## Guidelines for MIHCSME Template

The metadata template is composed according to REMBI (Recommended Metadata for Biological Images) recommendations and ISA (Investigations, Studies and Assays) methodology to ensure template gives a basis for organized structuring of experimental procedures and metadata recording. A large part of the template can be filled in before the start of experimental procedures and can be completed direct after acquisition. The main goal is to record required metadata describing the image data during experimentation procedures and reduce the burden at the end of the projects while making data available to community. In its current state, the template does not include analysis results, but links to the protocols used for the analysis should be provided.

There are several parts in this template as represented in 4 different worksheets in excel. MIHCSME consists of:

**Investigation information**

This worksheet contains an overview of data owners information and details related to investigation.

**Study Information**

This worksheet gives an overview of study related information that is common to all subsequent assays performed, e.g., Species, library, and protocols.

**Assay Information**

This worksheet provides assay related information, describing bio-sample, imaged entities, technology type and link to image data e.g., Screen.

**Assay Conditions**

This worksheet provides the well-level annotations for the experiment of all plates, relating the well name identifiers to treatment conditions annotations.

For each sheet and field there is a brief description/example included in the template. More detailed up to date information and more template examples are provided at

https://gitlab.services.universiteitleiden.nl/cellobs/usertemplates\_mihcsme/

## MIHCSME investigation compared to REMBI recommendations and IDR template

MIHSCME follows REMBI guidelines. It additionally follows the ISA recommendations, which were required to make MIHSCME interoperable with other data sets, and also to make MIHCSME more coherent with other templates that have been developed previously. ISA components and the JERM ontology enable connections to other related assays (e.g., experiments) performed within the same study. In Figure 1, the structure of MIHCSME (A) and REMBI (B) are shown next to each other, and some main differences are summarized in Figure 1C.

Archiving screen e.g. submission to IDR or biostudies require some additional metadata that must be provided. These blocks are outlined in figure 1B, which consists of three main points not covered in MIHSCME. i) Analysis results and scripts (which should be attached with screen data in OMERO), ii) providing licensing details (from your DMP) , and iii) publication details when applicable.



*Figure 1: A) Diagram of MIHCSME structure and its described components. In orange, outlined components contain identifiers connecting related assays (e.g., experiments). B) Diagram of REMBI (Recommended Metadata for Biological Images)* *structure and described components. C) Components of MIHCSME (green outlined in A) visualizing more detailed attributes which are added, different or formalized compared to REMBI. In MIHCSME, assay information contains “assay technology type” and “assay type”, which are consistent terminologies with other metadata recommendations (e.g., MIAME and MAGE-tab) and can be described using existing ontological terms. Image data attributes were changed from single string notation (e.g., XnYnCnZnTn) to single attributes based on users' feedback. With this feedback, additional biosample attributes were included for reproducibility purposes. Specimen descriptions with entities and visualization methods for each channel must be provided in MIHSCME template.*