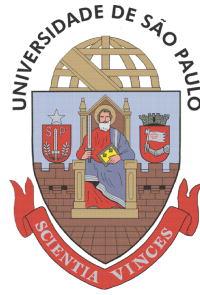**UNIVERSITY OF SÃO PAULO**

AsympPDC Package 1.0
User Guide

Preliminary Guide Version

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Abstract

This manual describes AsympPDC Package user level functionality aimed at inferring multivariate time series connectivity structure via Partial Directed Coherence (PDC) (and its variants gPDC and iPDC) via frequency domain null hypothesis tests that employ PDC's asymptotic statistics. The package also provides PDC confidence limits when connectivity cannot be rejected. Twelve examples from the literature illustrate its functionalities and capabilities.

1.0 Introduction

This is the first public release of an implementation of asymptotic statistics for partial directed coherence (PDC) that allows frequency domain Granger causality estimation via multivariate time-series vector autoregressive modeling by testing for the null hypothesis of significant PDC via its computed asymptotic statistical properties [Takahashi et al., 2007, 2010, de Brito et al., 2010]. In this release only MATLAB code is provided. A future release including a Python implementation is planned.

This document describes only basic package organization and aims at allowing data analysts quick access to the present methods for application on their own data sets. Didactic examples are included in the package to illustrate its use and functionality together with the nature of possible results.

This user manual is organized as follows: after the present brief introduction, Section 2.0 discusses installation and legal aspects. This is followed by a description of the package's organization (Section 3.0), its main routines and folder structure. Note that Section 3.2 presents a brief list of the illustrations provided in the package. Section 4.0 describes a template file whose comments point to details of how to call each function while Section 5.0 portrays the results of running one of the provided examples. Finally Section 6.0 lists known issues.

To provide expedited access to the present computational methods, this release does not provide a user friendly interface environment of the type often provided by real world professional data analysis packages. This is made up by providing the full integrated code for PDC estimation and null hypothesis testing. In doing so, our goal is to provide tools to explain/clarify the key concepts, PDC's advantages and limitations and (2) to give data analysts the chance to experiment the methods on their own data in way that they can incorporate the code in their own analysis procedures.

2.0 Installation and Legal Aspects

2.1 Installation and Requirements

The compressed package distribution file, asymppdc.zip, can be downloaded from PDC website.[1] After uncompressing it, copy/transfer the folder structure to your working folder. Then set MATLAB path access to that folder and subfolders using File Set Path... command from Matlab Desktop window. The **asymppdc** folder contains three folders, **routines**, **examples** and **supporting**, and a pair of files, a comprehensive template m-file for PDC connectivity analysis, **pdc_analysis_template.m** (see

---

[1]http://www.lcs.poli.usp.br/~baccala/pdc/

Appendix A), and a **readme.txt** file.

The AsympPDC package has been tested on Windows, Mac OS X and Linux-Ubuntu platforms running Matlab version 7.0 and higher. The package uses routines from Signal Processing, Statistics, and Control System toolboxes.

2.2   License and Distribution

This beta release of the AsympPDC package is a Matlab version of PDC connectivity tools for time series analysis and its content (not including **supporting folder**'s codes) is released as open source code under the GNU general public license version 3.

Matlab©is a product from Mathworks Inc™.

3.0   General Organization

A short description of folder (module) content follows.

3.1   Routines Module

There are four main routine types: (1) the MVAR module itself that estimates the VAR model via four algorithm options and the choice of different model order selection criteria; (2) a time domain Granger causality test (GCT) implementation that includes an instantaneous Granger causality test (IGCT); (3) the PDC and asymptotic statistics calculation routine (**asymp_pdc.m**) implementing all three PDC formulations and finally (4) a basic plotting routine, **pdc_xplot**, that provides graphic representation of the asymp_pdc routine results.

These modules and auxiliary m-files are briefly described:

Module and routine descriptions

- **A_to_f.m**

  Computes $\mathbf{A}(f)$ matrix in the frequency domain.

