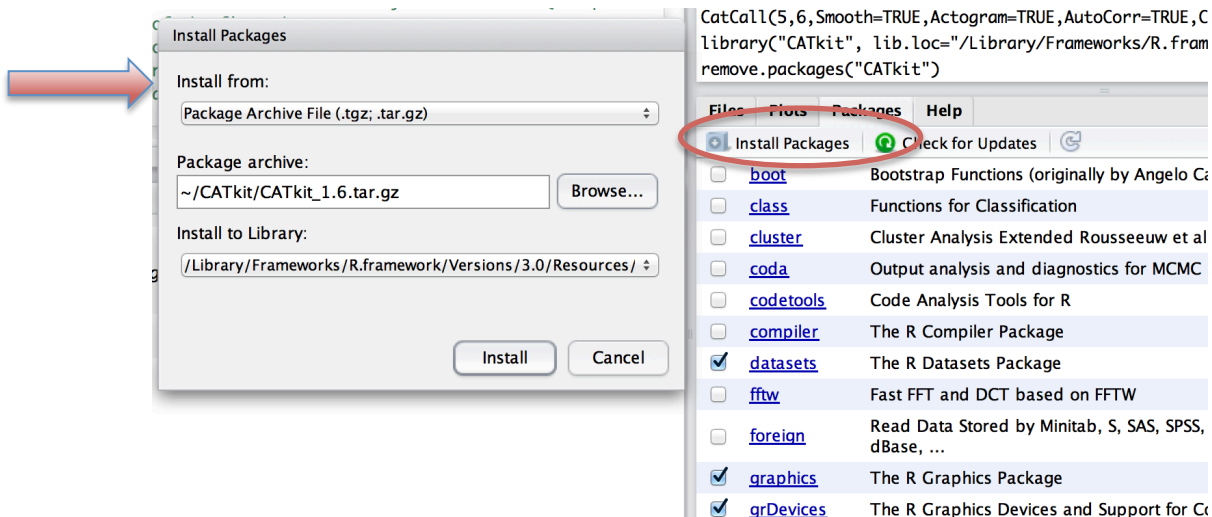
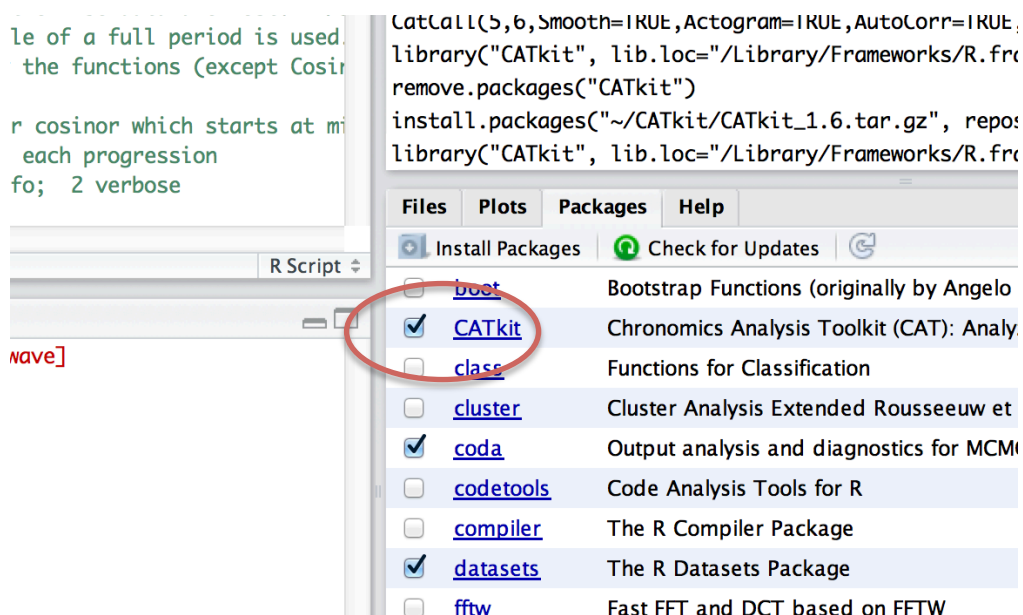


Installing CATkit from tar.gz file

- Download CATkit package to an easily accessible location. **Do not unpack!** Download from: <http://564394709114639785.weebly.com/installing-cat.html>
- Open RStudio
- Click on **Install Packages** tab in the lower right window in RStudio. (See figure below.) A pop-up window will open.
- In the top drop down, select **Package Archive file (tar.gz, or zip)**
- Browse to find the CATkitx.x.tar.gz file
- With CATkitx.x.tar.gz selected, click Open button
- Click Install button



CATkit is now installed. To load it into the environment, check the checkbox next to the package name in the list of packages, as shown in the figure below. Try it out!



