

# HINT Tutorial

Joshua Lukemire

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## Downloading HINT and the example data

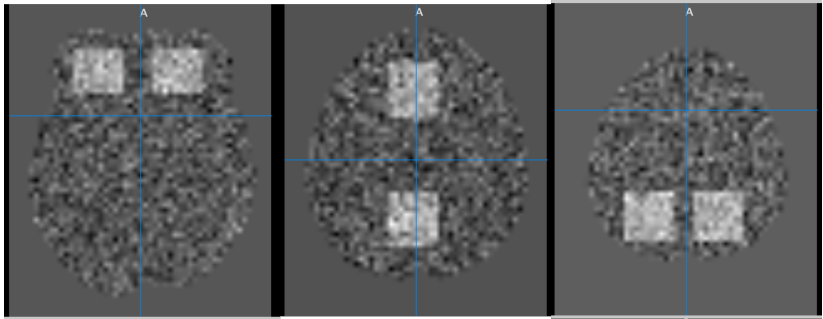
The current version of HINT can be downloaded from github at:  
<https://github.com/Emory-CBIS/HINT>

The tutorial data, as well as these slides, can be downloaded from  
github at:  
<https://github.com/JoshLukemire/HINTTutorial>

## Opening the toolbox

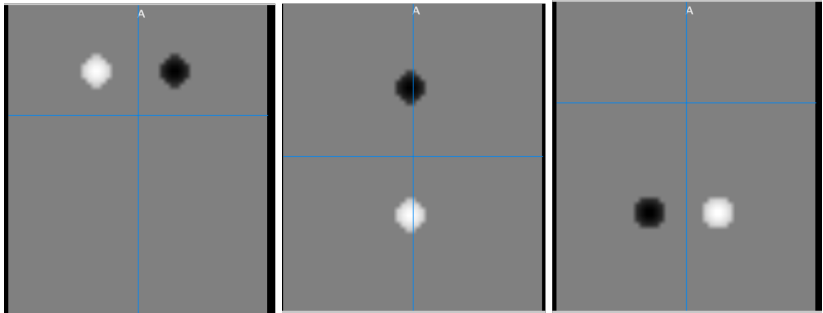
- Navigate to the HINT folder you downloaded from github
- Open the "hint.m" file in Matlab
- Click run to start up the GUI

The example data is just three brain slices. The baseline maps, which are common to all subjects, look like this:



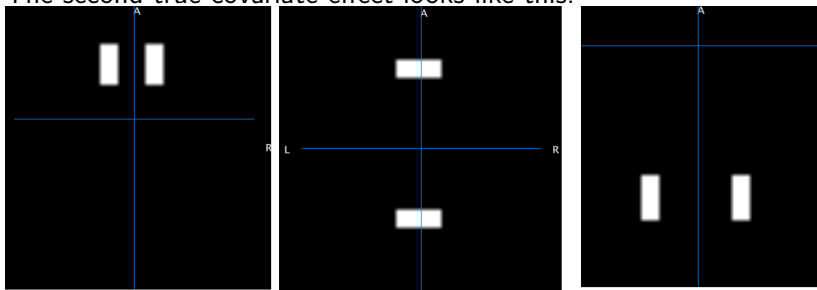
## Covariate Effect 1

The first true covariate effect looks like this:



## Covariate Effect 2

The second true covariate effect looks like this:



# HINT GUI

The HINT GUI consists of three panels, each corresponding to a part of an hc-ICA analysis.

- 1 Prepare Analysis
- 2 Run Analysis
- 3 Visualize



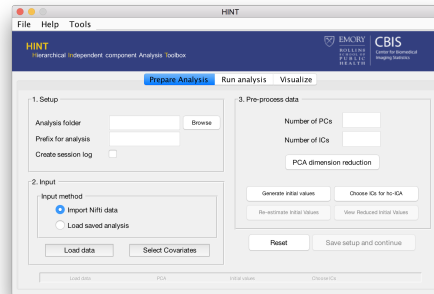
# Setup

- Specify the output folder
- Specify a prefix. All analysis output will start with this prefix.

