Instructions: Cortisol_PreProcessing.py

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Step 1
Download the appropriate files from GitHub

- Go to:

  https://raw.github.com/HappyPenguin/MRIMPACT_CODE/master/CORTISOL/Cortisol_PreProcessing.py
- Right click and save wherever you'd like (I'd suggest a dedicated scripts directory).

- Go to:

  https://raw.github.com/HappyPenguin/GENERAL_CODE/master/MyCoolFunctions.py
- Right click and save as MyCoolFunctions.py in the same folder as your copy of Cortisol_PreProcessing.py.

- Go to:

  https://raw.github.com/HappyPenguin/MRIMPACT_CODE/master/CORTISOL/Cortisol_SelectionCriteria.py
- Right click and save in your Cortisol analysis directory. For example that might be /home/kw401/CORTISOL/

Step 2a
Personalise your Selection Criteria file

- Make a copy of the Cortisol_SelectionCriteria.py file (in eg: SCRIPTS) and save wherever you want your output.

- Now open up this file (the new copy you just made) and edit it with all the right options.

- These are the instructions you'll see at the top of the file.

```
'''
Please fill in the following questions with the words True or False
True always means yes, and False always means no.
Please make sure to capitalize True and False

For example:
    need_2_am = True
    require_whole_day = False
    excl_wakemin_gt_10 = True

If you choose True for either of the questions about filtering according
to what's in an external file, please make sure that you have access to
that file, and that it contains the information you need. If it doesn't you'll
have to update the path and file to fit your needs.

Remember to keep these file names between ' ' quotes.

Note that you can enter ' ' as a filename if you don't want to use that
particular filter. For example, if you want to *exclude* a couple of subjects
but don't have a filelist of subjects to *include* then you can set:

    filter_subs = True
    include_subs_list = ' '
    exclude_subs_list = '/work/imagingA/mrimpact/workspaces/CORTISOL/exclude_subjects.txt'

'''
```

Step 2b
Personalise your Selection Criteria file

```python
# Do you require all cortisol values to be < 3?
cort_lt_3 = True

# Do you require the comment for each cortisol value to be '1000'
# (signifiying there isn't a problem, although not necessarily
# signifying that there _is_ a problem)
comment_1000 = True

# Do you want to exclude waking measures that were collected more than
# 10 minutes after waking?
minawake_lt10 = True

# Do you require a whole day's worth of data to consider it in the average?
require_whole_day = True

# Do you require two am values on the same day to calculate that day's maximum am value?
need_2_am = False

# Do you wish to exclude the CAR value if it is negative?
# (implying that this participant does not meet your model of cortisol
# awakening response and therefore you can't accurately interpret it?)
excl_neg_CAR = False

#---------------------------------------------------------------------------
# Would you like to exclude participants who are taking medication on
# this list:
excl_med = True
medlist_file = '/work/imagingA/mrimpact/workspaces/CORTISOL/Cortisol_MedicationList.txt'
medlist_special_cases_file =
'/work/imagingA/mrimpact/workspaces/CORTISOL/Cortisol_ExcludeMedications_SpecialCases.txt'

# Would you like to filter the list according to another list of subjects?
# (for example, a list of subIDs representing participants who have usable
# mri data)
filter_subs = False
include_subs_list = '/work/imagingA/mrimpact/workspaces/CORTISOL/MRIMPACT_subs.txt'
exclude_subs_list = ' '
```

Step 3
Run your code

Make sure you have all the files you need:

- data file: tab delineated version of the SPSS file
- selection criteria file: the file you just edited in step 2
- any filter files that you mentioned in the selection criteria file (eg: filter by sublist or medications)

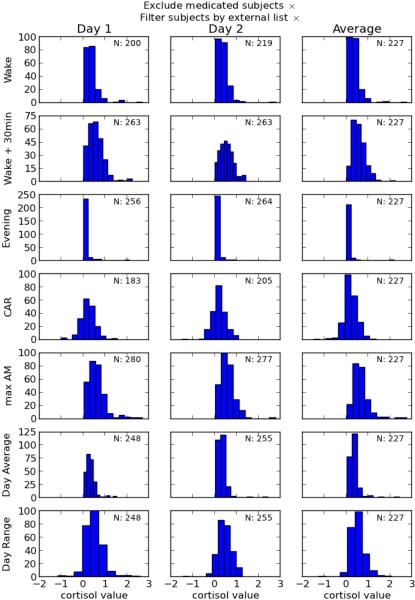Then just decide on your ouput name and you're ready to go!

If you forget you can see the usage by just typing the file name of Cortiosol_PreProcesing.py (with its path) with nothing else after it:

```
Check your input files
USAGE: Cortisol_PreProcessing.py  <data_filename> <selection_criteria_filename> <output_filename>

        <data_filename> is a TAB delineated file containing the cortisol data
        <selection_criteria_filename> is a python file that contains the answers (True or False) to selection criteria
        <output_filename> is, as it says, the TAB delineated output file
        For example:
                ./Cortisol_Preprocessing.py IMPACT_Cortisol_data.txt selection_criteria.py cortisol_output_April2013.txt
```

Output

You'll have two outputs: a tab delimited file with all the data and this figure

DISTRIBUTIONS OF CORTISOL MEASURES
USING THESE FILTERS:
Cort measures less than 3 ✓ Comment must be "1000" ✓
Mins awake less than 10 ✓   Require whole day's worth of data ✓
Require two measures in the morning to calc max ✕
Exclude medicated subjects ✕
Filter subjects by external list ✕