CATkit Vignettes

After installing CATkit, try these examples. A script file containing the sample calls can be found in this folder. More information regarding parameterization and function usage can be found at: <http://564394709114639785.weebly.com>

CATkit contains several functions, called with two different calls:

1. CatCall can run a number of functions: Smooth, Actogram, AutoCorr, CrossCorr
2. CATCosinor runs various cosinor-based functions.

These Vignettes provide sample runs of CATkit to assure CATkit has been successfully installed, and demonstrate its parameterization. Be sure CATkit checkbox is checked!

In the folder where you found this document, you will also find four Vignette folders, and a script to run the vignettes, Vignette.r. These folders contain input data and the expected output from sample runs of CATkit. Be sure to unzip the files after downloading – not just view them in the archive – and place them in a conveniently accessible location. (Right click on the zip file, and select “extract all...”.) The data files will not work if still zipped. Note: file paths are written different for a Mac than a PC (see examples below). (You may need to check the checkbox for CATkit, in the packages tab in RStudio, to load it.) All instructions assume RStudio is installed.

Vignette 0: Multiple-component Cosinor fit to blood pressure data

Fits a multiple-component cosinor model, composed of 3 cosine curves with periods of 24, 12 and 8 hrs. A model with multiple periodic components is used to improve the fit over a single cosine model. Three variables (three columns) are analyzed, sampled every 30 minutes: systolic blood pressure, diastolic blood pressure and heart rate.

```
> install.packages("~/Documents/Cathy/Neuroscience
papers/capstone/CAT/CATkit_1.8.tar.gz", repos = NULL, type = "source")
Warning in install.packages :
  package '~/Documents/Cathy/Neuroscience papers/capstone/CAT/CATkit_1.8.tar.gz' is
not available (for R version 3.0.2)
* installing *source* package 'CATkit' ...
** R
** preparing package for lazy loading
** help
*** installing help indices
** building package indices
** testing if installed package can be loaded
* DONE (CATkit)
> CATCosinor(TimeCol=2, Y=c(4,6,7), Components=3, window="noFilt", RefDateTime
="201302030000", timeFormat="%Y%m%d%H%M", RangeDateTime=list(Start=0, End=0
), Units='Hour', dt=0, Progressive=list(Span=0, Increment=0), Period=list(Set
=c(24,12,8),Start=0,Increment=1,End=0),header=F, Skip=0, Colors="BW",Graphics
="pdf",Output=list(Txt=F,Dat=T,TxtAmp=F,Doc=T,HeatMap=F,LineGraphs=F),Console
=F,Debug=FALSE,fileName=fileName,functionName='CallCos3varProg')
```



1. Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette0 script lines below (delete # at start of lines);
2. Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette0"          # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette0"    # PC
fileName<-file.path(filePath,'clgi001.dat')
```

```
CATCosinor(TimeCol=2,Y=c(4,6,7), Components=3, window="noTaper",
  RefDateTime="201302030000", timeFormat="%Y%m%d%H%M",
  RangeDateTime =list(Start=0, End=0), Units='hours', dt=0,
  Progressive=list(Interval=0,Increment=0),Period=
  list(Set=c(24,12,8),Start=0,Increment=1,End=0),header=FALSE,
  Skip=0,Colors="BW",Graphics="pdf",Output=list(Txt=FALSE,Dat=TRUE,
  Doc=TRUE,Graphs=TRUE),Console=FALSE,Debug=FALSE,IDcol="fileName",
  fileName=fileName,functionName='Vignette0')
```

3. To save and run the updated script, check the "Source on Save" checkbox, and press the diskette icon next to the checkbox.
4. The function will run using specified parameters. Date and time are in column 2 (**TimeCol=2**) of file **fileName**. Columns 4, 6 and 7 (**Y=c(4,6,7)**) are each analyzed with a multiple-component model (**Components=3**), using 24-hr, 12-hr and 8-hr cosine curves (**Set=c(24,12,8)**). Graphing is turned on (**Graphs=T**), enabling graphs to be produced. Computer-readable and human-readable file-output are also enabled, via **Dat=T, Doc=T**, respectively. The parameter **functionName** is used to give each call/configuration a unique name, for ease of associating a call with its output (**functionName='Vignette0'**) -- the **functionName** appears in the output file names. Once it completes, your results file will be found in the same folder as the input file, Vignette0. The console will list the file name when the run completes. Computer-readable results are in the .dat file, and human -readable results are in the .rtf file.
5. Once completed, compare the resulting files to expected result files:
clgi001.datnoTaper—[ddmmmyy—HH-MM-SS]Vignette0Cos.pdf,
clgi001.datnoTaper—[ddmmmyy—HH-MM-SS]Vignette0Cos.rtf,
clgi001.datnoTaper—[ddmmmyy—HH-MM-SS]Vignette0Cos.dat
 Your output should match these results.

6. The following are the default parameters, if a parameter is unspecified:

