Steps for running Modmap at the CfA (updated July 13, 2016)

In the following computer output is in small type, prompts end with ":" or ">", comments are in **boldface** (with command names in quotes), and that which the types is in *italics*:

The following should bring up Modmap:
/data/saku10/software/modmap/bin/modmap

Following which you should see this start-up text:

```
=========================================
MODMAP running on keiko
Tue Oct 5 15:48:24 2010
Version 1.0 Danny Steeghs
=========================================
modmap>
Commands:
C ... Conventional Doppler mapping
V ... Setup velocity grid/rest
F ... Fake data nw: 100 nphi: 80
D ... Load molly Data
O ... Generate optimal starting image
P ... Plot fit
R ... Annotate plots with lobe
M ... MEM iterations
S ... Save maps/data to disk file
L ... Load maps from disk file
Q ... Quit
```

To load a molly file (.mol file) into modmap we use the command "d" and enter the filename. Generally the file should consist of a set of spectra trimmed to capture the line of interest (and including a reasonable amount of continuum on each side).

```
modmap> d
MOLLY file to load ? [empty]test.mol
Rest wavelength:[0= 6562.76]
6562.76
MOLLY File opened : test.mol
Error reading MOLLY headers

43  spectra read.

DEBUG: 36.461834604179366 251 0. 0. 6529.491

Data is uniform in velocity

Covering  6431.364  - 6629.919  Angstrom

Data covers phases  0.73045653  - 1.5451138

*** Warning, there were  1320  ( 29.803568 %)  negative pixels!

Readmolly done

Found  103  pixels between - 1868.9  and  1868.9 km/s

Velocity dispersion of data : 36.3573  km/s

Velocity resolution of tomogram : 34.32323

FWHM of local profile : 60.

Filled array OBSN with real data... 103 x 43
Filled array SIGMA with real errors...oc
```

The command “v” is used to setup the parameters of the system. If unknown, use your best guess for γ (radial velocity); you can check this using different values in modmap. (250 pixels at 0.8angstroms/pixel; better to oversample)

```
modmap> v
Rest wavelength (A) : 6562.75788                    The rest wavelength of the feature to be used
Gamma velocity : -44                                          The system's radial velocity
Number of pixels in velocity grid : 100
Maximum velocity in tomogram: 2000
FWHM of local line profile: 100
Velocity grid set to  100  x  100  pixels
Spanning +/- 2000.  @  40.40404  km/s/pixel
Origin corresponds to  6562.758 A +  -44.  km/s
```

Next, we use the command “o” to generate the optimal starting image:

```
modmap> o
Performing optical scaling of starting image
============== op0 === 5 0.
pregauss: 50000 0.00008499622
  scale factor =  0.15342808
```

This optimizes Chi squared starting on the mean map (sets pixel level).

The command “m” gets us into 'MEMSYS', to fit the data.

```
modmap> m
Ready for MEMSYS iterations
Velocity grid = 100  x  100
Data grid = 103  x  43
Using  5  images to map modulations
image pixels= 50000  data values= 4429
MEMCORE - configuring MEM data and image buffers.
Image dimensions (X,Y,Z)= 50000 1 1
 Data dimension = 4429
9  images in 9  files.
1 50001 100001 150001 200001 250001 -9999999 -9999999 -9999999 -9999999 -999999
9 -9999999 -9999999 -9999999 -9999999 -9999999 -9999999 400001 300001 350001
8  data vectors in 8  files.
450001 454430 458859 463288 467717 472146 476575 481004 -9999999 -9999999 -9999
999 -9999999 -9999999 -9999999 -9999999 -9999999 -9999999 -9999999 -9999999 -999
9999
 Image pixels: 450000  = 92.700935  %
  Data values: 35432  = 7.2990656  %
```

```
Total storage: 485432  = 17.978964  % of buffer: 2700000
Divisor for weights: 0.9
  values: 0.0001 0.15342808
defaults: 0.001 0.16342808
 weights: 0.5 1.
============== op0 === 5 0.
Chi^2/ 4429  =  24.33169
============== fixdef ===
------------------------------------------------
 Iter= 0     CPU= 0.  CPU/Iter= 0.
 Elapsed realtime= 0.
 Mode= 1030   Level= 20
 Ndat= 4429    Nimg= 50000
 SumF= 0.    Caim= 1.  Chi^2/N= 24.33169
 Sold= 0.    Cold= 0.
 Snew= 0.    Cnew= 0.
  Alp= 0.  -2AlpS= -0.
 Stru= -0.371579    Nfit= 0.
 Rmax= 0.2    Step= 0.     TEST= 0.
Take  1  iterations on each GO.
Update default every  -1  iterations.
MEMITER >
```

