```
%~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
%
% PlotEQ14Spec.m
%
% dT/dt spectra are saved w/ GetAllSpecEQ14.m in file AllSpec_[dz].mat,
% where dz is the # of spectra to skip (too many to save all).
%
%-----------------
% 08/04/16 - A.Pickering
%~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

```
clear ; close all

addpath /Users/Andy/Cruises_Research/GenMatlabFunctions/
addpath /Users/Andy/Cruises_Research/mixingsoftware/general
% Load file with saved spectra
load('AllSpec_50.mat')
```

Plot for two different ranges of epsilon & chi (from chameleon)

```
% Ratios of chipod method to chameleon
clear chirat epsrat
chirat=AllSpec.all_chi_chi ./ AllSpec.all_chi_cham;
epsrat=AllSpec.all_eps_chi ./ AllSpec.all_eps_cham;

% (1) high eps,chi, and larger (negative) bias in chi
epsrange1=[-6.2 -6];
epsrange1=[-5.8 -5.6];
epsrange1=[-5.6 -5.4];
chirange1=epsrange1;
ig1=find(  log10(AllSpec.all_eps_cham)> epsrange1(1) & log10(AllSpec.all_eps_cham)< epsrange1(
    & log10(AllSpec.all_chi_cham)> chirange1(1) & log10(AllSpec.all_chi_cham)< chirange1(2) &

% (2) low eps,chi, and smaller bias in chi
epsrange2=[-8.8 -8.6];
chirange2=epsrange2;
ig2=find(  log10(AllSpec.all_eps_cham)> epsrange2(1) & log10(AllSpec.all_eps_cham)< epsrange2(
    & log10(AllSpec.all_chi_cham)> chirange2(1) & log10(AllSpec.all_chi_cham)< chirange2(2) &

%
figure(1);clf
agutwocolumn(1)
wysiwyg
set(gcf,'defaultaxesfontsize',15)

ax1=subplot(211);
loglog(AllSpec.ki,AllSpec.speci(ig1,:),'.')
hold on
loglog(AllSpec.ki,nanmean(AllSpec.speci(ig1,:)),'k','linewidth',2)
% Plot the (chi-pod method) fits
loglog(AllSpec.ki,(AllSpec.speci_fit(ig1,:)),'b','linewidth',1)
```

```matlab
% Plot kraichnan spectra for this range too
nu=1e-6;
tdif=1.5e-7;
qq=7;
% eps=10^(nanmean(epsrange1))
% chi=10^(nanmean(chirange1))
for ii=1:length(ig1)
    eps=AllSpec.all_eps_cham(ig1(ii));
    chi=AllSpec.all_chi_cham(ig1(ii));

    kb = (((eps./(nu.^3)).^.25 )/2/pi).*sqrt(nu./tdif);
    [spec_vals]=kraichnan(nu,AllSpec.ki,kb,tdif,chi,qq);
    hcham=loglog(AllSpec.ki,spec_vals,'m','linewidth',2);
end

grid on
xlim([0 300])
ylim([1e-14 1e0])
freqline(2);
freqline(7);
title([num2str(epsrange1(1)) ' < log_{10}\epsilon < ' num2str(epsrange1(2)) ...
    ' AND ' num2str(chirange1(1)) ' < log_{10}\chi < ' num2str(chirange1(2))])
xlabel('wavenumber')

ax2=subplot(212);
loglog(AllSpec.ki,AllSpec.speci(ig2,:),'.')
hold on
loglog(AllSpec.ki,nanmean(AllSpec.speci(ig2,:)),'k','linewidth',2)
% Plot the (chi-pod method) fits
loglog(AllSpec.ki,(AllSpec.speci_fit(ig2,:)),'b','linewidth',1)

