**Atrial Fibroblast Signaling Model**

This repository contains MATLAB code and data files to reproduce the figures from: Khorasani et al., The Journal of Physiology, 2025.

**Folder: ‘Network\_Model’**

Contains the model structure Excel file and files needed for running and visualizing simulations:

|  |  |
| --- | --- |
| File or Folder Names | Description |
| Khorasani\_Atrial\_Fibroblast\_Model.xlsx | Our model “xlsx” file for Netflux simulations |
| Netflux Documentation.docx | Instructions for using Netflux |
| Netflux SBGN style.xml | Style file for visualizing the network in Cytoscape |
| simulations\_in\_Netflux\_BL\_Ang\_Ca\_120h.txt | The file needed for Visualizing a Netflux network model with Cytoscape |
| simulations\_in\_Netflux\_BL\_TGFB\_Ca\_120h.txt | The file needed for Visualizing a Netflux network model with Cytoscape |

**Folder: ‘Validation\_Sensitivity\_Analysis\_Netflux’**

Contains code and data for reproducing the main figures in the paper:

|  |  |
| --- | --- |
| File or Folder Names | Description |
| Validation\_Code.m | plots **Fig. 2.** |
| Netflux\_NJ\_for\_predefined\_inp | Running the Netflux code using the provided initial values for **w** vector |
| Netflux\_NJ.m | plots **Fig. 3** (sensitivity analysis) |
| dataNJ\_ and dataNJ\_high\_1 | All the output files from “Netflux\_NJ\_v2.m” script |
| Netflux.m | The original Netflux Matlab code ploting **Figs. 4A–B and 6A–B** |
| +gui, +util, utilities folders | Containing the functions required to run the original Netflux MATLAB code |
| barPlot\_CaCalcineurinCamk.m | plots **Figs. 4C** and **D** |
| barplots\_CaCalcineurinCamKII\_files | Containing “txt” data files corresponding to “barPlot\_CaCalcineurinCamk.m” script |
| barplots\_for\_AF\_TRPC\_KD\_CaMKII\_KD.m | plots **Figs. 4E** and **F.** |
| barplots\_for\_AF\_TRPC\_KD\_CaMKII\_KD\_files | Containing the “txt” data files you need for “barplots\_for\_AF\_TRPC\_KD\_CaMKII\_KD.m” |
| barplots\_for\_CI\_CIII\_upstream\_species\_role | plots **Fig.7.** |
| barplots\_for\_CI\_CIII\_upstream\_species\_role\_files | Containing the “txt” data files corresponding to barplots\_for\_CI\_CIII\_upstream\_species\_role.m script |

**Notes on Other Figures**

* **Fig. 1**: Created using Netflux + Cytoscape (see ‘Network\_Model’ folder for the corresponding materials)
* **Fig. 5**: Created manually in Inkscape.

**‘txt’ Data Files**

All .txt’ data files were generated using ‘Netflux.m’, following the input protocols described in the Methods section of our paper1 and the workflow in \*Clark et al.2.

**Reference:**

1. N. Khorasani, H. Ni, J.J. Saucerman, D. Dobrev, S. Morotti, and E. Grandi. Computational modeling of cardiac fibroblast signaling reveals a key role for Ca2+ in driving atrial fibrillation-associated fibrosis. The Journal of Physiology, 2025.
2. A.P. Clark, M. Chowkwale, A. Paap, S. Dang and J.J. Saucerman. Logic-based modeling of biological networks with Netflux. *PLOS Computational Biology*, 2025.