```
(TimeCol=1,Y=2, Components=1, window="noTaper", RefDateTime=NA,
timeFormat="%Y%m%d%H%M", RangeDateTime=list(Start=NA, End=NA),
Units="hours", dt=0, Progressive=list(Interval=0, Increment=0),
Period=list(Set=0,Start=0,Increment=1,End=0),header=FALSE,
Skip=0, Colors="BW",Graphics="pdf",Output= list(Txt=FALSE,
Dat=TRUE, Doc=TRUE,Graphs=FALSE),yLabel="",Console=FALSE,
Debug=FALSE,IDcol="fileName", fileName=fileName,functionName="")
```

Vignette 1: Least Squares Spectrum of two pure sine waves

An artificially generated test series, containing two pure sine waves of 48 and 24-hr periods, is analyzed. The call to CAT performs a sweep of frequencies, a spectrum analysis, to identify where there are periodicities present in the data.

1. Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette1 script lines below (delete # at start of lines);
2. Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette1"          # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette1"      # PC
fileName<-file.path(filePath,'Signal10-20.txt')
```

```
CATCosinor(TimeCol=1,Y=2, Components=1, window="noTaper",
RefDateTime="0", timeFormat="%Y%m%d%H%M", RangeDateTime=
list(Start=0, End=0), Units='hours', dt=0, Progressive=
list(Interval=0, Increment=0), Period=list(Set=0,Start=144,
Increment=1,End=4),header=FALSE, Skip=0,Colors="BW",Graphics="pdf",
Output=list(Txt=FALSE,Dat=TRUE,Doc=TRUE,Graphs=TRUE),Console=F,
Debug=FALSE, fileName=fileName,functionName='Vignette1')
```

3. To save and run the updated script, check the "Source on Save" checkbox, and press the diskette icon next to the checkbox.
4. CATCosinor will run using specified parameters. Analysis is performed across a frequency range corresponding to periods from 144 to 4 hrs. The harmonic increment is one, meaning trial periods are 144/1, 144/2, 144/3, 144/4, ... 144/36 (= 4) hrs. (**Period=list(Set=0,Start=144,Increment=1,End=4)**). The data, two sine waves of periods 48 and 24 hrs, are plotted in the PDF file, versus time. Amplitudes are also plotted -- versus frequency. Maximum amplitudes are seen at the 3rd and 6th frequencies, corresponding to periods of 144/3=48 and 144/6=24 hrs, correctly identifying the periodicities present in the data. Green dots represent the SE on either side of the amplitude. Once the run completes, the result file will be found in the same folder as the input file, Vignette 1. The console will display the full file name when the run completes. Computer-readable results are in the .dat file, and human-readable results are in the .rtf file.
5. Once completed, compare the resulting files to expected result files:
Signal10-20.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette1Cos.pdf;
Signal10-20.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette1Cos.rtf;
Signal10-20.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette1Cos.dat.
Your output should match these results.

Vignette 2: Gliding spectrum: heatmap of progressive least squares spectral analysis cosinor

Using systolic blood pressure data from the first month of a newborn's life, a progressive analysis is performed across successive sub-spans of the full time-series, and for a Fourier range of frequencies for each sub-span. The rhythm components in this time-series (periodicity, amplitude) have been found to be changing over time (they are non-stationary). This progressive analysis across spans of data is used to provide us a look at rhythm characteristics of small sections of the time series. In this vignette, a least squares spectrum analysis, as demonstrated in Vignette 1, is combined with a progressive analysis of sub-spans of the time-series, allowing analysis of a time series where periodicities may change across time. The heatmap provides macroscopic visualization of rhythmicity.

1. Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette2 script lines below (delete # at start of lines);
2. Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette2"          # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette2"      # PC
fileName<-file.path(filePath,'FWedited.txt')
```

```
CATCosinor(TimeCol=1,Y=2, Components=1, window="noTaper",
RefDateTime = "199210192152", timeFormat="%Y%m%d%H%M",
RangeDateTime= list(Start="199210200000", End="199211300000"),
Units='hours', dt=0, Progressive=list(Interval=168, Increment=12),
Period=list(Set=0, Start=168,Increment=.5,End=9.5),header=FALSE,
Skip=0, Colors="BW", Graphics="pdf",Output=list(Txt=FALSE,Dat=TRUE,
Doc=TRUE, Graphs=TRUE),Console=F,Debug=FALSE,fileName=fileName,
functionName='Vignette2')
```

3. To save and run the updated script, check the "Source on Save" checkbox, and press the diskette icon next to the checkbox. This run takes longer to run than the others.
4. CATCosinor will run using specified parameters. Analysis is performed on progressive spans of data, each 168 hours in length, incremented by 24 hours from one span to the next (**Progressive=list(Interval=168,Increment=12)**). Thus these spans overlap each other by 156 hours. Data in each span are analyzed by least square spectrum in a range of trial periods from 168 to 9.5 hrs, using a harmonic increment of .5 between consecutive frequencies. (**Period=list(Set=0,Start=168,Increment=.5,End=9.5)**). This three-dimensional analysis is graphically represented by a heatmap of frequency vs. time, with amplitude at each point represented by color. (This progressive analysis can also be performed at specified periods instead of a spectrum – in this case it is called a chronobiologic serial section analysis). Once completed, the result file will be found in the same folder as the input file, Vignette 2. The console will display the full file name when the run completes. Computer-readable results are in the .dat file, and human -readable results are in the .rtf file.

- Once completed, compare the resulting file to expected result file:
FWedited.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette2Cos.pdf;
FWedited.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette2Cos.rtf;
FWedited.txtnoTaper—[ddmmmyy—HH-MM-SS]Vignette2Cos.dat
 Your output should match these results.

Vignette 3: Smoothing, Actogram, Autocorrelation, Crosscorrelation

Activity data are collected from mice over several days, by counting breaks in a laser beam. After a period of exposure to social stressors, activity data were again collected. This call to CatCall allows evaluation of both sets of data for gaps (Smoothing), and to look for periodicity (Actogram, Autocorrelation). The Crosscorrelation will tell us if the stress resulted in any changes in phase (or period length) in the activity levels.

- Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette3 script lines below (delete # at start of lines);
- Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette3"          # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette3"    # PC
fileName<-file.path(filePath,'activity stress c57--stress
copy2-part.txt')
file2Name<-file.path(filePath,'good-6d-2m-part.txt')
```

```
CatCall(TimeCol=c(1,2), timeFormat="%d/%m/%y %H:%M:%S",
lum=NA, valCols=5, sumCols=c(), Avg=FALSE, export=TRUE,
sizePts=2, binPts=30, Span = 0, Increment=0, k=5, yLab=NA,
modulo=1440,Rverbose=0,RmaxGap=3000, Skip=0,header=TRUE,
Smoothing=TRUE,Actogram=TRUE,AutoCorr=TRUE,CrossCorr=TRUE,
Console=FALSE, Graphics="pdf",Darkness=0,LagPcnt=1,
fileName=fileName, file2=list(Name=file2Name,TimeCol=c(1,2),
timeFormat="%d/%m/%y %H:%M:%S", lum=NA, valCols=5,
sumCols=c(),sizePts=2, binPts=30,Darkness=0))
```

- To save and run the updated script, check the “Source on Save” checkbox, and press the diskette icon next to the checkbox.
- The function will run using some explicitly specified parameters, as well as some default parameters (see default parameters, below). Activity data are sampled at 2-minute intervals, so sizePts is set to 2. We want them binned into 60 min time slots, so binPts is set to 30. k=6 defines the number of points to be averaged for Smoothing. There is a header in the data file, so header=TRUE. No data rows must be skipped, so the default Skip=0 is used. (For more details on parameterization see: <http://564394709114639785.weebly.com/running-cat.html>) Results files will be put into the same folder as the input file. The console will list the file name when the run completes.

5. Once completed, compare the main results file to the expected result file, found in the Vignette3 folder ending in **"output.pdf."** Your output should match these results. Other result files are also produced:
 - a. Two files ending in **"...binned.txt"** contain the data from the 2 files after binning (binned according to parameters **binPts** and **sizePts**), and before applying any of the functions.
 - b. For each data file analyzed, one additional file is output by each function (except Actogram, which creates no output), ending in **"...(function).txt"**, and containing the data after the function is applied. The Periodogram function outputs one file for each column of data (**lum=4, valCols=3, sumCols=c(5,6)**), so there will be four additional files produced from each input file. Overall, 13 output files are produced by the functions, in this case.

