



[Dick de Ridder](#) (M.Sc. in Computer Science, 1996; Ph.D. in Pattern Recognition and Image Processing, 2001; both from [Delft University of Technology](#), The Netherlands) in 2003 moved into bioinformatics starting at [Erasmus University Medical Centre](#), Rotterdam. In 2005 he was tenured as assistant professor at Delft University of Technology, where he currently conducts research in data-driven bioinformatics, particularly focusing on problems in biotechnology and microbial systems biology.

His interest lies in the integration of high-throughput measurement data with prior knowledge about a problem to be solved by machine learning algorithms. Challenges occur at the “interface” between generic algorithms and specific bioinformatics problems. How can biological prior knowledge be transformed and used to achieve optimal generalisation at minimal experimental cost?

Over the last years, he has developed several data analysis algorithms, and has studied more generally the application of bioinformatics tools to patient-cohort studies, in particular in [immunological diseases](#). Recently, he focused on developing integrative bioinformatics tools for use in microbial systems biology (of bacteria, yeasts and fungi) with applications in biotechnology, i.e. in modeling metabolic networks, their regulation and evolution and in improving industrial processes. He is an author on over 60 peer-reviewed publications in journals and at international conferences.

Key publications

R.J.P. van Berlo, [D. de Ridder](#), J.-M. Daran, P.A.S. Daran-Lapujade, B. Teusink and M.J.T. Reinders, “Predicting metabolic fluxes using gene expression differences as constraints”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 8(1):206-216, 2011

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M.J.L. de Groot, R.J.P. van Berlo, W.A. van Winden, P.J.T. Verheijen, M.J.T. Reinders and [D. de Ridder](#), “Metabolite and reaction inference based on enzyme specificities”, *Bioinformatics* 25(22):2975-2982, 2009

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