

# Introductory Course on Spectral Clustering Assignment

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As we have discussed in the final lecture, you have the option of using the provided data and Matlab files to carry out the assignment for the course. Provided in the “Assignment.zip” file are:

1. The directory **Local\_Hopkins155\_slim** which contains all the data. For information it is the Hopkins155 motion segmentation dataset from <http://www.vision.jhu.edu/data/hopkins155/>
2. The main evaluation file **fullDatabaseRun.m** which you should use for doing your assignment
3. Other supporting files and directories

When you unzip everything into a directory and run **fullDatabaseRun.m** from Matlab, the code will go through every directory in **Local\_Hopkins155\_slim**, and calculate 4 different affinity matrices for each sequence. I have included 156 sequences in total.

The main calculation in **fullDatabaseRun.m** is done between lines 64-100. The 4 different affinities matrices are A1, A2, A3 and A4.

You will need to build your own spectral clustering code and insert it some place after line 82. There is also an evaluation function call to **classification\_error.m**. This will take as input the ground truth segmentation labels in **s** and the ones you have recovered (e.g **I**) and produce a error percentage for each. If the error is 0 then the segmentation is correct.

You may look into any of the issues we have discussed in the final lecture. For example, affinity combination, parameter search, kernel choices etc. For kernel choices you will have to go into the code for each method and change the kernel function. It is not that hard. The 4 different methods are **Affinity\_TK**, **Affinity\_LCV**, **Affinity\_SCC** and **Affinity\_SLBF**. In general, unless you are experimenting with different kernels you should not need to change anything outside **fullDatabaseRun.m**.

You may also decide to create your own method that generates affinity matrices. But be warned! this is not trivial. As this is motion trajectory data you will need to use multi-way affinities. We would not recommend to explore this option and instead use the provided methods.