- **arfitcaps.m**

  If available, the **ARfit package** can be used as an alternative for the natively implemented VAR estimation algorithms. The ARfit package was developed by Tapio Schneider and Arnold Neu-

maier. Please visit Tapio Schneider's site. For further information about ARfit see [Scheneider and Neumaier, 2001].

arfitcaps.m is capsule routine for calling the arfit.m, which is part of the "ARfit: Multivariate Autoregressive Model Fitting" package. If you would like use ARfit algorithm for VAR model estimation, you can get it at http://www.gps.caltech.edu/tapio/arfit/index.html

Please also read the allied license term before using it.

- **asymp_pdc.m**

  Computes the PDC connectivity measure and its asymptotic statistics taking as input arguments the time series.

- **cmlsm.m**

  VAR least squares estimator.

- **coh_alg.m**

  Calculates the cross coherence functions from spectral density matrix.

- **gct_alg.m**

  Performs the Granger causality test, including instantaneous causality.

- **getCij.m**

  Extracts the (i,j) index variable structure from the c structure that results from asymp_pdc and employs the following syntax

  ```
  Cij(f) = getCij(c,i,j,nFreq)
  ```

  c is a structured variable that stands for either c.pdc, c.th, c.ic1, c.ic2, c.SS, c.coh, or p.pdc_th, as returned by **asymp_pdc.m** and **pdc_alg.m**.

- **mcarns.m**

  Calculates the coefficients of vector auto-regressive matrix using the Nuttall-Strand algorithm (a generalization of single channel harmonic method).

- **mcarvm.m**

  Calculates the coefficients of vector auto-regressive matrix using the Vieira-Morf algorithm, a generalization of single-channel geometric method.

- **mvar.m**

  Estimates the VAR matrix based on algorithm choice and model order selection criteria

- **mvarresidue.m**

  Residues test for whiteness.

- **pdc_alg.m**

  Computes partial directed coherence measure from the time series given by "options". If you want just to calculate PDC measure, and the asymptotic statistic this is probably the most useful routine

- **pdc_xplot.m**

  Connectivity plot in matrix layout with power spectra along the main diagonal.

- **pdc_xplot_title.m**

  This is an auxiliary routine that can be used with pdc_xplot.m to put a text title above the matrix layout plot.

- **ss_alg.m**

  Calculates the spectral density function (SS) given the auto-regressive matrix, A, and covariance residue.

- **standardize.m**

  Data transformation by standardization of time series imposing zero mean and unit standard-deviation.

3.2 Examples Module

The folder **examples** contains 12 examples borrowed from the literature, four auxiliary m-files used by the examples (**example_analysis_parameters.m**, **example_pre_processing.m**, **example_mvar_estimation.m**, and **example_pdc_analysis.m**), and a batch file that runs all the examples in batch-mode (**run_all_examples.m**) for operating system compatibility testing purposes.

Those curious about the performance and characteristics of PDC, gPDC and iPDC please play along with the examples in the folder, read the comments and try alternatives.

The examples presented in this package have been borrowed from Andrews and Herzberg [1985]), Sunspot-Melanoma 1936-1972 series, and from the literature, Baccalá and Sameshima [2001a], Baccalá and Sameshima [2001b], Schelter et al. [2005], Schelter et al. [2006], Schelter et al. [2009], Guo et al. [2008], Gourévitch et al. [2006], and an extended variant of Winterhalder et al. [2005].

All examples can be run in batch to verify if all routines and necessary toolboxes are available and Matlab path has been set by running the example batch command

>>run_all_examples

3.3   Supporting Module

Mostly comprised of user-contributed MATLAB code:

- **shadedplot.m**

- **subplot2.m**

- **suplabel.m**

- **suptitle.m**

- **tilefigs.m**

  Figure tiling routine for organizing the visualization of several open figures. See for instance **andrews_herzberg.m**, the Sunspot-Melanoma example.