The screenshot shows a dialog box titled "1. Setup". It contains three fields: "Analysis folder" with a text input field and a "Browse" button to its right; "Prefix for analysis" with a text input field; and "Create session log" with an unchecked checkbox.

## Prepare analysis panel

- Specify analysis folder and prefix
- Load the data and setup the model
- Preprocess the data
- Obtain an initial guess for the EM algorithm
- Remove unwanted independent components from the analysis

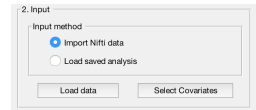


# Loading the data

Two options for loading the data

**Import Nifti data** Start a new analysis by selecting the Nifti files, the mask file, and the covariate file.

**Load saved analysis** Load a previous HINT analysis by selecting a runinfo file (more on this later).



# Loading the data

The image shows a screenshot of a software window titled "Load .nii data". The window has a standard macOS-style title bar with red, yellow, and green window control buttons. The main content area is divided into three sections, each with a label and a form:

- Load subject data**: Contains a "Browse .nii files" button, a text input field, and a question mark icon in a small box.
- Load mask**: Contains a "Browse .nii file" button, a text input field, and a question mark icon in a small box.
- Load covariates**: Contains a "Browse .csv file" button, a text input field, and a question mark icon in a small box.

At the bottom right of the window, there are some small, faint icons that appear to be part of a larger application interface.

# Model Specification

The screenshot shows the 'Model Specification' window with the following components:

- Table:** A table with 4 columns: Subject, x1, x2=a, and an unlabeled column. It contains 8 rows of data for subjects sub1 through sub8.
- Annotations:**
  - Red text 'View the design matrix For each subject' points to the table.
  - Red text 'Change covariates from categorical/continuous' points to the 'Specify Covariates' panel.
  - Red text 'Add and remove covariates from the model' points to the 'Available Covariates' panel.
  - Red text 'Add and remove interactions from the model' points to the 'Interaction List' panel.
- 1. Model Specification:** A panel with two lists: 'Available Covariates' (containing x1, x2) and 'Covariates in Model' (containing x1, x2). It includes 'Add', 'Remove', 'Add All', and 'Remove All' buttons.
- 2. Specify Covariates:** A panel with two boxes: 'Categorical' (containing x2) and 'Continuous' (containing x1). It includes 'Make Continuous' and 'Make Categorical' buttons.
- Add Interaction Terms:** A panel with two dropdown menus (both showing x1) and 'Add interaction' and 'Remove Interaction' buttons.
- Interaction List:** An empty list box for managing interactions.
- Close Window:** A button at the bottom center.

	Subject	x1	x2=a
1	sub1	-1.1279	1
2	sub2	-1.2645	0
3	sub3	-1.7945	0
4	sub4	-0.5057	0
5	sub5	-0.3678	1
6	sub6	1.2812	1
7	sub7	1.8394	0
8	sub8	-0.1949	0

Analyses in HINT require the data to be demeaned and prewhitened. Two things to select:

