VORTEX FOR BIOINFORMATICS

Vortex is a powerful, easy-to-use data analysis and visualization program that is widely adopted for scientific research. Vortex for Bioinformatics extends Vortex with capabilities that allow scientists engaged in biologics drug discovery and other biology research to easily analyze and visualize their data, including antibody sequences, genomic, proteomic, metabolomic, and peptide data.

VORTEX FOR BIOINFORMATICS – EASILY ANALYZE AND VISUALIZE BIOLOGICAL DATA

Vortex for Bioinformatics intrinsically understands biological data types, enabling standard bioinformatics analysis to be run directly from the graphical UI. It also includes novel analyses such as biological structure/sequence activity relationship (BSAR) and matched pair analysis, supporting scientific decision making in order to accelerate the progress of discovery projects.

- Enables bioscientists to analyze their own data. Users do not need to be an expert bioinformation or proficient at scripting to use Vortex for Bioinformatics
- Suitable for a broad range of bioscience disciplines including antibody design, genomics, proteomics, and metabolomics
- Natively handles biological data types including sequences, conjugates, oligomers, proteins and peptides as well as small molecules
- Standard bioinformatics analyses are built in and fully integrated including sequence alignment (multiple methods), cross alignment, sequence clustering, Prosite searching, and library search (e.g., CDR and ORF detection)
- High performance visualization and analysis on all data volumes – fast enough for interactive visualization and analysis of a whole genome, or millions of shorter sequences, on a standard business laptop

INTEGRATES WITH EXISTING CHEMINFORMATICS STATISTICS AND CHARTING

Vortex for Bioinformatics leverages the Vortex program that has been widely adopted across the pharma and biotech industry for cheminformatics, and statistical analysis and visualization. It seamlessly integrates the new bioinformatics capabilities with the existing cheminformatics, statistics and charting.

Key Features

- Load data from FastA, FastQ, (HELM in development) or directly from databases via Dotmatics Browser
- Native handling of scientific data types including sequences, conjugates, oligomers, proteins and peptides, as well as small molecules
- Display sequences in hyberbolic or linear one line, or multiline representations of one letter or three letter codes
• Annotate sequences with text, other sequences, small molecules or oligomers
• Search and browse sequence annotations
• Supports antibody CDR numbering schemes such as Kabat and Chothia
• Sequence edit mode allows direct editing of sequences for mutations, insertions, and deletions
• Display 3D structures of proteins and antibodies in a variety of modes include ribbon, CPK and surface
• Display oligomer representations
• Sequence alignment (multiple methods), cross alignment, antibody CDR alignment, sequence clustering, BLAST and Prosite searching, library search, ORF detection
• BSAR (Biological Sequence/Structure Activity Relationship) analysis
• Visualizations – CIRCOS plots, BSAR plots, in addition to a wide variety of regular plots (e.g. bar, scatter, pie, heatmap, tree and many more)
• Load and display OBO and OWL ontologies

VORTEX IS A POWERFUL, VERSATILE AND EASY TO USE VISUALIZATION TOOL WHICH ENABLES YOU TO VIEW YOUR DATA IN AN INTUITIVE AND MANNER