4.0   PDC Analysis Getting Started Template File

The **pdc_analysis_template.m** file is meant to be self-explanatory. Please read and play with it. The file contains a description of how to interconnect the various routines to make the analysis of one's data. The **pdc_analysis_template.m** file is listed in Appendix 1.0 for convenience.

5.0   Sample Run

5.1   Sunspot-Melanoma 1936-1972 Series: andrews_herzberg.m

This is an interesting very short data set, 37 data points in all (see Figures 1 and 2), which can be used to investigate the interdependence between the cycles of solar activity given by the annual sunspot number and the epidemiological record of the number annual melanoma cases in the state of Connecticut from 1936 to 1972. The data are provided in the **sunmeladat.m** file contained in the **extras** directory.

Original PDC estimation of detrended but not standardized times series yields the result depicted in Figure 3.

Using generalized PDC for $\alpha = 1\%$ leads to the results in Figure 4 where the apparent contradictory results from Figure 3 become resolved.
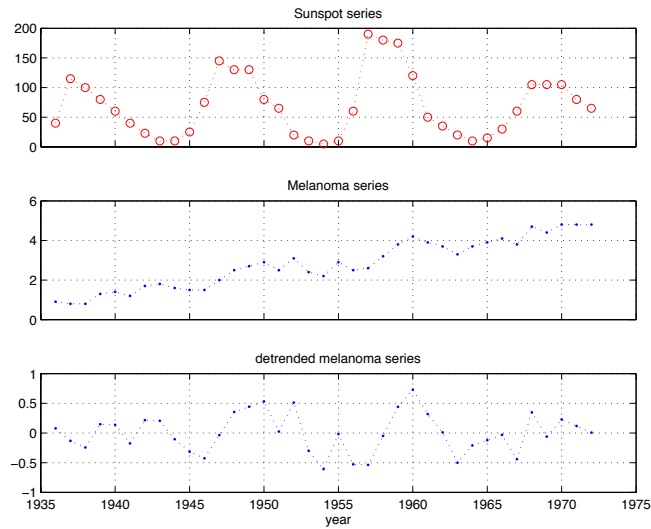
Figure 1: Detrended Sunspot-Melanoma 1936-1972 Series .
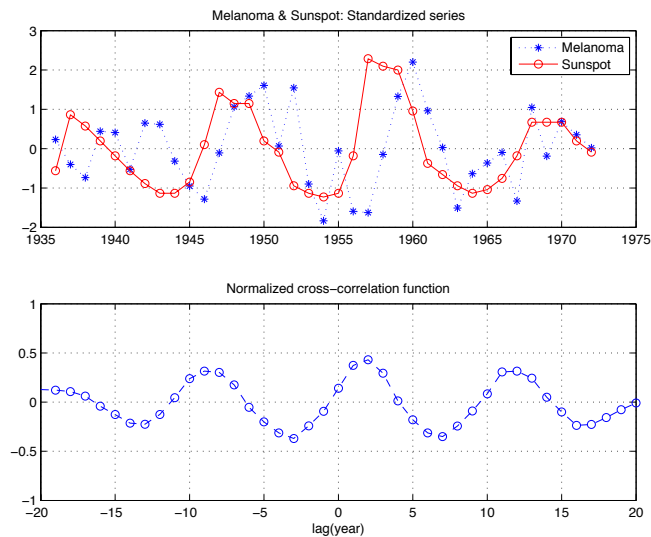
Figure 2: Standardized Sunspot-Melanoma series plotting and corresponding normalized cross-correlation function. Note that the peak of cross-correlation of 2 years lag led by the sun's activity.