%eps=10^(nanmean(epsrange2))
%chi=10^(nanmean(chirange2))
for ii=1:length(ig2)
    eps=AllSpec.all_eps_cham(ig2(ii));
    chi=AllSpec.all_chi_cham(ig2(ii));

    kb = (((eps./(nu.^3)).^.25 )/2/pi).*sqrt(nu./tdif);
    [spec_vals]=kraichnan(nu,AllSpec.ki,kb,tdif,chi,qq);
    hcham=loglog(AllSpec.ki,spec_vals,'m','linewidth',2);
end

grid on
xlim([0 300])
ylim([1e-14 1e0])
freqline(2);
freqline(7);
title('log_{10}\epsilon > -8')
xlabel('wavenumber')
title([num2str(epsrange2(1)) ' < log_{10}\epsilon < ' num2str(epsrange2(2)) ...
    ' AND ' num2str(chirange2(1)) ' < log_{10}\chi < ' num2str(chirange2(2))])

linkaxes([ax1 ax2])
```
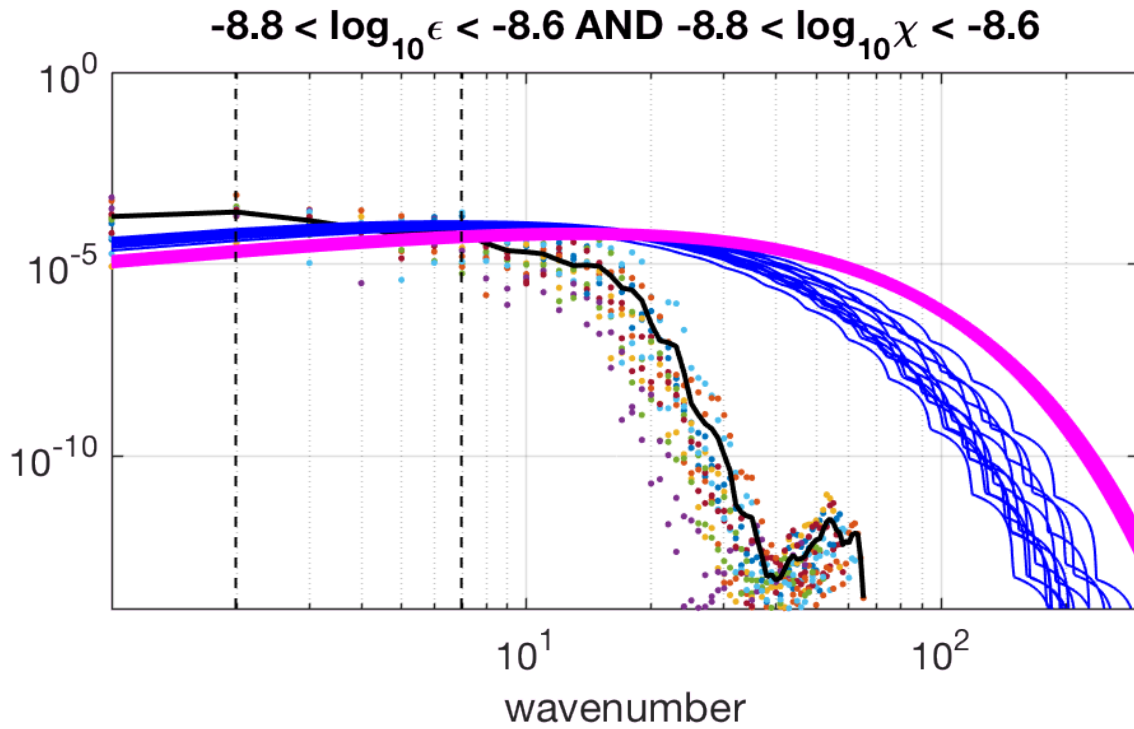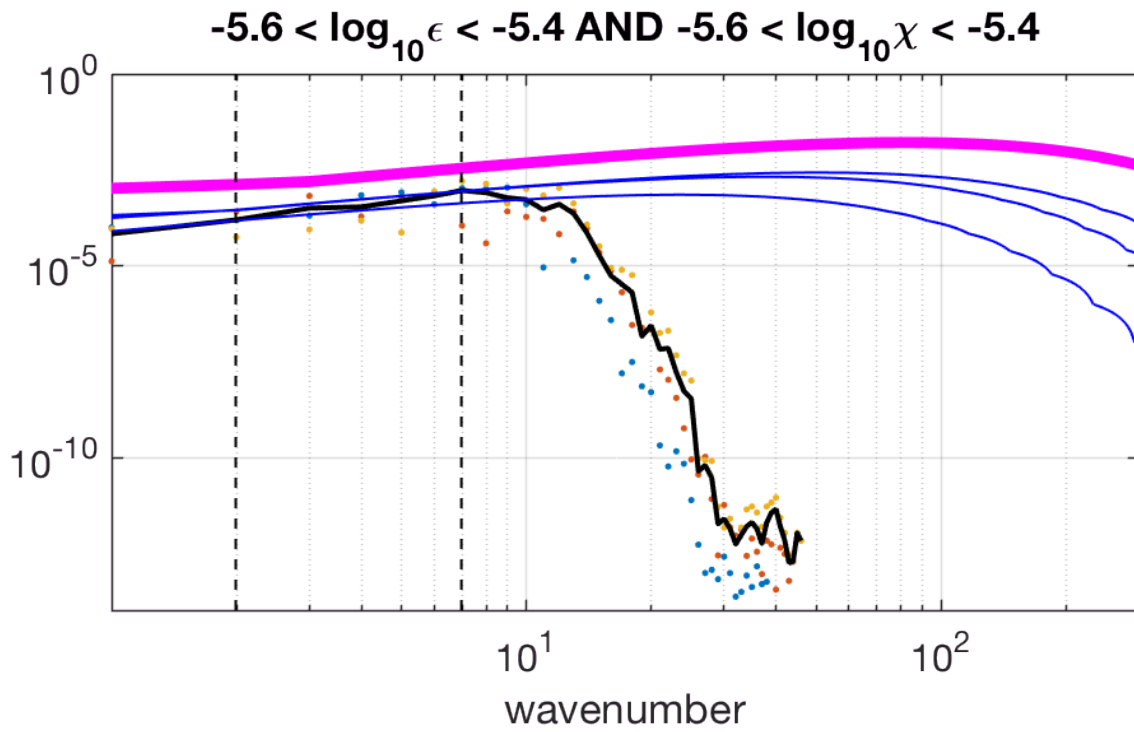
-5.6 < log$_{10}\epsilon$ < -5.4 AND -5.6 < log$_{10}\chi$ < -5.4

wavenumber

-8.8 < log$_{10}\epsilon$ < -8.6 AND -8.8 < log$_{10}\chi$ < -8.6

wavenumber

\# - For high values of the true (chameleon) \epsilon and \chi (top panel), the \chi pod fit spectra (blue) are all lower in magnitude than the Kraichnan spectra (magenta) for the true values. However the \chi pod fit spectra appear to match the observed spectra well (the 'true' spectra are too high).

\# - For low values of the true (chameleon) \epsilon and \chi (lower panel), the \chi pod fit spectra (blue) are higher in magnitude at low wavenumbers and lower at higher wavenumbers..