**Number of PCs** The number of principal components used by the tc-GICA approach to get an initial guess.

**Number of ICs** The number of independent components for the analysis.

3. Pre-process data

Number of PCs

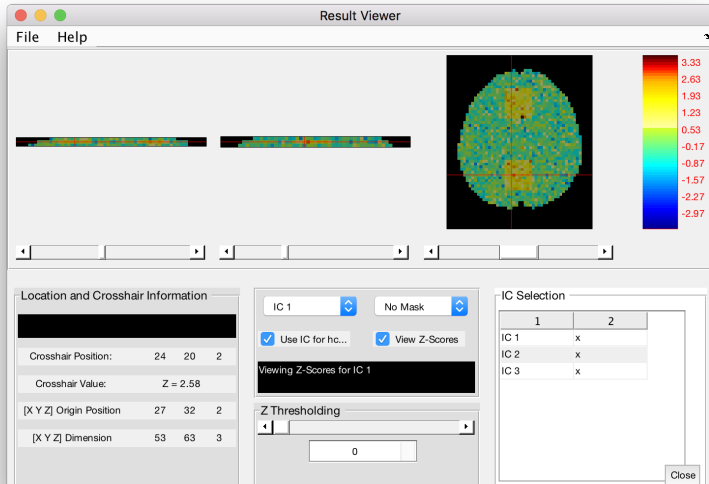
Number of ICs

PCA dimension reduction

Generate initial values    Choose ICs for hc-ICA

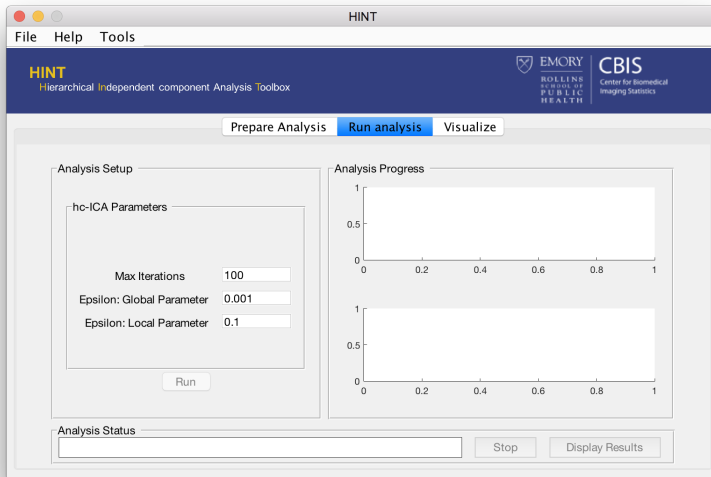
Re-estimate Initial Values    View Reduced Initial Values

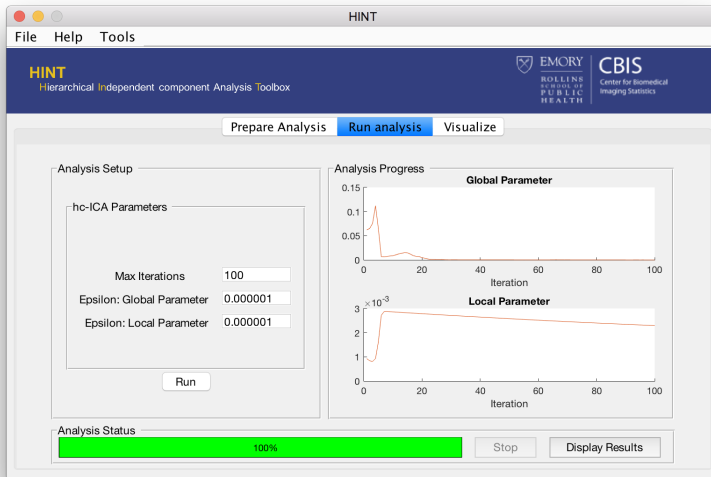
After obtaining an initial guess, you will see the following window:



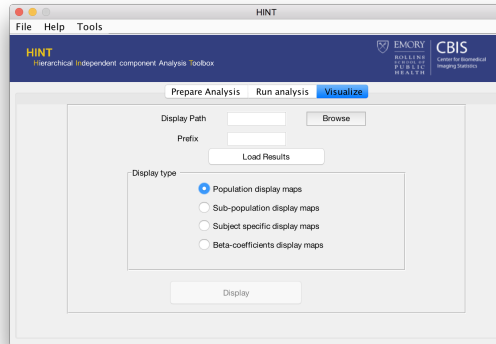
After verifying that the initial guess looks reasonable, click “saved setup and continue to move to the second panel. Clicking this also creates a file called the “runinfo” file in the output directory with all information needed to replicate or change the initial setup.