Checking asympPDC package log output on Command Window in more detail:

```
=====================================================================
      Andrews and Herzberg's Sunspot and Melanoma 1936-1972 Data
                Sunspot --> Melanoma or other way?
=====================================================================

Setting up default analysis parameters.
Running simple data pre-processing routines.
Time series were detrended.
Running MVAR estimation and GCT analysis routines.
maxOrder limited to 30
IP=1  vaic=418.156614
IP=2  vaic=415.350982
IP=3  vaic=409.454496
IP=4  vaic=411.220477


Number of channels = 2 with 37 data points; MAR model order = 3.
```

6

```
------------------------------------------------------------------------
                    MVAR Residues test for whiteness
========================================================================
Good MAR model fitting! Residues white noise hypothesis NOT rejected.
Pass =
    0.0250
st =
   85.8928
------------------------------------------------------------------------
                        GRANGER CAUSALITY TEST
========================================================================
Connectivity matrix:
Tr_gct =
    -1     0
     1    -1
Granger causality test p-values:
pValue_gct =
   -1.0000    0.0796
    0.0000   -1.0000
------------------------------------------------------------------------
                 INSTANTANEOUS GRANGER CAUSALITY TEST
========================================================================
Instantaneous connectivity matrix:
Tr_igct =
    -1     0
     0    -1
Instantaneous Granger causality test p-values:
pValue_igct =
   -1.0000    0.0762
    0.0762   -1.0000
>>>> Instantaneous Granger causality NOT detected.
(...)
%========================================================================
            End of Sunspot-Melanoma series analysis example.
%========================================================================
```

6.0 Known Issues

1. The x-axis scaling plot label does not work for any other than normalized unit frequency, i.e. $fs = 1$.

2. The **asymp_pdc**.m routine as provided is not optimized. Setting $alpha = 0$, provides PDC without its asymptotic statistics, and is thus much faster.

3. A known issue among Matlab subplot users is that any figure reformatting with subplot requires replotting of everyone of its components which accounts for the slow speed of the pdc_xplot routine.

Please help us by referencing your use of this package and by reporting any bugs you find. You may do so by email to ksameshi@usp.br or baccala@lcs.poli.usp.br.
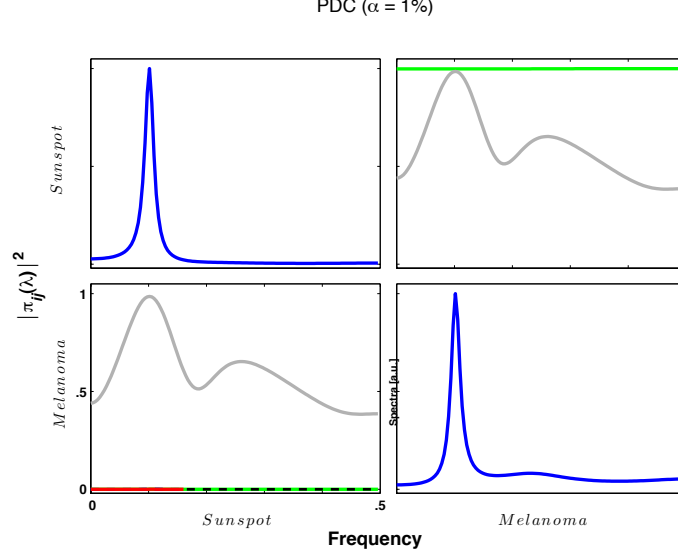
Figure 3: Matrix layout plot of squared original PDC ([Baccalá and Sameshima, 2001a]) calculated from detrended but nonstandardized sunspot and melanoma series. The direction of influence is from column to row variables. Observe that in this case the magnitude of PDC from $Melanoma \rightarrow Sunspot$ is high, close to 1, yet as the green line indicates, PDC is not significant. In the reverse direction, i. e. $Sunspot \rightarrow Melanoma$ even though PDC's magnitude seems almost zero, one can see a red line at the lower frequencies indicating significant connectivity in this direction. The gray lines depict coherence function, a symmetric measure.

7.0   Acknowledgements

Figure 4: Matrix layout plot of squared generalized PDC ([Baccalá and Sameshima, 2007]) estimates of the same sunspot and melanoma series of Figure 3. Now one observes that $|gPDC(f)|^2 < 0.3$ for the Melanoma to Sunspot activity, but more importantly it is not statistically significant. In the reverse direction, $Sunspot \rightarrow Melanoma$ now reveals a clear picture of Sun's activity onto the number of melanoma cases, with a peak at the lower frequency range, which correponds to approximately 11-year cycle indicating significant (red line) connectivity in this direction. In the gPDC plots, the black dashed-line indicates the 1% significance level, and the pair of blue dashed-lines the 99% confidence interval of the significant range of gPDC.