The subroutine “c” uses iterations to reduce the value of chi squared to try and find a good fit. It is extremely unlikely that system will ever get a reduced Chi square of 1; if the initial Chi square is say 30 (in the example above it is 24.33), start by aiming for 20 - if it looks like it is improving, steadily reduce to 10 and so on. To set final Chi square value to aim for, use “c”. This will also ask for an initial guess and number of iterations:

```
MEMITER > c
== Auto C-aim stepper === test version
Enter final C-aim
8
Enter test value to go ahead with
2.0
Enter number of iterations per step
2
Enter number of steps to reach final CAIM
2
New C-aim ;  8. 1
Iter= 14     CPU= 89.01747  CPU/Iter= 6.358391
```

```
 Elapsed realtime= 88.9855
 Mode= 1030   Level= 20
 Ndat= 4429    Nimg= 50000
 SumF= 996.9127    Caim= 8.  Chi^2/N= 8.5955305
 Sold= -0.037704766    Cold= 8.700225
 Snew= -0.06027075    Cnew= 8.595371
  Alp= 0.0025477018  -2AlpS= 0.0003071038
 Stru= -0.371579    Nfit= 0.00094667246
 Rmax= 0.2    Step= 0.2     TEST= 0.21966195
Take  5  iterations on each GO.
Update default every  -1  iterations.
MEMITER >
-------------------------------------------------
```

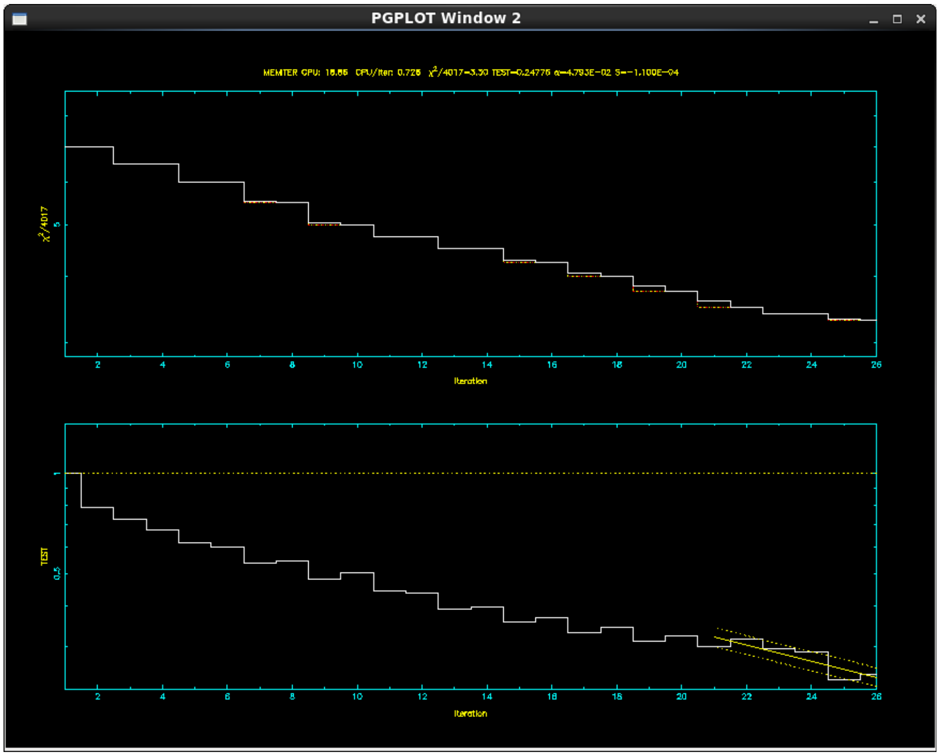
“g” does one iteration. You can also use “i 5”, for example, to set "g" do (5) iterations. The “g” command will then start the iterations.

“p” shows the Chi square convergence; lower values should be approached in a straight line; if values go up and down sporadically, you are trying for too low a Chi square value. In this case, you will have to restart modmap and stay within a more reasonable limit. Once you have reached the desired reduced Chi square, you will still need to iterate to minimize Maximum Entropy.

