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## Elena Sabbioni

Elena Sabbioni is a Ph.D. student in Biostatistics, currently affiliated with the SmartData@Polito research center and the Department of Pure Applied Mathematics (DISMA) and of Politecnico di Torino. She obtained her bachelor degree in 2019 and her master degree in 2021, both at the University of Trento, where she studied Mathematics. Her research field is Bayesian Statistics applied to biological and genetics models, using both simulated and real data to infer the parameters of the models.



## Bayesian approach for modelling RNA velocity

## ABSTRACT

RNA velocity is a biological quantity related to the evolution of cells at different stages of maturity and can be used to interpret cellular differentiation. The mathematical model behind this quantity describes the biological transformation from DNA to RNA, which can be modelled as a set of ordinary differential equations, whose rate constants need to be estimated from collected experimental data bv single-cell RNA sequencing. The principal method used in RNA velocity literature to estimate the parameters of the model is scVelo. Since it has already been criticized over various aspects, we propose a model that is mathematically better founded, using Bayesian statistics to infer the parameters. Our approach clarifies which parameters can be estimated and it is able to estimate appropriately the parameters of the system.

