

Curriculum Vitae - Dr. Amit Fliess

Profession: Bioinformatician
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Objective

Computational data analysis and Information retrieval, mainly analysis of biological data.

Work experience

2013	<u>Computational Genomics Scientist:</u> Evogene Ltd., Computational Genomics Department, 13 Gad Feinsein st. Rehovot. - Information retrieval from the web including: public biological databases and tables & lists of various crops traits. Merging those tables & lists into a single table. - Semi-automatic text mining of annotations in Genbank and Uniprot files mainly by using regular expressions. - Updating and correction of the taxonomic data in Evogene.
2010	<u>Bioinformatician:</u> Dr. Shimon Meir and Dr. Sonia Philosoph-Hadas Lab., Department of Post-harvest Science of Fresh Produce, ARO, The Volcani Center, Bet-Dagan, with the help of Dr. Ron Ophir. - Microarray computational analysis, mainly by Clustering.
2009	<u>Bioinformatician:</u> Dr. Nativ Dudai Lab., Medicinal and Aromatic Plants Unit, Newe Ya'ar Agricultural Research Center, Ramat Yishay. - Correlation analysis between volatile compounds in spice plants. - Curve fitting of accumulation of volatile compounds in leaves.
2006-2008	<u>Post doctorate:</u> Dr. Eitan Rubin Lab., Health Sciences Faculty, Ben-Gurion University. - Data mining of medical data, mainly the study of the relationships between clinical biomarkers and age. - Cluster analysis based on composition of volatile compounds for classification and characterization of aromatic plant, A joint project with South Judea R&D Center and Newe Ya'ar Agricultural Research Center.
2003-2005	<u>Post doctorate:</u> Prof. Ron Unger Lab., Life Science Faculty, Bar-Ilan University. - Classification of biological term in biomedical literature for a joint free text mining project with Dr. Ronen Feldman Lab. - Computational prediction of the structure of human histone deacetylases and their binding to butyrate.
2002	<u>Research assistant:</u> Prof. Hanah Margalit Lab., Department of Molecular Genetics & Biotechnology, the Hebrew University of Jerusalem. - Semi-automatic text mining of yeast protein-protein interaction sites.
1993-1994	<u>Research assistant:</u> Prof. Ephraim Katzir Lab., Weizmann Institute. - Computational prediction of heparin binding to fibroblast growth factors. - Information retrieval of protein electrostatics computation.

Education

1996-2002	Ph.D. : Prof. Ron Unger Lab., Life Science Faculty, Bar-Ilan University. Thesis: Swaps in Biological Macromolecules.
1990-1992	M.Sc. : Prof. Amiram Goldblum Lab., School of Pharmacy, the Hebrew University of Jerusalem. Thesis: The main factors in the dimerization of HIV-1 protease.
1987-1988	Diploma of Librarian-Information specialist: School of Library & Archive, the Hebrew University of Jerusalem.
1983-1985	B.Sc. : Faculty of Agriculture Rehovot, the Hebrew University of Jerusalem.

Professional skills

Category	Computational tools
Text processing , mostly by utilizing Regular Expressions	Perl, Unix shell & Ruby
High throughput computational analysis	Unix shell, Perl, Ruby & R
Data analysis by Clustering	R & T-Mev
Data-mining packages	KNIME, Clementine & Weka
macromolecule 3D-cartesian coordinate files analysis	R, Matlab & Unix shell(especially awk)
Semi-automatic text mining	
Basic Statistical analysis	R & SPSS
Information retrieval	
Websites design (especially for automatic table making)	Html

Award

The Hebrew University of Jerusalem Medical School prize for an outstanding M.Sc. research thesis.

Publications

Fliess A, Ragolsky, M, Rubin E .

Reverse Translational Bioinformatics: A Bioinformatics Assay Of Age, Gender And Clinical Biomarkers.

Translational Bioinformatics Proceedings, San Francisco, CA, 10 to 12 March 2008: 11-15 [AMIA, Bethesda, MD, ISCB, La Jolla, CA, 2008]

Fliess A, Motro B, Unger R .

Swaps in protein sequences.

PROTEINS 48: 377-387 [2002]

Uliel S, Fliess A, Unger R .

Naturally occurring circular permutation in proteins.

PROTEIN ENGINEERING 14: 101-110 [2001]

Uliel S, Fliess A, Amir A, Unger R .

A simple algorithm for detecting circular permutation in proteins.

BIOINFORMATICS 15: 930-936 [1999]

Gorinstein S, Zemser M, Fliess A, Shnitman I, Paredes-Lopez O, Yamamoto K, Kobayashi S, Taniguchi H .

Computational analysis of the amino acid residue sequences of amaranth and some other proteins.

BIOSCIENCE BIOTECHNOLOGY AND BIOCHEMISTRY 62: (10) 1845-1851 [1998]

Goldblum A, Rayan A, Fliess A, Glick M .

Extending crystallographic information with semiempirical quantum-mechanics and molecular mechanics - a case of aspartic proteinases.

JOURNAL OF CHEMICAL INFORMATION AND COMPUTER SCIENCES 33: (2) 270-274 [1993]

Rayan A, Fliess A, Kotler M, Chorev M, Goldblum A .

Theoretical models of aspartic proteases: active site properties, dimer stability and interactions with model inhibitors.

ADVANCE IN EXPERIMENTAL MEDICAL BIOLOGY 306: 555-558 [1991]

For recommendations please contact:

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