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Nota di contenuto	Modeling and Parameter Estimation for Single-Cell Data -- ODE Constrained Mixture Modeling for Multivariate Data -- Approximate Bayesian Computation Using Multivariate Statistics.
Sommario/riassunto	Carolin Loos introduces two novel approaches for the analysis of single-cell data. Both approaches can be used to study cellular heterogeneity and therefore advance a holistic understanding of biological processes. The first method, ODE constrained mixture modeling, enables the identification of subpopulation structures and sources of variability in single-cell snapshot data. The second method estimates parameters of single-cell time-lapse data using approximate Bayesian computation and is able to exploit the temporal cross-correlation of the data as well as lineage information. Contents Modeling and Parameter Estimation for Single-Cell Data ODE Constrained Mixture Modeling for Multivariate Data Approximate Bayesian Computation Using Multivariate Statistics Target Groups Researchers and students in the fields of (bio-)mathematics, statistics, bioinformatics System biologists, biostatisticians, bioinformaticians The

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