features has been extended: for each feature a "history" of annotation is stored. This allows the user to track back changes made within individual annotations of features and to restore previous annotations.
- Initiation of translation can be defined for each translation (e.g. some translations start at second initiation)
- User-defined color definitions for feature identification quality, labelling of imported or unknown features

Frame analysis

- Module entirely redesigned!
- New user-adjustable sequence layout display
- Incorporation of "zoom scroller"
- Real-time editing of the sequence updates frame analysis results, start- and stop codons, protein translations of affected open reading frames
- Mapping of intron-exon structure of eukaryotic genes on the frame analysis
- Fully automated gene prediction for prokaryotes, viruses and eukaryotes by importing screening results of the powerful GeneMark gene prediction algorithms (used by EMBL and GenBank for gene annotation).

Comparative chromosome analysis

- Implementation of user-defined seeds for screening initiation
- Possibility to screen with several different seeds (higher screening sensitivity)
- Possibility to calculate only rows of comparison matrix (pairwise comparison of one entry against all other).
- New user-adjustable sequence layout display
- Incorporation of "zoom scroller"
- Stretch identity and stretch distance cut-off slider bars for interactive displaying of genome synteny on pairwise comparisons.
- Algorithms for finding homology stretches making up the genome synteny: finding genome alignment paths based on superstretch composition

- New user-defined color codes for mapping stretches based upon identity, stretch orientation, superstretch inclusion...

New application: Chromosome Alignment!

- Based upon homology stretch screening results obtained from a comparative chromosome analysis project, chromosome alignments can be carried out. A template genome is selected, query genomes are aligned against this template sequence.
- Alignment considers sequence inversions and sequence rearrangements
- No limits on sequence lengths and sequence numbers
- Alignment can be edited by the user
- Search algorithms for synonymous and non-synonymous mutations, deletions and insertions
- Export of SNP / mutation tables
- Search functions within the alignment for features, sequences, positions
- Fully scriptable accession to the input and output
- Excellent assembly results for 454 *de novo* or 454 assembled sequence data