Peter De Rijk

Neuromics Support Facility - Bioinformatics
VIB-UAntwerp Center for Molecular Neurology
University of Antwerp

Education
BSc in Chemistry, University of Antwerp, 1988
MSc in Biochemistry, University of Antwerp, 1990
PhD in science, University of Antwerp, 1995

Position
1999 Postdoc
2002 Jr Staff Scientist
2009 Staff Scientist
2011 Research Associate

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Keywords
Bioinformatics – high-throughput genetics/genomics technology – data management - sequence analysis – genotyping – non coding RNA

Function
My work is focused on the design, development, implementation and support of work-flows and software tools to enhance the research of complex diseases. Over the years, I developed software covering management, setup and analysis of a very diverse set of genotyping technologies, ranging from STR analysis and Sanger sequencing to next generation sequencing. During the analysis of some of early complete genomes, I made software for comparing, annotating, filtering and validating complete genome data (Genomecomb). This is developed further to integrate the in-house analysis of gene panel and exome sequencing using state of the art publicly available tools and local enhancements. We are further exploring new ways to extract meaning from sequencing data by integrating new analyses and technologies such as nanopore sequencing.

I am also responsible for the (further) development and support of the in-house LIMS system managing the data-flow in the center from sample management to experimental results, and provide bioinformatics expertise, advice and support to the center.

Expertise
- sequencing, genomics, genetics
  - ngs analysis (whole genome, exome, targetted)
  - technology development, workflow design
  - pedigrees, linkage, association analysis
  - structural variants
  - miRNA
- programming
  - software design en implementation
  - low level languages (C, fortran, ...)

    - high-level languages (Tcl, R, Julia, …)
- databases
    - technical: several relational (Postgresql, Firebirdsql, sqlite, ...) as nosql (berkeley, mongodb, ...) databases
    - applied: sequence databases, structure, lims
- general bioinformatics
    - sequence analysis
    - structure
    - evolution
- general it
    - cluster management and application
    - Unix/Linux
    - networks
    - hardware

Selected Publications

Cammaerts,S., Strazisar,M., Dierckx,J., Del-Favero,J., **De Rijk,P.**: miRVaS: a tool to predict the impact of genetic variants on miRNAs. Nucleic Acids Research 44(3): e23 (2016) Epub: 17-Sep-2015 (PMID: 26384425) (I.F.: 10.162)

Strazisar,M., Cammaerts,S.,Van Der Ven,K., Forero,D.A., Lenaerts,A.S., Nordin,A., Almeida-Souza,L., Genovese,G., Timmerman,V., Liekens,A., **De Rijk,P.**, Adolfsson,R., Callaerts,P., Del-Favero, J.: MIR137 variants identified in psychiatric patients affect synaptogenesis and neuronal transmission gene sets. Mol Psychiatry. 20(4):472-481 (2015) Epub 3-Jun-2014 (PMID: 24888363) (I.F.: 15.147)

Kancheva,D.*, Atkinson,D.*, **De Rijk,P.**, Zimon,M., Chamova,T., Mitev,V., Yaramis,A., Fabrizi,G.-M., Topaloglu,H., Tournev,I., Parman,Y., Battaloglu,E., Estrada-Cuzcano,A.*, Jordanova,A.* (* equal contribution): Novel mutations in genes causing hereditary spastic paraplegia and Charcot-Marie-Tooth neuropathy identified by an optimized protocol for homozygosity mapping based on whole-exome sequencing. Genetics in Medicine 18(6): 600-607 (2016) Epub: 22-Oct-2015 (PMID: 26492578) (I.F.: 8.229)

Reumers,J.*, **De Rijk,P.***, Zhao,H., Liekens,A., Smeets,D., Cleary,J., Van Loo,P., Van Den Bossche,M., Catthoor,K., Sabbe,B., Despierre,E., Vergote,I., Hilbush,B., Lambrechts,D., Del-Favero,J.: Optimized filtering reduces the error rate in detecting genomic variants by short-read sequencing. Nature Biotechnology 30(1): 61-68 (2012) Epub: 18-Dec-2011 (PMID: 22178994) (I.F.: 23.268)

Momozawa,Y., Mni,M., Nakamura,K., Coppetiers,W., Almer,S., Amininejad,L., Cleynen,I., Colombel,J.-F., **De Rijk,P.**, Dewit,O., Finkel,Y., Gassull,M.A., Goossens,D., Laukens,D., Lémann,M., Libioulle,C., O'Morain,C., Reenaers,C., Rutgeerts,P., Hugot,J.P., Zelenika,D., Lathrop,M., Del-Favero,J., Hugot,J.P., de Vos,M., Franchimont,D., Vermeire,S., Louis,E., Georges,M.: Resequencing of positional candidates identifie low frequency IL23R coding variants protecting against inflammatory bowel disease. Nature Genetics 43(1): 43-47 (2011) Epub: 12-Dec-2010 (PMID: 21151126) (I.F.: 35.532)

All Publications