

# HINT Tutorial

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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

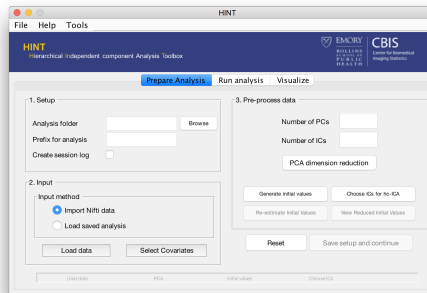
# HINT GUI

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

## 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

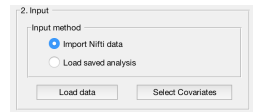


## Loading the data

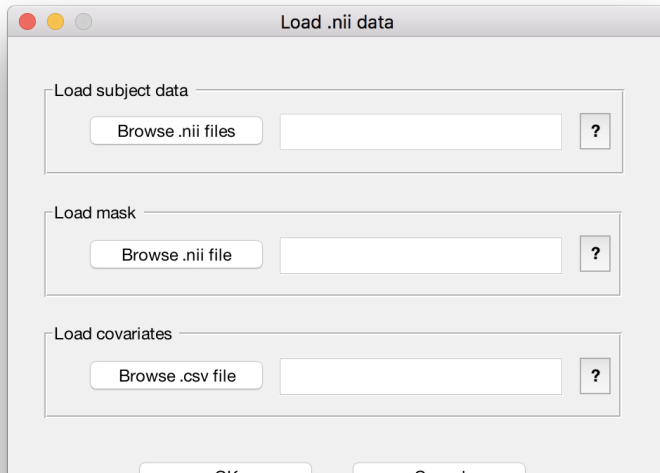
Two options for loading the data

**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





# Model Specification

The screenshot shows the 'Model Specification' dialog box. It contains a table of data, two panels for specifying covariates, and an interaction terms section. Red annotations highlight key features: 'View the design matrix For each subject' points to the data table; 'Change covariates from categorical/continuous' points to the 'Specify Covariates' section; 'Add and remove covariates from the model' points to the 'Available Covariates' list; and 'Add and remove interactions from the model' points to the 'Interaction List'.

	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

1. Model Specification

Available Covariates: x1, x2

Covariates in Model: x1, x2

2. Specify Covariates

Categorical: x2

Continuous: x1

Make Continuous: [button]

Make Categorical: [button]

Close Window: [button]

Add Interaction Terms

x1 [dropdown] x1 [dropdown]

Add interaction: [button]

Remove Interaction: [button]

Interaction List

Add and remove interactions from the model: [text area]

