

Guidelines for Model Entries in Spreadsheet

v1.0

1. Entries in the spreadsheet with following specs would be imported:

- * Entity = single cell
Artefact Type = model / model fit
- * Entity = network
Artefact Type = model / model fit / model collection
- * Entity = subcellular / intrasignalling
Artefact Type = model / model fit
- * Entity = molecular
Artefact Type = model / model fit

Note: let us know if we have missed a relevant category/sub-category

2. Models of ion channels, synapses, intracellular signalling pathways, etc ... should be assigned "Entity = subcellular" (and not as 'single cell')

3. Please ensure that the 'Entity' is specified from the drop down list. Currently some sheets such as the 'Molecular Models' sheet seems to some different values... e.g. "subcellular - molecular" (select either 'subcellular' or 'molecular', whichever is most appropriate). Selecting values from the dropdown options makes the automated import into model catalog less error-prone.

4. Ensure that each of the entries in (1) have the following set appropriately:

Note: mandatory unless explicitly stated as optional

- * Author
- * Author Organization (*optional*)
- * Collab ID to be linked to the model

Note: a new column needs to be added to each of the sheets for this info
E.g. of Collab ID = '7840'

You can pick this up from the URL once inside a Collab (example below):

<https://collab.humanbrainproject.eu/#/collab/7840/nav/59620>

-> Collab_ID = 7840

- * Species

5. [Optional]: If you intend to link to a specific version of the model (by providing url), then set the following appropriately:

Note: mandatory unless explicitly stated as optional

- * Version (e.g. '1.0' or 'dev_1')

* Version description (*optional*) (e.g. 'model from Abcde et al. (2018)' or 'model with STP')

* Version parameters (*optional*): list any specific parameter values which you wish to link to this model version) (e.g. `gnabar_hh = 0.44`)

* Location: the url to the model (either inside Collab storage or an external link)

Note: the 'Location' field currently contains basic info such as "VoxelBrain" or "BBP server". This should be updated to contain a URL or Collab path.

Note: without the above info, the entry in the Model Catalog would simply consist of metadata (species, brain region, cell type, author, organization, etc) and would not contain info regarding the implementation of the model itself.

6. Regarding 'Model Collection': If you intend to add examples of individual models inside a 'model collection', then do the following:

a) Add a column named "Link_to_child"

b) Add an entry (row) for the 'model collection'

c) Add entries (rows) for the individual sample models

d) Set the "Link_to_child" parameter of the parent (b) to the row number(s) of the child (c); e.g. "23, 45" (comma separated).... where row #23 and #45 are example models of the parent model collection.

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