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D. Y. Takahashi, L. A. Baccalá, and K. Sameshima. Connectivity inference between neural structures via partial directed coherence. *Journal of Applied Statistics*, 34:1259–1273, 2007.

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M. Winterhalder, B. Schelter, W. Hesse, K. Schwab, L. Leistritz, D. Klan, R. Bauer, J. Timmer, and H. Witte. Comparison of linear signal processing techniques to infer directed interactions in multivariate neural systems. *Signal Processing*, 85:2137–2160, 2005.

1.0   Appendix A — PDC_ANALYSIS_TEMPLATE listing

```
1   % Edit this file to analyze your data. You might want to choose analysis
2   % parameters followed by comment containing "<***>". Check bellow.
3   %
4   % Some important input and output parameters and variables:
5   % input:
6   %         u    - data in columns
7   %         fs   - Sampling frequency
8   %         maxIP - externally defined maximum IP
9   %         alg  - for algorithm (1: Nutall-Strand),(2: mlsm) ,
10  %                           (3: Vieira Morf),  (4: ARfit)
11  %         criterion - for AR order selection =>
12  %                                1: AIC; 2: Hanna-Quinn; 3: Schwartz;
13  %                                4: FPE, 5: fixed order in MaxIP
14  %         alpha - PDC test significance level
15  %
16  % output:
17  %         c.pdc - original/generalized/informational PDC
18  %         c.th - threshold level by Patnaik approximation
19  %         c.pdc_th - above threshold pdc values otherwise equal NaN
20  %         c.ic1,c.ic2 - superior and inferior confidence interval
21  %         c.p - VAR model order
22  %         c.SS - Power spectrum
23  %         c.coh - coherece function
24
25
26  %==========================#
27  % Times series for analysis /
28  %==========================#
29  % u    - data in columns.
30  %         The variable u must contain the time series
31  %         If flgExample=1 the template file will analyze a
32  %         5 variables Gaussian independent noises.
33  format compact
34  clear all; clc
35  % Choose Example 1 == Five independent random variables model
36  %              2 == Sunspot-melanoma time series
37  %              3 == Baccalá & Sameshima (2001) 5 variables linear model
38  %              4 == Takahashi(2009) Thesis' example model
39  flgExample=4;
40
41  disp('==================================================================');
42  disp('============= PDC analysis getting started template =================')
43  disp('==================================================================');
44
45  switch flgExample
46     case 1,
47        u=randn(2000,5);    %<***> Example (1)
48        disp('          Random Independent Process with 5 variables')
49        disp('==================================================================');
50
51     case 2
52        u=sunmeladat([4 3]); %<***> Example (2)
53        disp('     Andrews and Herzberg''s Sunspot and Melanoma Example');
54        disp('             Sunspot --> Melanoma or other way?');
55        disp('==================================================================');
56     case 3
57        u=baccala2001a_ex5data(200);
58     case 4,
59        u=takahashi_thesis_dat(200);
```

```matlab
      otherwise
         error('Wrong example selection.')
   end;

   fs = 1; %<***> Sampling frequency

   [nSegLength,nChannels]=size(u);
   if nSegLength < nChannels, error('The data might be transposed.'); end;

   %===========================#
   %  Channel identification    /
   %===========================#

   switch flgExample
     case 1,
       chLabels  = {'x_1';'x_2';'x_3';'x_4';'x_5'}; %<***> Example (1)
       strTitle2 = 'Five independent Gaussian noises '; %Title info
     case 2
       chLabels  = {'Sunspot';'Melanoma'}; %<***> Example (2)
       strTitle2 = 'Sunspot & Melanoma 1936-1972 ';
     case 3,
       chLabels  = [];                       %<***> Example (3)
       strTitle2 = 'Five variables Baccalá+Sameshima(2001) examples ';
     case 4,
       chLabels  = {'X'; 'Y'; 'Z'};          % Takahashi thesis example