When plotting, modmap will ask you which plotting device you would like to use. To open the graph in a window, choose /xs (xserve). To open multiple windows simultaneously, use successive numbers followed by /xs, e.g. 1/xs, 2/xs etc, each new number opening a new window. To save a plot, type the filename followed by /ps, e.g. file.ps/ps.

```
MEMITER > p
Iterations: 14 1 14
Graphics device/type (? to see list, default /NULL): 1/xs
-------------------------------------------------
 Iter= 14     CPU= 89.01747  CPU/Iter= 6.358391
 Elapsed realtime= 88.9855
 Mode= 1030   Level= 20
 Ndat= 4429    Nimg= 50000
 SumF= 996.9127    Caim= 8.  Chi^2/N= 8.5955305
 Sold= -0.037704766    Cold= 8.700225
 Snew= -0.06027075    Cnew= 8.595371
  Alp= 0.0025477018  -2AlpS= 0.0003071038
 Stru= -0.371579    Nfit= 0.00094667246
 Rmax= 0.2    Step= 0.2     TEST= 0.21966195
Take  5  iterations on each GO.
```

```
Update default every  -1  iterations.p
```

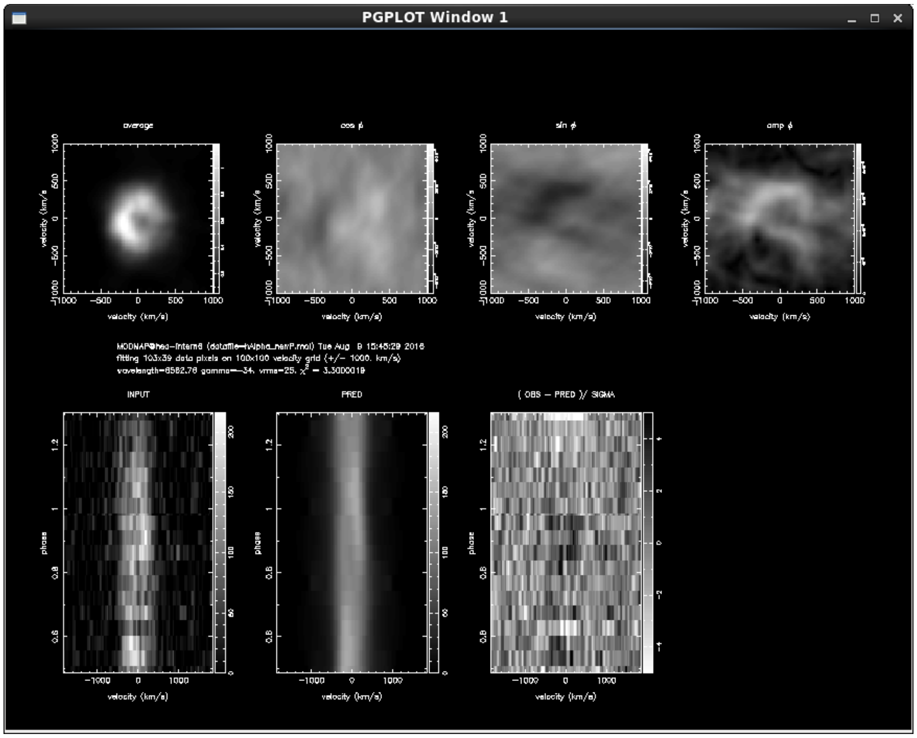


The Chi squared convergence. The values should steadily decrease. If the values go up and down sporadically, you have decreased Chi squared too low and must restart.

The command"f" plots the modulated maps

```
MEMITER > f
=============== plotfit ===
=============== op0 === 5 0.
Graphics device/type (? to see list, default /NULL): /xs
--------------------------------------------------
 Iter= 14     CPU= 89.01747  CPU/Iter= 6.358391
 Elapsed realtime= 88.9855
 Mode= 1030   Level= 20
 Ndat= 4429    Nimg= 50000
 SumF= 996.9127    Caim= 8.  Chi^2/N= 8.5955305
 Sold= -0.037704766    Cold= 8.700225
 Snew= -0.06027075    Cnew= 8.595371
  Alp= 0.0025477018  -2AlpS= 0.0003071038
 Stru= -0.371579    Nfit= 0.00094667246
 Rmax= 0.2    Step= 0.2     TEST= 0.21966195
Take  5  iterations on each GO.
```

```
Update default every  -1  iterations.
```


