



Jeroen de Ridder received his Masters degree in Electrical Engineering from the Delft University of Technology (TUD) in 2005 (*cum laude*). Subsequently, he started a PhD to work on pathway discovery in insertional mutagenesis data. This work was carried out in the Delft Bioinformatics lab (Reinders group, TUD) and at the Netherlands Cancer Institute (Wessels group). His PhD work resulted in a statistical framework for the analysis of retroviral insertional mutagenesis data [6,7] to identify cancer genes in mice and was used in the analysis of several mutagenesis datasets in collaboration with researchers at the Netherlands Cancer Institute and the Wellcome Trust Sanger Institute (Hinxton, UK) [2,3,4]. More recently, he published a method for pathway inference from multimodel genomics data [1]. During his PhD, Jeroen has gained international experience during two three-month visits to the Shmulevich lab at the Institute for Systems Biology (Seattle, USA), where he worked on multi-scale methods for genomic data analysis. In addition, Jeroen has been an active member of the national and international bioinformatics communities, first as member of the board of the Dutch Regional Student Group, co-initiated by NBIC, and later as the elected chair of the Student Council, an initiative of the International Society for Computational Biology (ISCB). Jeroen currently holds a position as Assistant Professor in the Delft Bioinformatics Group.

#### Key publications

[1] Pérez-Mancera, P. A., A. G. Rust, L. van der Weyden, G. Kristiansen, A. Li, A. L. Sarver, K. A. T. Silverstein, R. Grützmann, D. Aust, P. Rümmele, et al., "The deubiquitinase USP9X suppresses pancreatic ductal adenocarcinoma.", vol. 486, issue 7402, pp. 266-270, 2012, *Nature*

[2] de Ridder J, Gerrits A, Bystrykh L, de Haan G, Reinders M, Wessels L. Inferring Combinatorial Association Logic Networks in Multimodal Genome-Wide Screens, vol. 26, issue 12, pp. i149-57, 2010, *Bioinformatics*

[3] Mattison J, Kool J, Uren A, de Ridder J, Wessels L, Jonkers J, Bignell G, Butler A, Rust A, Brosch M, Wilson C, van der Weyden L, Largaespada D, Stratton M, Futreal PA, van Lohuizen M, Berns A, Collier L, Hubbard T, Adams D. Large-scale cross-species comparative oncogenomics identifies candidate oncogenes and tumour suppressor genes, 2009, *Cancer Research*

[4] Uren GA, Kool J, Matentzoglou K, de Ridder J, Mattison J, van Uiter M, Lagcher W, Sie D, Tanger E, Cox T, Reinders M, Hubbard T, Rogers J, Jonkers J, Wessels L, Adams DJ, van Lohuizen M, Berns A. Large-Scale Mutagenesis in p19ARF- and p53-Deficient Mice Identifies Cancer Genes and Their Collaborative Networks. 2008, *Cell*

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[7] de Ridder, J, Uren, A, Kool, J, Reinders, M, and Wessels, L. Detecting statistically significant common insertion sites in retroviral insertional mutagenesis screens. 2006, *PLoS Comput Biol*