```
nanmean(log10(chirat(ig1)));
nanmean(log10(epsrat(ig1)));

nanmean(log10(chirat(ig2)));
nanmean(log10(epsrat(ig2)));
```

Plot histgram of chi_chi to chi_cham

```
% ratio of chi_chi to chi_cham
chirat=AllSpec.all_chi_chi ./ AllSpec.all_chi_cham;

figure(1);clf
agutwocolumn(0.5)
histogram(log10(chirat))
freqline(nanmean(log10(chirat)));
```
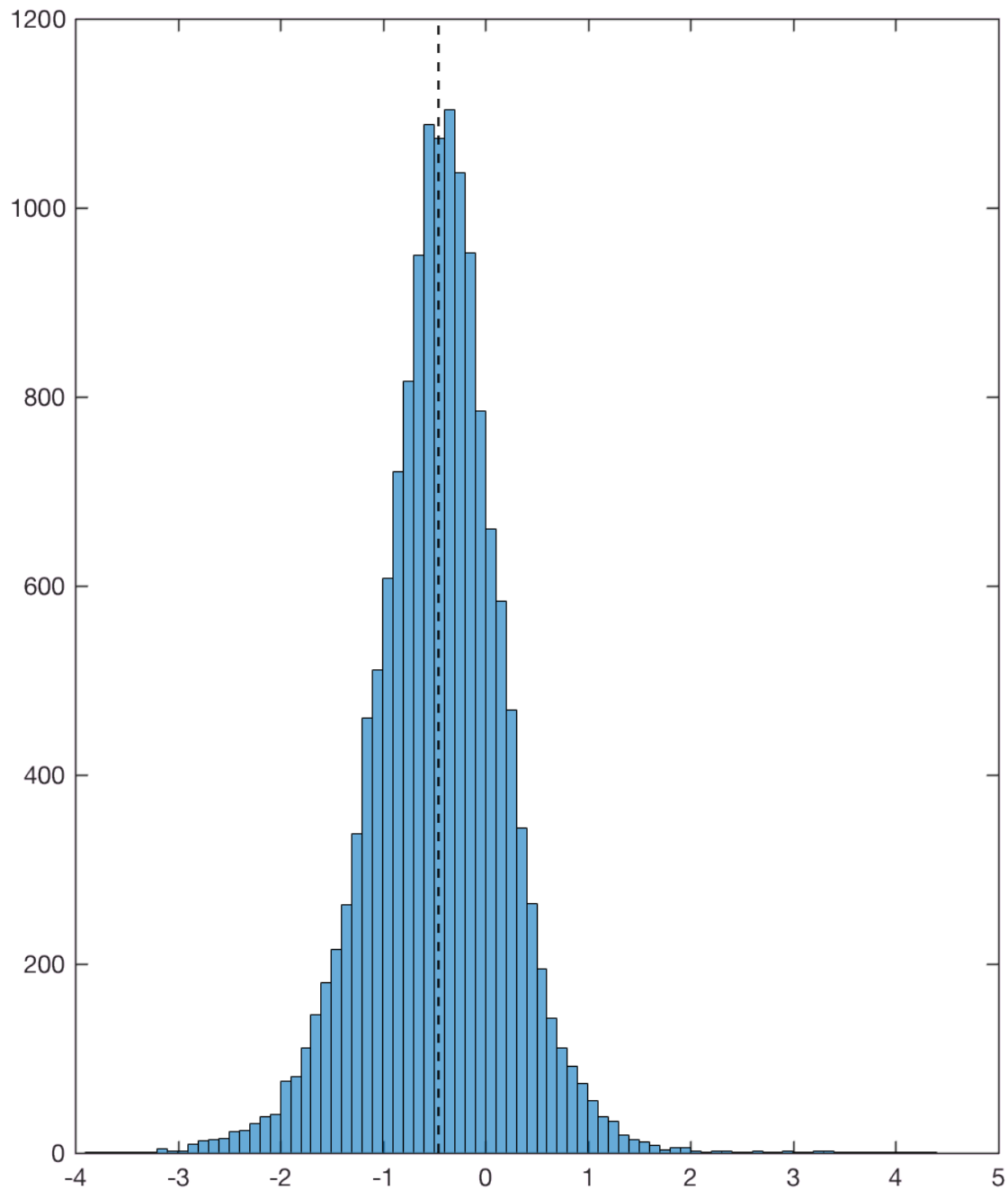
Plot histograms of chi and eps (from chameleon) where ratio is low; this shows bias is lowwhere true epsilon and chi are large