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

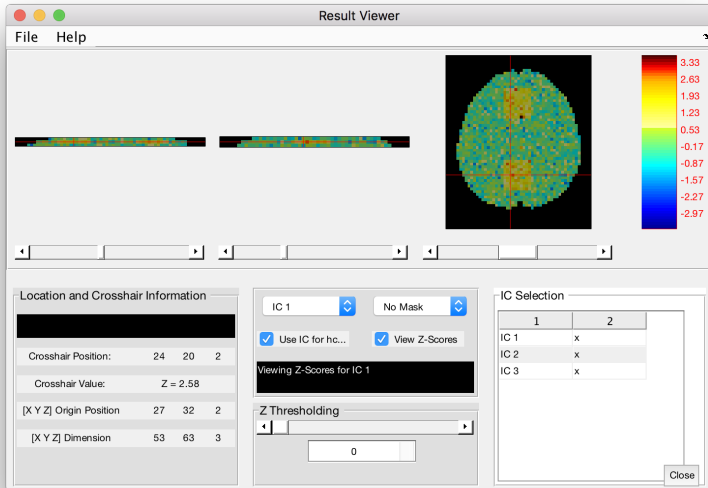
Number of ICs

PCA dimension reduction

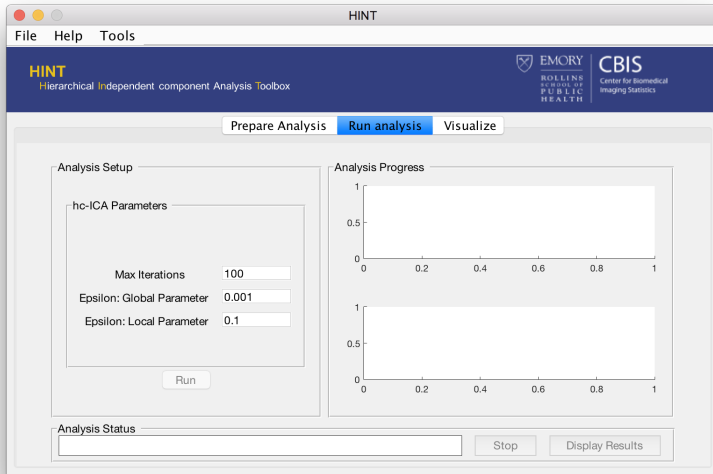
Generate initial values Choose ICs for hc-ICA

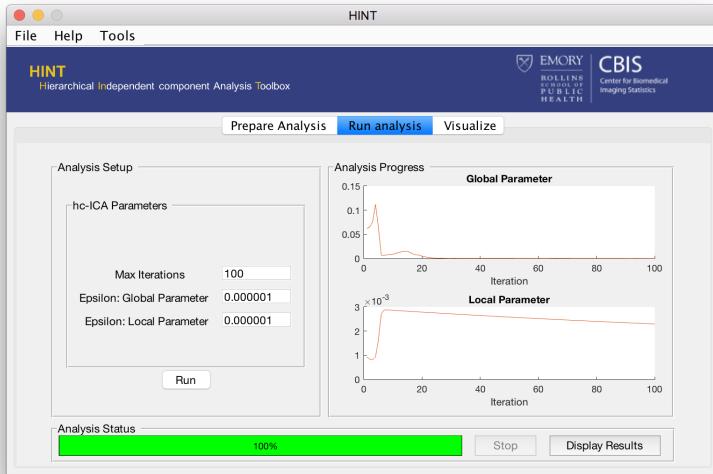
Re-estimate Initial Values View Reduced Initial Values

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

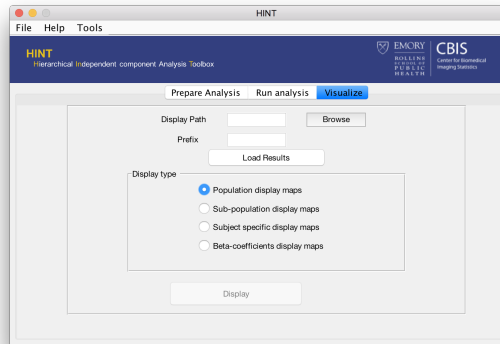


After verifying that the initial guess looks reasonable, click “saved setup and continue to move to the second panel. Clicking this also creates a file called the “runinfo” file in the output directory with all information needed to replicate or change the initial setup.

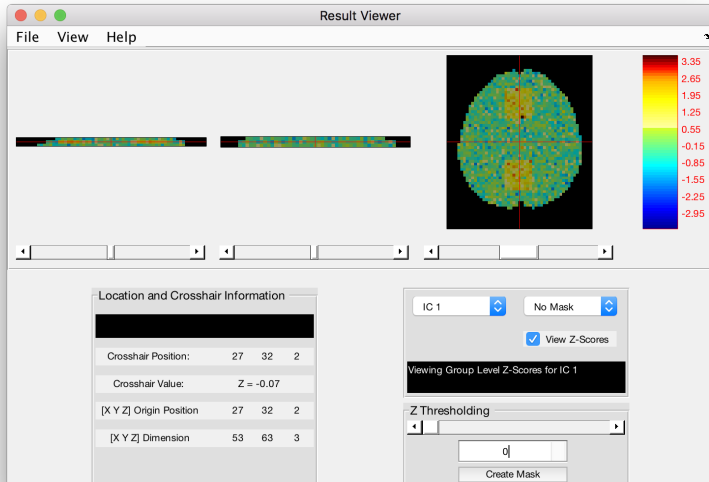




- ① Population Level Results
- ② Sub-population Level Results
- ③ Subject Specific Display Maps
- ④ Beta-coefficient Display Maps

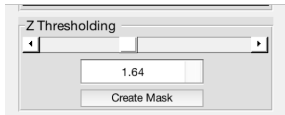


# Population Level Results

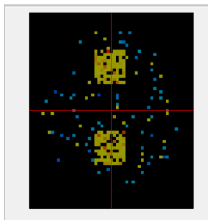




# Creating a mask

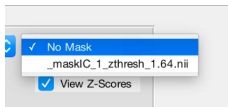


1. Drag the slider to the desired level, or type it into the box.



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.

