Peter De Rijk

BioInfo Unit

Department of Molecular Genetics, VIB, Antwerp, Belgium
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

E-mail: Peter.DeRijk@molgen.vib-ua.be

Phone: +32 (3) 265 1030

Keywords

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

Function

My work is focused on the design, development and implementation of work-flows and software tools to enhance the research of complex diseases. Over the years, I developed software covering the 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, software was developed for comparing, annotating, filtering and validating complete genome data (Genomecomb). This is now also used 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 the variants. One way this is done is through the discovery of new potential targets. Our large scale reanalysis of public sequencing data discovered a large number of novel miRNAs, which will be used to annotate variants. We will also further implement ways to combine genomic data with downstream transcriptome, proteome and phenotypic information in order to gain more insight into the disease process.

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

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)

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)

Liekens,A., De Knijf,J., Daelemans,W., Goethals,B., **De Rijk,P.**, Del-Favero,J.: Biograph: Unsupervised biomedical knowledge discovery via automated hypothesis generation. Genome Biology 12(6): R57 (2011) Epub: 22-Jun-2011 (PMID: 21696594) (I.F.: 9.036)

Goossens,D., Moens,L.N., Nelis,E., Lenaerts,A-S., Glassee,W., Kalbe,A., Frey,B., Kopal,G., De Jonghe,P., **De Rijk,P.**, Del-Favero,J.: Simultaneous mutation and copy number variation (CNV) detection by multiplex PCR-based GS-FLX sequencing. Human Mutation 30(3): 472-476 (2009) (PMID: 19058222) (I.F.: 6.887)

All Publications