QBiC CDB JOINT SEMINAR

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Thursday, July 19, 2012

15:00 ~ 16:00

RIKEN CDB Bldg. A, 7th Floor Seminar Room

There will be a video broadcast in OLABB 3F conference room

Systematic single-cell analysis of development: worm and beyond

Summary

Recent progress in *in toto* imaging of metazoan embryogenesis and image analysis algorithms for automated cell tracking offers an exciting opportunity for systematic single-cell analysis of development. In *C. elegans*, we have optimized the technologies so that we can lineage 5,000 embryos per year with a dedicated spinning disc confocal microscope. In addition to mapping gene expression onto identifiable individual cells, we have developed methods for not only automated phenotype detection (systematic single-cell measurements of how a mutant embryo is different from the wild type), but also automated interpretation (inferring mechanisms and complex gene function from the differences) based on a set of surprisingly simple rules. More complex organisms provide a greater challenge both in terms of the sheer number of cells and in interpreting variable cell lineages. We are developing a statistical framework to infer consensus developmental programs from multiple data sets containing both variable cell lineages and tracking errors. Together with methods for automated phenotype interpretation, this statistical framework will provide the essential computational tools needed to enable systematic single-cell analysis of development in complex model organisms.

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