PGPLOT Window 1
average
cos ϕ
sin ϕ
amp ϕ
velocity (km/s)
−1000 −500 0 500 1000
MODMAP@hea-Interns (datafile=hAlpha_newP.mol) Tue Aug 9 15:45:29 2016
fitting 103x39 data pixels on 100x100 velocity grid (+/− 1000. km/s)
wavelength=6562.76 gamma=−34. vrms=25. χ² = 3.3000018
INPUT
PRED
(OBS − PRED)/ SIGMA
phase
0.6
0.8
1
1.2
50
100
150
200
−1000 0 1000

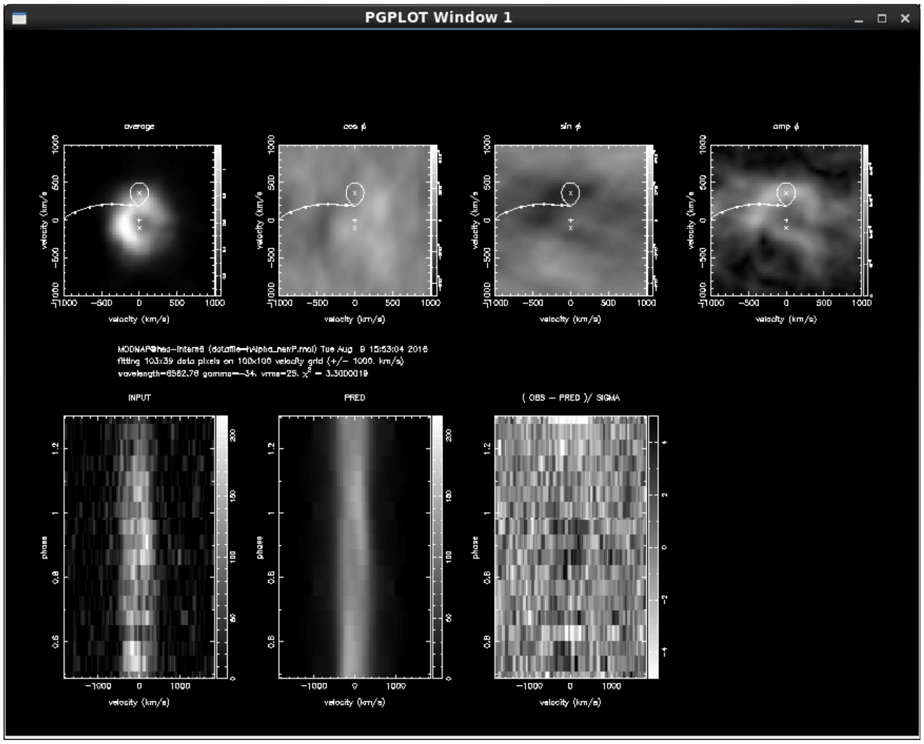
The modulated maps. The predicted trail should match the input trail. If the tomograms (in the top row) become too splotchy/spotty, you may be overfitting the data. In this case, you have decreased Chi squared too low and must restart.

To plot the modulated maps with the companion star, etc plotted over them, you must first get out of memitter with q then run r and give the K1 and K2 values. Then go back into memitter and run f.