The default parameters for CatCall, when a parameter is not explicitly stated, are:

```
(TimeCol=1, timeFormat="%Y%m%d%H%M", lum=4, valCols=c(3,4),
sumCols=c(5,6), Avg=FALSE, export=F, sizePts=2, binPts=5,
Span = 0, Increment=0, k=6, yLab="Activity Level (au)",
modulo=1440, Rverbose=0, RmaxGap=400, Skip=0, header=FALSE,
Smoothing=FALSE, Actogram=FALSE, AutoCorr=FALSE,
CrossCorr=FALSE, Console=FALSE, Graphics="pdf", Darkness=1,
LagPcnt=.33, tz="GMT", fileName, file2=list(Name=NULL,
TimeCol=1, timeFormat="%Y%m%d%H%M", lum=4,
valCols=c(3,4), sumCols=c(5,6), sizePts=2, binPts=5,
Darkness=0))
```

Vignette 4: Population-Mean Cosinor (PMC)

Behavioral and lipid profiles are collected every 6 hours from healthy subjects over the period of one day. From the collected data, a single cosinor has been performed for each subject behavior and lipid profile. A population mean cosinor (PMC) can now be performed on the resulting parameters from each behavior and lipid: MESOR, Amplitude and Acrophase. The PMC will tell us what the population models look like for each behavior and lipid profile, and combinations.

3. Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette4 script lines below (delete # at start of lines);
4. Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette4"          # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette4"    # PC
fileName<-file.path(filePath, 'cos02x03.csv')

cosdat <- c("PR", "MESOR", "Amp", "Phi", "age_grp", "id",
"act_age", "Lipids", "gender", "smoking"), "diet")
```

```
CATpmc(fileName=fileName, colNames=cosdat, VarID=8,
GrpID=c(5,10),header=FALSE,sep=",",functionName="V8,G5,10",
title="PMC V8,G5,10")
```

6. To save and run the updated script, check the “Source on Save” checkbox, and press the diskette icon next to the checkbox.
7. The function will run using some explicitly specified parameters, as well as some default parameters (see default parameters, below). There is no header in the data file, so column names are set in cosdat. (For more details on parameterization see: <http://564394709114639785.weebly.com/running-cat-pmc.html>) Results files will be put into the same folder as the input file. The console will list the file name when the run completes.
8. Once completed, compare the main results file to the expected result file, found in the Vignette4 folder ending in “**PMC.rtf**.” Your output should match these results.

The default parameters for CATpmc, when a parameter is not explicitly stated, are:

```
CATpmc(data, fileName, colNames, VarID=NA, GrpID = NA, alpha
= 0.05, header=FALSE, sep="\t", Output=list(Doc=TRUE,
Txt=FALSE), functionName="", title="")
```

Vignette 5: Population-Mean Cosinor Parameter Test (PMCTest)

Once we have prepared the data, and run the PMC, we will choose which populations to compare. The PMCTest compares rhythm parameters (M, A, Phi, [A,Phi]) and tests for equivalency. In this way, we can see if models are different or not.

5. Open the Vignette.r script file with RStudio (or double click on the script file), uncomment the Vignette4 script lines below (delete # at start of lines);
6. Change the filePath sample in the script to your filePath (note: the format is different for Mac or PC).

```
filePath<-"~/file_path/Installing CAT/Vignette5" # mac
# filePath<-"c:\\file_path\\Installing CAT\\Vignette5" # PC
fileName<-file.path(filePath, 'cos02x03.csv')

cosdat <- c("PR", "MESOR", "Amp", "Phi", "age_grp", "id",
"act_age", "Lipids", "gender", "smoking", "diet")
CATparam(fileName=fileName, colNames=cosdat, VarID=8,
GrpID=c(5,10),header=FALSE,sep=",",functionName=" V8,G5,10",
title="PMCTest V8,G5,10")
```

9. To save and run the updated script, check the “Source on Save” checkbox, and press the diskette icon next to the checkbox.
10. The function will run using some explicitly specified parameters, as well as some default parameters (see default parameters, below). There is no header in the data

file, so column names are given in `cosdat`. (For more details on parameterization see: <http://564394709114639785.weebly.com/running-cat-pmctest.html>) Results files will be put into the same folder as the input file. The console will list the file name when the run completes.

11. Once completed, compare the main results file to the expected result file, found in the Vignette5 folder ending in "**ParamTest.rtf**." Your output should match these results.

The default parameters for `CATparam`, when a parameter is not explicitly stated, are:

```
CATparam(data, fileName, colNames, GrpID = NA, VarID = NA,  
alpha = 0.05, header=FALSE, sep="\t",  
Output=list(Doc=TRUE,Txt=FALSE), functionName="", title="")
```