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Data Article

# Analysed cap mesenchyme track data from live imaging of mouse kidney development

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ABSTRACT

This article provides detailed information on manually tracked cap mesenchyme cells from timelapse imaging of multiple *ex vivo* embryonic mouse kidneys. Cells were imaged for up to 18 h at 15 or 20 min intervals, and multiple cell divisions were tracked. Positional data is supplemented with a range of information including the relative location of the closest ureteric tip and a correction for drift due to bulk movement and tip growth. A subset of tracks were annotated to indicate the presence of processes attached to the ureteric epithelium. The calculations used for drift correction are described, as are the main methods used in the analysis of this data for the purpose of describing cap cell motility. The outcomes of this analysis are discussed in "Cap mesenchyme cell swarming during kidney development is influenced by attraction, repulsion, and adhesion to the ureteric tip" (A.N. Combes, J.G. Lefevre, S. Wilson, N.A. Hamilton, M.H. Little, 2016) [1].



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**Specifications Table**

| | |
|---|---|
| Subject area | *Biology* |
| More specific subject area | *Cell motility in kidney development* |
| Type of data | *Tables* |
| How data was acquired | *Confocal Microscope, Zeiss 710 and 780, analysis in Imaris (Bitplane 8.0.1) and R* |
| Data format | *Analysed* |
| Experimental factors | *Cellular compartments within the developing mouse kidney were labeled with transgenic reporters and imaged in organ culture using confocal microscopy* |
| Experimental features | *Quantitative analysis of cell migration data, computed information* |
| Data source location | *Institute for Molecular Biosciences, The University of Queensland, Brisbane, QLD, Australia*<br>*Murdoch Childrens Research Institute, Melbourne, VIC, Australia* |
| Data accessibility | *Data is included in this article* |

**Value of the data**

- Timelapse imaging dataset from complex developing organ including methods to correct for drift and compute relationships between cells and local features in a dynamic environment.
- Includes data on position and movement of cap mesenchyme cells relative to ureteric tip.
- Available for further analysis and modelling of cell motility.
- Provides benchmark for studying mutant phenotypes.

## 1. Data

The data consists of 3 tables formatted as Excel files, and an additional Excel file containing detailed metadata. Supplementary Table 1 gives the primary cap mesenchyme cell dataset summarised in Table 1, Supplementary Table 2 gives the same dataset with position and derived fields transformed according to the drift correction described below, while Supplementary Table 3 contains tip extremity tracks that were used for drift correction. Each table row corresponds to a single measurement and contains sample, crop, track and track branch identifiers as well as the time step, position and additional calculated data fields.

**Table 1**
Data Summary.

| *Sample id* | *Crops* | *Time step (minutes)* | *Experiment duration (hours)* | *Tracks (may be branched)* | *Analysis tracks (unbranched)* | *Total observations (spots)* |
|---|---|---|---|---|---|---|
| 1 | 1 | 15 | 11.75 | 1 | 3 | 95 |
| 4 | 1 | 15 | 12.00 | 102 | 118 | 3753 |
| 5 | 1 | 15 | 17.25 | 5 | 9 | 474 |
| 6 | 1 | 15 | 18.00 | 10 | 14 | 707 |
| 11 | 5 | 15 | 16.25 | 249 | 281 | 8593 |
| 13 | 1 | 20 | 18.67 | 38 | 92 | 2262 |
| 14 | 1 | 20 | 18.00 | 47 | 77 | 1917 |
| 16 | 4 | 20 | 18.00 | 125 | 189 | 5295 |
| 17 | 4 | 20 | 17.67 | 47 | 69 | 2391 |
| **total** | **19** | | | **624** | **852** | **25,487** |