

## Getting The Data

The zebrafish embryogenesis data (38,731 cells, 12 developmental time points from 3.3–12 hours post fertilization) can be obtained in two forms:

1. **The processed counts matrix** can be downloaded and used as a starting point for your own analysis: ([https://singlecell.broadinstitute.org/single\\_cell/data/public/SCP162/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis?filename=URD\\_Dropseq\\_Expression\\_Log2TPM.txt.gz](https://singlecell.broadinstitute.org/single_cell/data/public/SCP162/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis?filename=URD_Dropseq_Expression_Log2TPM.txt.gz) — requires logging into the Broad Single-cell Portal).
2. **BAM files** are deposited in NCBI GEO under accession number [GSE106587](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE106587).

## Getting URD

**URD** is an R package designed for reconstructing transcriptional trajectories underlying specification or differentiation processes in the form of a branching tree, using single cell RNA-sequencing data. URD is hosted in Github (<https://github.com/farrellja/URD>). Detailed installation instructions and tutorials are located in the repository.

## Browsing the Processed Data

The URD reconstructed developmental trajectories of zebrafish embryogenesis can be browsed in two forms:

1. **Easiest/Quickest:** The Broad Single-cell Portal ([https://portals.broadinstitute.org/single\\_cell/study/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis](https://portals.broadinstitute.org/single_cell/study/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis)). This allows plotting the expression of genes of interest on the 3D force-directed layout, tSNE projection, or spatially assigned 50% epiboly cells.
2. **Best:** The pre-processed URD object ([https://singlecell.broadinstitute.org/single\\_cell/data/public/SCP162/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis?filename=URD\\_Zebrafish\\_Object.rds](https://singlecell.broadinstitute.org/single_cell/data/public/SCP162/single-cell-reconstruction-of-developmental-trajectories-during-zebrafish-embryogenesis?filename=URD_Zebrafish_Object.rds) — requires logging into the Broad Single-cell Portal). This allows more responsive plotting on the 3D force-directed layout, the dendrogram layout, or the tSNE projections (including dual-color plotting of multiple genes), as well as isolation of particular cell populations, differential expression, and more.