

# Applied Maths

## KODON VERSION 3.0/3.10: LIST OF NEW FEATURES

Version 3.00 Release – 5 August 2005

Version 3.10 Release – 9 March 2006

### Startup window

- Wider database list field
- Double-click on database name to launch Kodon with selected database

### General

- Context-sensitive menu of commands in all applications

### Database

- Possibility to lock or unlock selected sequences directly from the database
- Export selected sequences in a database directly to the clipboard as FASTA, EMBL or GenBank
- Export selected sequences in a database as a TXT file in FASTA, EMBL or GenBank format
- Edit the *Connected Database settings* for databases under Microsoft Access, SQL Server, Oracle or other engines
- New **database of oligo nucleotides**
  - o Name and comment fields for each oligo
  - o Calculation settings per oligo
  - o Thermodynamic Properties calculator
  - o Storage of primers and primer pairs
- Local BLAST databases can be generated (NBLAST and PBLAST) (Version 3.10)

### Primer and PCR design

- Improved thermodynamics calculation
- Possibility to store and reuse primer and PCR calculation settings
- New thermodynamic properties calculator
- Possibility to store and retrieve primers and oligos in *Oligo nucleotide database*
- New powerful project-based application for **multiplex PCR design**
  - o Multiplex PCR from multiple sequences up to chromosome size
  - o Check for various parameters such as product length difference, false priming, distance between target regions, etc.

### Sequence editor

- Choice to enable or disable automatic inversion of sequence according to selected feature
- New multiline graphical sequence overview in *Sequence Editing mode*
- Continuous zoom using “zoom-slider” on graphical sequence overview

- Direct creation of new entry from a selection on a sequence
- Shortcut keys for Cut, Copy, Paste, Delete, Undo, Select all, etc.
- Local BLAST screening of nucleotide and amino acid (sub)sequences or CDS features (**Version 3.10**)

#### **Frame analysis**

- Local BLAST screening (NBLAST and PBLAST) for selected ORFs (**Version 3.10**)

#### **DNA-based comparative chromosome mapping**

- Possibility to choose sequence entry labels on identity matrix and clustering
- All-way synchronization between dot-plot, feature list and feature overview in pairwise comparison (*Cell view*)
- Differential coloring according to homology for stretches of features (graphical overview map)

#### **New CDS-based comparative chromosome mapping**

- Similar project as DNA-based comparative chromosome mapping but based on *annotated CDS features*
- Matrix of *features versus sequence entries* to show all hits and understand gene similarities/parallelisms
- Search for CDS classes based on gene similarities and gene ontologies
- Clustering and pairwise alignment of CDS features

#### **New automated chromosome annotation**

- Project-based automated annotation of full or partial chromosome sequences based on comparison with selections of annotated chromosomes
- Annotations based on gene similarities and surrounding parallelisms
- Optional additional NCBI BLAST for CDS features that could not be annotated using selected chromosomes
- Local BLAST screening (NBLAST and PBLAST) for selected ORFs (**Version 3.10**)