Alternatively, exit memitter with q, give K1 and K2 values with r, and then plot with p before resuming memitter.

```
MEMITER > q
 MEMITER retired.
 ============== op0 === 5 0.
 modmap> r
 Roche lobe will be plotted
 Enter K1,K2 (km/s)
93,360
 modmap> m
 Ready for MEMSYS iterations
 Velocity grid = 100  x  100
 Data grid = 79  x  39
 Using  5  images to map modulations
 image pixels= 50000  data values= 3081
 MEMCORE - previous configuration retained.
```

```
Divisor for weights: 0.9
  values: 0.0000068954596 0.24392265
defaults: 0.00001629452 0.11646019
 weights: 0.5 1.
=============== op0 === 5 0.
Chi^2/ 3081  =  2.926773
=============== fixdef ===
-------------------------------------------------
 Iter= 6     CPU= 0.  CPU/Iter= 0.
 Elapsed realtime= 0.
 Mode= 1030   Level= 20
 Ndat= 3081    Nimg= 50000
 SumF= 117.30066    Caim= 2.9  Chi^2/N= 2.926773
 Sold= -0.0015340447    Cold= 2.9568884
 Snew= -0.029639808    Cnew= 2.926739
  Alp= 0.004909638  -2AlpS= 0.00029104145
 Stru= -0.73224443    Nfit= 0.003595055
 Rmax= 0.2    Step= 0.20000002     TEST= 0.2207666
Take  2  iterations on each GO.
Update default every  -1  iterations.
MEMITER > f
=============== plotfit ===
=============== op0 === 5 0.
Graphics device/type (? to see list, default /NULL): 3/xs
-------------------------------------------------
 Iter= 6     CPU= 0.  CPU/Iter= 0.
 Elapsed realtime= 0.
 Mode= 1030   Level= 20
 Ndat= 3081    Nimg= 50000
 SumF= 117.30066    Caim= 2.9  Chi^2/N= 2.926773
 Sold= -0.0015340447    Cold= 2.9568884
 Snew= -0.029639808    Cnew= 2.926739
  Alp= 0.004909638  -2AlpS= 0.00029104145
 Stru= -0.73224443    Nfit= 0.003595055
 Rmax= 0.2    Step= 0.20000002     TEST= 0.2207666
Take  2  iterations on each GO.
Update default every  -1  iterations.
MEMITER > q
```



```
MODMAP@hea-intern6 (datafile=hAlpha_narrP.mol) Tue Aug  9 15:53:04 2016
fitting 103x39 data pixels on 100x100 velocity grid (+/- 1000. km/s)
wavelength=6562.76 gamma=-34. vrms=25. χ² = 3.3000019
```

The modulated maps with the Roche lobe of the companion star, the center of mass of the companion star, system, and compact object, and the accretion stream plotted over them.

To save the data produced, use the command "s". This will ask you whether you wish to save the data or the maps. Choose using LOWER CASE 'd' or 'm' to save the data or maps respectively, then enter the filename to save:

```
modmap> s
Dump (D)ata or (M)aps?
d
=============== dumpdata ===
File to SAVE data in : file.data
data dumped...
type name.ps/ps to save images onto a file name.ps


modmap> s
Dump (D)ata or (M)aps?
m
=============== dumpdata ===
File to SAVE data in : file.maps
data dumped...
type name.ps/ps to save images onto a file name.ps
```

Plotresults.

The directory /data/saku10/charith.dir/plotresults/bin/ has several different versions of plotresults in order to produce publishable plots once you have generate file.data and file.maps using MODMAP. So for example:

(black and white)

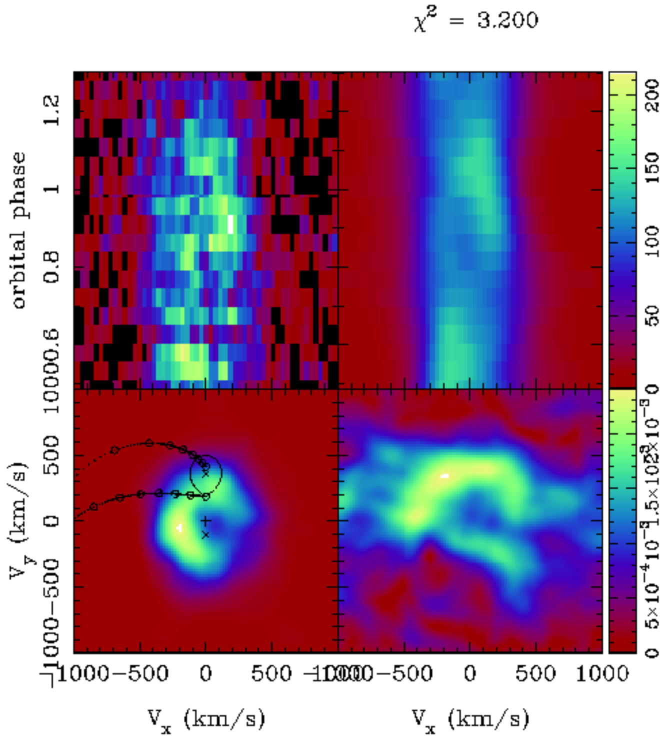
```
/data/saku10/Peris.dir/plotresults/bin/plotresults file.data file.maps savefilename.ps/cps K1 K2
```

or

(color)

```
/data/saku10/Peris.dir/plotresults/bin/plot4maps_1000 file.data file.maps savefilename.ps/cps K1 K2
```

NOTE: K1 and K2 must be real (decimal) numbers, not integers. Ex: 2.0, not 2



An example of the output of plot4maps_1000: Four panels showing the real trailed spectra, predicted trailed spectra, time-averaged tomogram, and modulation tomogram.