

Roughly ten years ago, the first gastruloid paper was published. Gastruloids are stem cell-based embryo models that recapitulate body axis formation and germ layer specification, without relying on extraembryonic tissues to provide spatial signalling cues. This makes the model particularly valuable, since the equivalent developmental processes in vivo take place after implantation in the uterine wall, which comes with significant technical and ethical constraints.

While extensive characterisation of the gastruloid system using single-cell omics and imaging has yielded many exciting insights, a full spatial transcriptomic profile of developing gastruloids is still missing. Capturing spatial transcriptomics before the symmetry-breaking event could reveal how cells are spatially organised prior to committing to a fate and self-organising along the body axis, whether this organisation is consistent across individual gastruloids, and potentially shed light on cell-to-cell communication and the underlying gene regulatory networks. The Visium HD platform used for our spatial transcriptomics data is genome-wide, going beyond the limited gene panels used in other spatial transcriptomics or imaging approaches applied to mouse gastruloids, and thereby enabling much deeper profiling of the gastruloid after symmetry breaking.

The aim of this internship is to analyse spatial transcriptomics data from mouse gastruloids across several developmental timepoints. In addition, we aim to build a 3D representation of an "average" gastruloid, for which the individual 2D gastruloid sections will need to be registered onto a 3D template using landmark detection or a comparable algorithm.

Programming (languages) to use

- Python
- Linux
- ImageJ / CellPose / Loupe browser

Skills

- Image analysis / segmentation / 3D registration
- Single-cell RNA sequencing analysis

Key literature

1. <https://journals.biologists.com/dev/article/141/22/4231/46516/Symmetry-breaking-germ-layer-specification-and>
2. <https://elifesciences.org/reviewed-preprints/109268v2>
3. <https://academic.oup.com/bioinformatics/article/40/9/btae546/7754061>
4. <https://www.nature.com/articles/s41592-024-02199-5>