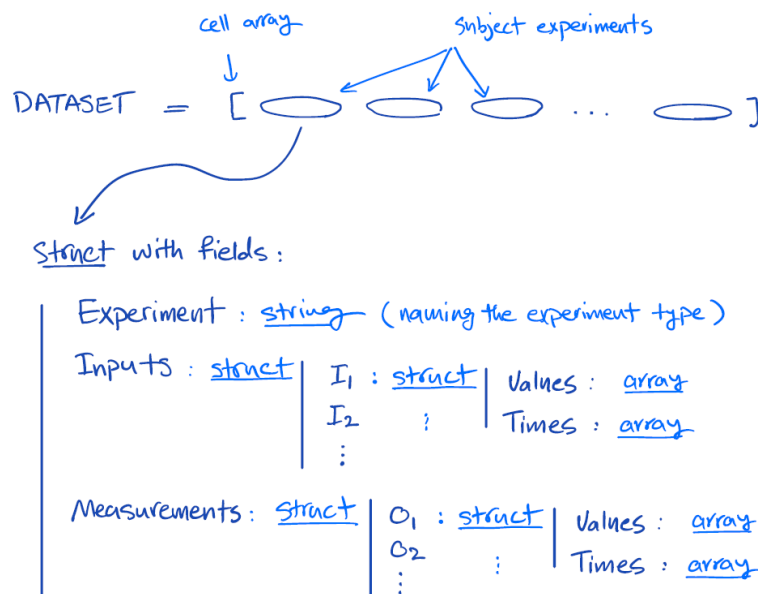


Collective Variational Inference (C-VI)

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C-VI is an inference algorithm that infers the (personalized and population-level) parameters of a physiological model from a low-information and heterogeneous dataset. To work, the algorithm needs two main definitions: (1) the dataset, and (2) the model.

* Defining the dataset: please refer to the file "[prepare_data.m](#)" to learn more about how to prepare the dataset. Here is an overview of the desired data structure:



The data structure is an array of cells. Each cell represents an experiment, so in each cell we have a struct with the following fields:

- (1) Experiment: this is a string indicating experiment type, for example 'HR' for hemorrhage resuscitation. This name is important because it tells the algorithm which type of virtual experiment to run in order to obtain the simulations relevant to this experiment.
- (2) Inputs: this is a struct containing input signals.
- (3) Measurements: this is a struct containing the output signals.

* Defining models: To define a model and its associated experiments for the algorithm, we need to provide the following:

(1) A Matlab function that runs the physiological experiment and gives the results. For an example, in the case of hemorrhage resuscitation, the file must receive the (i) hemorrhage and infusion inputs, and (ii) physiological parameters, and produce the resulting output signals for HCT, CO and MAP. The file name for this Matlab function is important and must be in the following format: "`XX_run_model.m`", where `XX` can be replaced by the experiment type specified in the dataset. In addition, the output of this file must be a structure that has the same output fields as the dataset. For more details, please refer to the example: "`HR_run_model.m`".

(2) A likelihood function that compares the outputs above to the available data and produces a likelihood value. The file name for this Matlab function is important and must be in the following format: "`XX_run_model.m`", where `XX` can be replaced by the experiment type specified in the dataset. For more details, please refer to the example: "`HR_log_likelihood.m`".

In addition, it is possible to define multiple experiment types. For example, one can define a hemorrhage resuscitation experiment using file names "`HR_run_model.m`" and "`HR_log_likelihood.m`" and a drug infusion experiment using file names "`DI_run_model.m`" and "`DI_log_likelihood.m`", and so forth. As long as the associated data are provided in the dataset, the appropriate experiment will be run.

* Running the C-VI algorithm: Having defined the dataset, models, and experiments as described above, it becomes fairly straightforward to run the algorithm. A step-by-step example is provided in the file "`run_collective_vi.m`". After running the algorithm, important variables are saved in the RESULTS folder. These variables include: TTA_MU containing the most-likely personalized models, TTA_SG containing standard deviations representing model uncertainties, PHI_MU containing the center of the generator which is the most typical subject, and PHI_SG, PHI_COV represent the spread of the subject generator.

* Using and analyzing the inference results: This is typically application-specific, but examples are included for the hemorrhage resuscitation example, which can be used as guidelines:

- (1) Plotting parameters and responses: "`view_personalized_parameters.m`" and "`view_personalized_responses.m`".
- (2) Generating virtual subjects: "`view_generation_results.m`".