

[Modelling and simulation for the interpretation of single-cell data](#)

Single-cell technologies have emerged as a groundbreaking technique in molecular biology, providing unprecedented insights into cellular heterogeneity. Their unique characteristics have stimulated the development of a vast generation of computational methods aimed at profiling cell differentiation trajectories, reconstructing cell-type-specific gene regulatory networks, or inferring cell-to-cell communication, among others.

The goal of this session is to bring together different Computational Biology researchers at the interphase of single-cell data studies and modelling to discuss advancements on both ends and facilitate exchanges that could help accelerate research. The session welcomes success stories about interesting single-cell analyses, modelling frameworks that would welcome single-cell data and novel methods that bring these two communities closer together.

Call for Abstracts

We accept abstracts about computational methods integrating single-cell data, focusing on mathematical modelling and simulation protocols to predict relevant cellular features in different biological scenarios. These abstracts will be peer-reviewed by a panel of specialists, and those selected will be included in the programme as 15 min selected talks.

Relevant topics for the call for abstracts:

- Genomic heterogeneity
- Network modelling
- Reconstruction of gene regulatory networks
- Integrative multi-omics models
- Cell-to-cell communication
- Multiscale modelling
- AI/ML applications

Click [here](#) to submit your abstract and [here](#) for the abstract template. **Submission deadline is 28 June.**

Registration

Click [here](#) for the registration form.

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