```
ig=find(log10(chirat)<-1.5);

figure(2);clf

subplot(211)
```

```
h1=histogram(log10(AllSpec.all_chi_cham),'Normalization','pdf');
hold on
h2=histogram(log10(AllSpec.all_chi_cham(ig)),h1.BinEdges,'Normalization','pdf');
xlabel('log_{10}\chi')
ylabel('pdf')
legend([h1 h2],'All','biased low')

subplot(212)
h1=histogram(log10(AllSpec.all_eps_cham),'Normalization','pdf');
hold on
h2=histogram(log10(AllSpec.all_eps_cham(ig)),h1.BinEdges,'Normalization','pdf');
xlabel('log_{10}\epsilon')
ylabel('pdf')
```
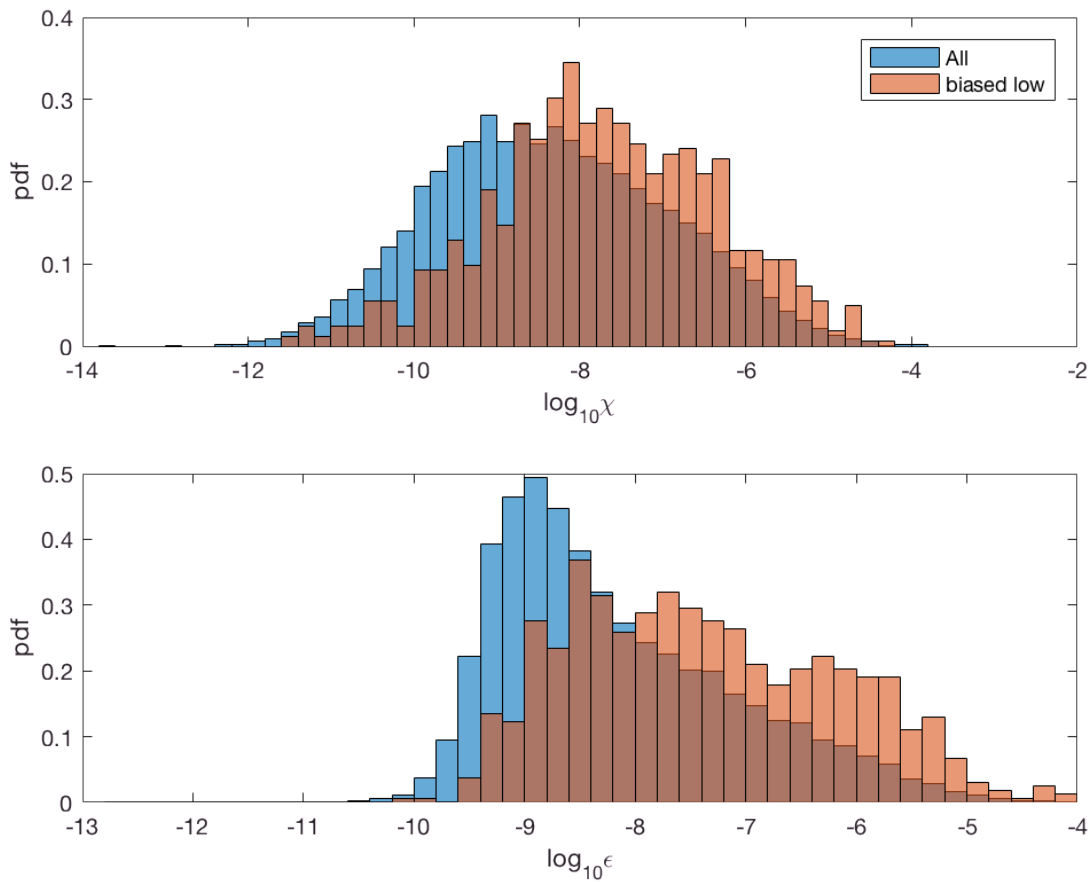


```
ig1=find(log10(AllSpec.all_eps_cham)<-8);
ig2=find(log10(AllSpec.all_eps_cham)>-8);

figure(2);clf

subplot(211)
imagesc(log10(AllSpec.speci(ig1,:)))
colorbar
caxis([-11 -0])
```

```
xlim([0 60])
title('log_{10}\epsilon < -8')

subplot(212)
imagesc(log10(AllSpec.speci(ig2,:)))
colorbar
caxis([-11 -0])
xlim([0 60])
title('log_{10}\epsilon > -8')
```