       strTitle2 = 'Takahashi 2008 (Thesis) example';
   end;

   flgLabels = ¬isempty(chLabels);
   if flgLabels,
     if nChannels ≠ max(size(chLabels))
       error('Numbers of labels and channels do not match.')
     end;
   end;

   %===========================#
   %       Action flags        /
   %===========================#
   flgDetrend=1;   %<***> Usually it's recommended to detrend the time series.

   flgStandardize=0; %<***> For PDCn estimation normalization has no effect.
   if flgStandardize,
     disp('Be aware that the data normalization does not affect the generalized')
     disp('   PDC estimates nor its statistics results, so that data normalization')
     disp('   is not necessary.')
   end;

   %===========================#
   %    Analysis parameters    /
   %===========================#
   nFreqs = 128; %<***> number of points on frequency scale;
                 %      use either 64 or 128.

   metric = 'info';
   %        metric   'euc'  - Euclidean     -> original PDC;
   %                 'diag' - diagonal      -> gPDC;
   %                 'info' - informational -> iPDC;

   maxIP = 30; % maxIP - externally defined maximum IP %<***>

   %===========================#
   %    MAR algorithm          /
   %===========================#
```

```matlab
123  % Choose one of algorithm for MAR estimation
124  % alg   - for algorithm  (1: Nutall-Strand),(2: mlsm) ,
125  %                        (3: Vieira Morf),  (4: QR artfit)
126  alg=1; %<***> Nuttall-Strand (alg=1) algorithm, it seems to be a good
127         %       and robust method.
128
129  %===========================#
130  %MAR order selection criteria/
131  %===========================#
132  % criterion - for AR order choice
133  %  1: AIC; 2: Hanna-Quinn; 3: Schwartz;
134  %  4: FPE, 5: fixed order in MaxIP
135  criterion = 1; %<***> AIC, Akaike information criterion (Our preferred one)
136
137  %===================
138  alpha = 0.05;        %<***> Significance level for PDC null hypothesis
139                       % testing, it is usually 1% or 5%
140                       %
141                       % IMPORTANT: if alpha == 0, no asymptotic statistics
142                       % calculation is performed and ASYMP_PDC (see bellow)
143                       % will only returns PDC. This option is interesting
144                       % if you want faster PDC calculation.
145                       %
146  gct_signif = alpha;  % Granger causality test significance. Choose other
147                       % value if you have good reason for using different
148                       % one from PDC statistical testing.
149  igct_signif = alpha; % Instantaneous Granger causality test significance level.
150  VARadequacy_signif = 0.05; % VAR model adequacy significance level
151
152  %=============================================================================
153  %                        Plotting options
154  %=============================================================================
155  flgColor = [0 1]; % Plotting option for automatic scaling for small PDC
156                    % values.
157                    % if flgColor = 0, y-axis scale = [0 1]
158                    % elseif flgColor = 1, the pdc_xplot routine rescales
159                    % the y-axis automatically according to the following
160                    % rules:
161                    %   if .001<=PDC(f) < .01 background-color = light-blue,
162                    %                          so that y-axis scale = [0 .1]
163                    %   elseif PDC(f) < .001 background-color = light-purple
164                    %                          and y-axis = [0 .01];
165                    % for flgColor=[0 1], both lay-outs are plotted.
166
167  %          [1 2 3 4 5 6 7]
168  flgPrinting=[1 1 1 1 1 0 2];
169  %           | | | | | | | 7 Power Spectra (0: w/o SS; 1: Linear; 2: Log-scale)
170  %           | | | | | | 6 Coherence
171  %           | | | | | 5 Plot lower confidence limit
172  %           | | | | 4 Plot upper confidence limit
173  %           | | 3 Significant PDC in red line
174  %           | 2 Patnaik threshold level in black dashed-line