Subpopulation Control

SubPop1

	x1	
SubPop1		

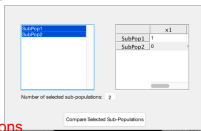
Add New Sub-Population

Compare Sub-Populations

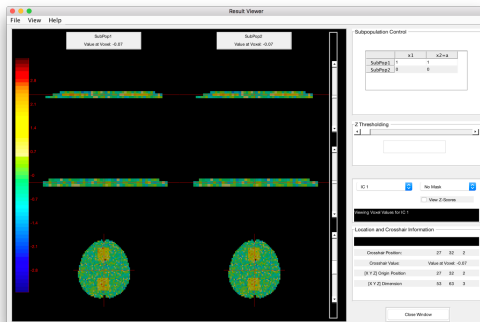
# Comparing Sub-populations

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

	x1	
SubPop1	1	1
SubPop2	0	0

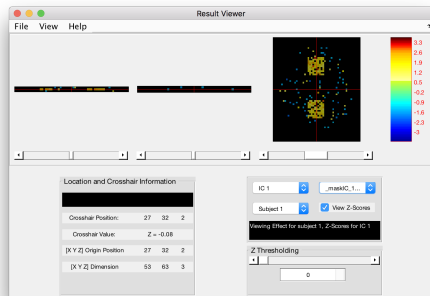


2. Select the  
 sub-populations  
 you wish to  
 compare

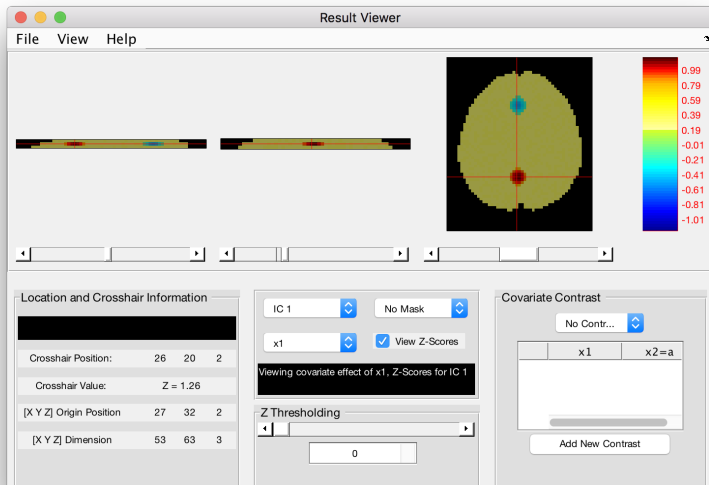


## Single Subject Viewer

- 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.



# Beta Coefficient Display



# Specifying Contrasts

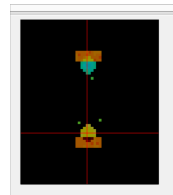
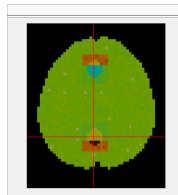
Covariate Contrast

C1

	x1	x2=a
C1	1	1

Add New Contrast

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



Viewing contrast C1, Z-Scores for IC 1

## 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

XXX



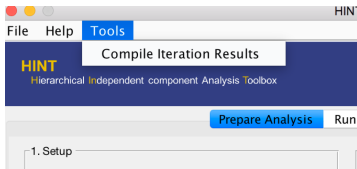
## Running the EM algorithm from a script

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.

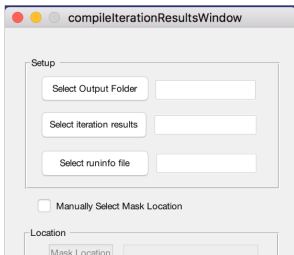
```
2  
3 - estimateFromSavedData('_runinfo.mat',... % location/name of the runinfo file  
4     'approx',... % Type of algorithm to run (always approx)  
5     100,... % Maximum number of iterations  
6     0.001,... % stopping crit: change in all non-beta terms  
7     0.1) % stopping crit: change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