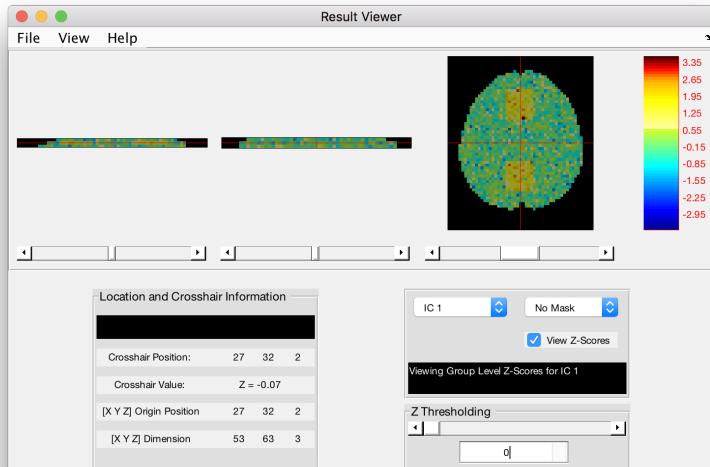
- ① Population Level Results
- ② Sub-population Level Results
- ③ Subject Specific Display Maps
- ④ Beta-coefficient Display Maps



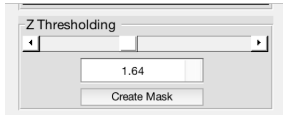
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**Visualization Panel**  
Other Functionality

Study Population-Level Viewer  
Sub-population Viewer  
Single Subject Viewer  
Beta Coefficient Display Map

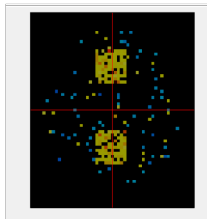
# Population Level Results



# Creating a mask

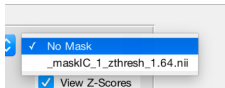


1. Drag the slider to the desired level, or type it into the box.



2. Verify that the map looks correct

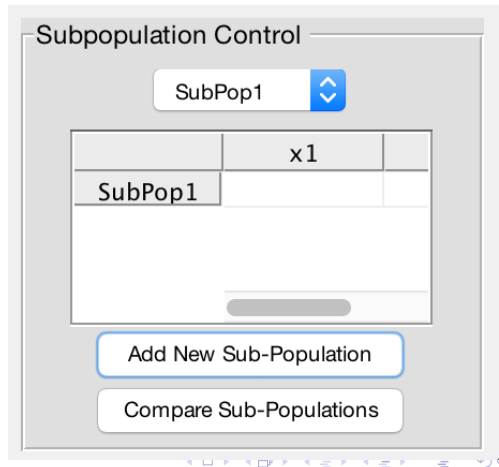
3. Click on Create Mask



The mask will now show up in the mask drop-down menu, and is saved to the output folder.

## Sub-population Viewer

- This window allows you to specify sub-populations of interest by entering their covariate values.
- Two sub-populations can be compared side-by-side by selecting the "compare Sub-populations" button.



# Comparing Sub-populations

1. Enter covariates for (at least) two sub-populations and click "compare Sub-populations"

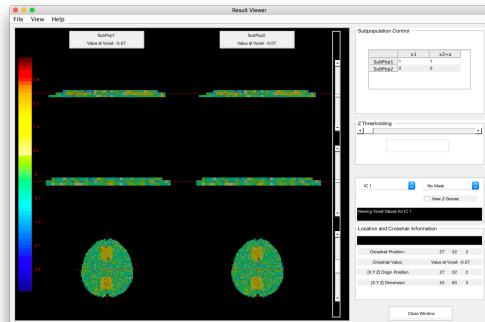
	x1	
SubPop1	1	1
SubPop2	0	0

2. Select the sub-populations you wish to compare

SubPop1	x1
SubPop1	1
SubPop2	0

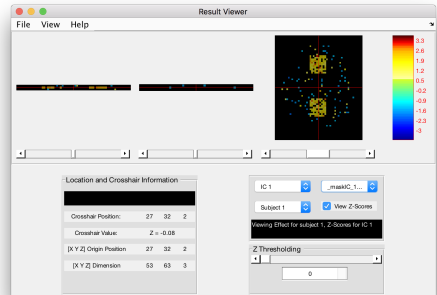
Number of selected sub-populations: 2

Compare Selected Sub-Populations



## Single Subject Viewer

- This window allows you to view the IC estimates for individual subjects.
- You can also apply any mask created using the population-level viewer to the subject level data.