175  %           1 PDC in green line
176
177  axis_scale = [0 0.50 -0.02 1.05];
178  w = fs*(0:(nFreqs-1))/2/nFreqs;
179  w_max = fs/2; %<***> Usually half of sampling frequency = Nyquist frequency
180
181  %=============================================================================
182  %=============================================================================
183  %         ATTENTION: BELOW THIS LINE PROBABLY YOU MIGHT NOT WANT TO EDIT,
184  %              UNLESS YOU WANT TO CUSTOMIZE YOUR ANALYSIS ROUTINE.
185  %=============================================================================
```

```matlab
186
187 %===========================================================================
188 %                        Detrend and normalization options
189 %===========================================================================
190 if flgDetrend,
191    for i=1:nChannels, u(:,i)=detrend(u(:,i)); end;
192    disp('Time series were detrended.');
193 end;
194
195 [nChannels,nSegLength]=size(u);
196 if nChannels > nSegLength, u=u.';
197    [nChannels,nSegLength]=size(u);
198 end;
199
200 if flgStandardize,
201    for i=1:nChannels, u(:,i)=u(:,i)/std(u(:,i)); end;
202    disp('Time series were scale-standardized.');
203 end;
204
205 %===========================================================================
206 % Additional info for title (optional)
207
208 strTitle1 = ['PDC(' '{\alpha = ' int2str(100*alpha) '%}' ') '];
209 switch metric
210    case 'euc'
211       %NOP
212    case 'diag'
213       strTitle1 = ['g' strTitle1];
214    case 'info'
215       strTitle1 = ['i' strTitle1];
216    otherwise
217       error('Unknown metric.')
218 end;
219 % or set strTitle1 = [];
220
221 %==================
222 switch alg
223   case 1
224     disp('VAR estimation using Nutall-Strand algorithm.')
225   case 2
226     disp('VAR estimation using least-squares estimator.')
227   case 3
228     disp('VAR estimation using Vieira-Morf algorithm.')
229   case 4
230     disp('VAR estimation using QR-ARfit algorithm.')
231 end;
232
233 %============================#
234 %MAR order selection criteria/
235 %============================#
236 switch criterion
237    case 1
238       disp('Model order selection criteria: AIC.')
239    case 2
240       disp('Model order selection criteria: Hanna-Quinn.')
241    case 3
242       disp('Model order selection criteria: Schwartz (BIC).')
243    case 4
244       disp('Model order selection criteria: FPE.')
245    case 5
246       disp('Model order selection criteria: fixed order in maxIP.')
247    otherwise
248       error('Model order selection criteria: NOT IMPLEMENTED YET.')
```

```matlab
249  end;
250
251  %===========================================================================
252  %                          VAR model estimation
253  %===========================================================================
254  [IP,pf,A,pb,B,ef,eb,vaic,Vaicv] = mvar(u,maxIP,alg,criterion);
255
256  disp(['Number of channels = ' int2str(nChannels) ' with ' ...
257    int2str(nSegLength) ' data points; MAR model order = ' int2str(IP) '.']);
258
259  %===========================================================================
260  %     Testing for adequacy of MAR model fitting through Portmanteau test
261  %===========================================================================
262     h = 20; % testing lag
263     aValueVAR = 1 - VARadequacy_signif;
264     flgPrintResults = 1;
265  [Pass,Portmanteau,st,ths]=mvarresidue(ef,nSegLength,IP,aValueVAR,h,...
266                                                    flgPrintResults);
267
268  %===========================================================================
269  %           Granger causality test (GCT) and instantaneous GCT
270  %===========================================================================
271     flgPrintResults = 1;
272  [Tr_gct, pValue_gct, Tr_igct, pValue_igct] = gct_alg(u,A,pf,gct_signif, ...
273                                                    flgPrintResults);
274
275  %===========================================================================
