**HWI Image Classification System**

The scripts and other files are installed in a base directory. On my laptop, the base directory is

BASEDIR=C:\Users\smith\Documents\Becky\HawkWatch\

**Restarting hwi\_sequence.py from Checkpoint**

The morphology program hwi\_sequence.py can take a long time to run for directories with a large number of images. If the run is interrupted before it completes, you can restart the program from the last checkpoint. The output is checkpointed to the directory $BASEDIR\scripts\checkpoint after each group of 600 images. Checkpoint files are called bird\_sequence.chkpt-xxx where x is the number of sequences processed.

To restart the run from the last checkpoint:

* Copy the last checkpoint file to the image directory that was being processed.
* Rename the checkpoint to hwi\_sequence\_out.csv.
* Open the checkpoint and get the last image number. You need to know the last image # plus 1.
* From the scripts directory run,

python hwi\_sequence.py -n last\_imagenum+1 -d image\_directory

* The program will restart from the image number you give it and you’ll see a question:

Output file exists. (a=append, o=overwrite, 9=exit):

Type ‘a’ to append, then you’ll see this message:

Appending to file: $image\_directory\hwi\_sequence\_out.csv

* Let the program run for a while and watch the checkpoint directory for the next checkpoint to be written into bird\_sequence.chkpt-200. This file will contain all the records from the restored checkpoint plus another 600. Visually inspect the file to make sure the image numbers are sequential around the image number where the restore started. This is to give you a warm fuzzy about the restore working properly.

**Clearing the Checkpoint Directory**

Clearing the checkpoint directory is not done automatically. You should delete the contents of the directory after a big run to free up disk space. This is left to user discretion since only you know when you no longer need the checkpoint files around.