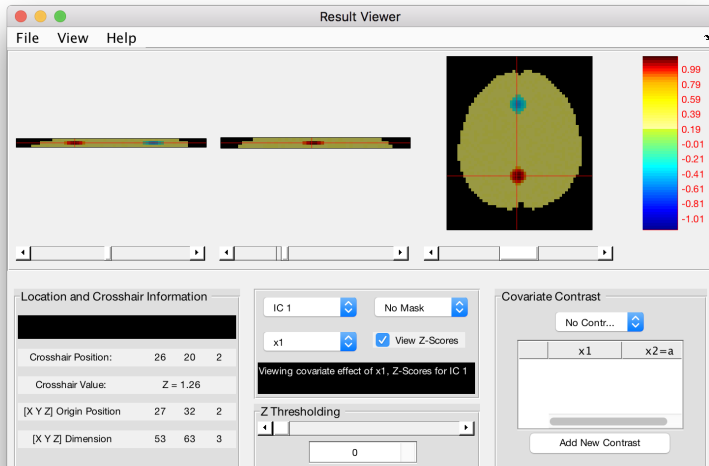




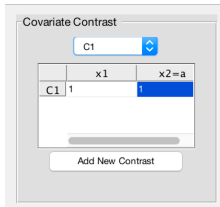
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**Beta Coefficient Display Map**

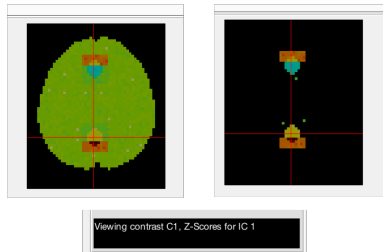
# Beta Coefficient Display



## Specifying Contrasts



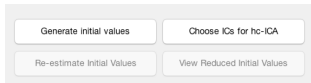
Select "Add New Contrast"  
and then select the contrast  
from the drop-down menu



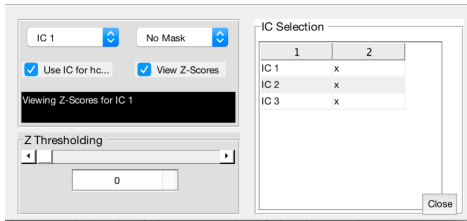
## Loading a saved analysis

Instead of re-starting everything, you can load a previous runinfo file using the "load a saved analysis" option and navigating to the runinfo file. Everything will auto-fill. However, if you want to re-run the initial guess, you will also have to re-run the preprocessing step. This is for memory reasons.

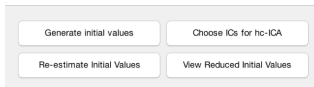
# Removing ICs from the analysis



1. Click on “Choose ICs for hc-ICA”



2. Find the ICs you are not interested in and uncheck the “use IC for hc-ica” box



3. Re-estimate the initial guess

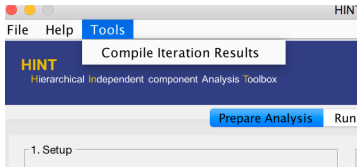
## Running the EM algorithm from a script

The matlab function `estimateFromSavedData()` allows you to run the EM algorithm from a script instead of the GUI. This is used if you want to submit to a cluster instead of running the algorithm on your machine.

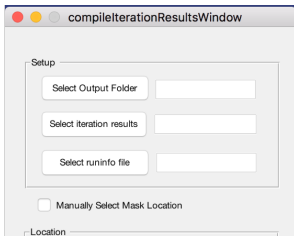
```
2  
3 - estimateFromSavedData('_runinfo.mat',... % location/name of the runinfo file  
4   'approx',... % Type of algorithm to run (always approx)  
5   100,... % Maximum number of iterations  
6   0.001,... % stopping crit: change in all non-beta terms  
7   0.1) % stopping crit: change in beta terms
```

## Compiling iteration results

If you terminate the EM algorithm early, you may want to use the results from whatever the final completed iteration was. To do this:



1. Select compile iteration results from the Tools menu



2. Fill out the location where you want the results saved, The location of the iteration results, and the location of the Runinfo file. Then click "compile results"