276  %             PDC, threshold and confidence interval calculation.
277  %===========================================================================
278
279  % if alpha == 0, no asymptotic statistics is performed. ASYMP_PDC returns
280  % only the PDC. This option is much faster!!
281   c=asymp_pdc(u,A,pf,nFreqs,metric,alpha);
282
283  % Power spectra and coherence calculation
284  c.SS = ss_alg(A, pf, nFreqs);
285  c.coh = coh_alg(c.SS);
286
287  % Statistically significant PDC on frequency scale
288  if alpha ≠ 0,
289     pdc_temp = ((abs(c.pdc)-c.th) > 0).*c.pdc + ((abs(c.pdc)-c.th) ≤ 0)*(-1);
290     pdc_temp(ind2sub(size(pdc_temp),find(pdc_temp == -1))) = NaN;
291     c.pdc_th = pdc_temp;
292  end;
293
294  %Adding further analysis details in the figure title.
295  %strTitle3 = ['[N=' int2str(nSegLength) '; IP=' int2str(c.p) ']'];
296  % or
297
298  strTitle3 = ['[N=' int2str(nSegLength) 'pts; IP=' int2str(c.p) '; ' ...
299     datestr(now) ']'];
300
301  % or leave emptied: strTitle3=[];
302
303  %===========================================================================
304  %              Matrix Layout Plotting of the Analysis Results
305  %===========================================================================
306
307  w_max = fs/2;
308  strTitle = [strTitle1 strTitle2 strTitle3];
309  strWindowName = 'PDC Analysis Template Example';
310
311  % The following "for loop"  thourgh flgColor values, 0 and 1, and yields a
```

```matlab
312   % pair of plots, one without and other with color scale rearrangment option.
313   % Value range of PDC and Coherence is from [0 1], but sometimes the maximum
314   % peak value is small (<0.1), or even smaller, (<.01), so in these cases it
315   % might be interesting to have a plot with finer smaller y-axis scale. The
316   % white-background plot indicates full-scale [0 1] y-axis, while
317   % light-blue-background stands for intermediate [0 .1] scaling and
318   % light-purple-background shows very fine detail of small, usualy not
319   % significant PDCs. Try flgColor = 0 or 1, or both [0 1].
320
321   for kflgColor = flgColor,
322      h=figure;
323      set(h,'NumberTitle','off','MenuBar','none', ...
324         'Name', strWindowName )
325
326      [hxlabel hylabel] = pdc_xplot(c,...
327          flgPrinting,fs,w_max,chLabels,kflgColor);
328   % The title suplabel command should (not sure) follow the pdc_xplot routine
329   % In MacOS X, for flgPrinting(7) = 4 or 5, the main diagonal plotting
330   % gets misaligned if suplabel with 't' option is used more than once.
331
332      [ax,hT]=suplabel( strTitle, 't' );
333      set(hT,'FontSize',8)
334   end;
335
336   %======================= pdc_xplot =======================================
337   %Plot legend:  Blue lines on the main diagonal = Power spectra;
338   %              Black dashed lines are Patnaik threshold for PDCn;
339   %              Green lines = non significant PDCn;
340   %              Red lines = significant PDCn;
341   %              Light-gray lines = coherence function.
342   %
343   % Notes:       a.The main diagonal of matrix layout contains power spectra.
344   %              b.Coherences are symmetric, e.g.,
345   %                  Coh_{Sunspot,Melanoma}(f) = Coh_{Melanoma,Sunspot}(f).
346   %              c.PDCn is asymmetric relation, and the PDCn graphics should
347   %              be read as if the flow of information is been from the
348   %              x-axis variable toward y-axis variable.
349   %
350   %              For sunspot and melanoma example, one only sees significant
351   %              PDCn from Sunspot to Melanoma, which could eventually be
352   %              interpreted that "Sunspot", or the Sun's activity
353   %              modulates the incidence of melanoma.
354   %======================= pdc_xplot =======================================
355   disp('======================================================================');
356   disp('==========PDC_ANALYSIS_TEMPLATE SUCCESSFULLY FINISHED ==============')
357   disp('======================================================================');
```