After the inference is performed for the community case, (which can be done by the script files), we perfrom various validation tests. Some of them are shown in this example notebook. All codes are avaible as scripts or tools.

Firstly we show tests for convergence:

```
load('./../figures/chain_combined.mat');

grand_mean = (mean_chain_1 + mean_chain_2 )/2;

%chain_1 and chain_2 are the chains.

B = N/(M-1) * ((mean_chain_1 - grand_mean).^2 + (mean_chain_2 - grand_mean).^2) ;

v_1 = (std(chain_1)).^2 ;
v_2 = (std(chain_2)).^2 ;

W = (1/M) * (v_1 + v_2) ;



R =  ( (N-1)/N * W + (B/N) ) ./W;
R(24) = [];
```

Now the Gelman Rubin test plots:

```
%% plot bars


figure(1)
subplot(2,1,1)
b = bar(R,'FaceColor','flat');

for i = 1:5
b.CData(i,:) = [211,23,24]./255;
end

for i = 6:14
b.CData(i,:) = [15,104,82]./255;
end

for i = 15:23
b.CData(i,:) = [211,119,46]./255;
end

for i=24:32
b.CData(i,:) = [62,137,168]./255;
end
```

```
b.CData(33,:) = [217,76,33]./255;
set(gca,'XTickLabel','');
hold on;
line([0.2, 35.8], [1.1, 1.1], 'Color', [0.1,0.1,0.1],'LineStyle','--',LineWidth=2);
set(gca,'FontSize',20);
xlim([0 35])
ylabel('R_{GR}')
ylim([0 1.2])
yticks([0 0.5 1 1.1]);
```

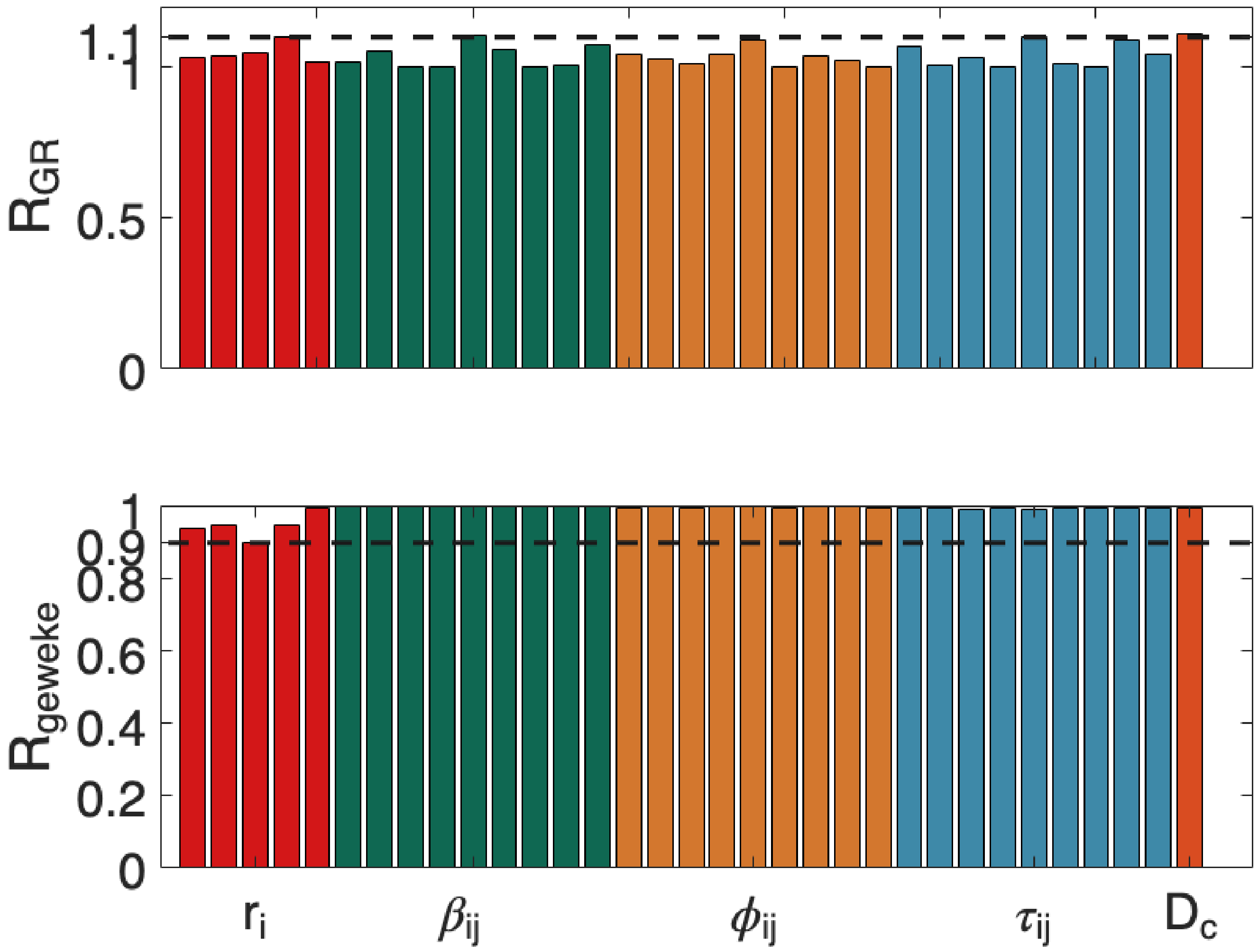
Now the geweke test bars

```
store = chainstats(chain_1);
```

```
MCMC statistics, nsimu = 10000

      mean         std      MC_err         tau      geweke
----------------------------------------------------------
  0.098496    0.017004   0.0015792      106.24     0.93956
  0.086781    0.022143   0.0023597      104.96     0.94899
  0.018441     0.01343   0.0014589      117.86     0.90139
   0.33332    0.017818   0.0025657      457.59     0.95099
    0.4875     0.02225    0.002355      117.59     0.99648
    285.41    0.027412   0.0036058      292.19     0.99995
    316.03    0.051235   0.0067916      211.32     0.99991
    426.23     0.03248   0.0038391      195.29     0.99994
    261.38    0.025038   0.0031335      218.59     0.99994
    86.125    0.033966   0.0034678       138.3     0.99981
     172.4    0.021483   0.0030284      348.54     0.99996
    395.47    0.027687   0.0034785      211.17     0.99996
     143.5    0.032051   0.0039558      176.96           1
    14.326    0.035882   0.0043197      160.67     0.99955
   -7.5826    0.028902   0.0038293      210.42     0.99823
   -7.5103    0.032121    0.003092      112.92     0.99995
   -7.3538    0.029977   0.0035721      159.32     0.99872
   -8.0602    0.024614   0.0032397      117.98     0.99983
   -7.1996    0.039248   0.0041699      111.94     0.99982
    -8.893    0.030788   0.0044936      311.13     0.99772
   -8.0558    0.023094   0.0026061      134.64     0.99947
   -7.8117    0.024538   0.0023767      88.026     0.99931
   -9.0365    0.028682   0.0037894      242.88     0.99911
    1.1321    0.014489    0.001683      154.98     0.99384
     4.718    0.019667   0.0021243       119.2     0.99791
    4.7531    0.032828   0.0042213      142.88     0.99772
    5.0989     0.03667   0.0049031      407.61     0.99204
    5.2102    0.049952    0.006766      263.93     0.99494
     4.092    0.023801   0.0025727      158.06       0.994
    8.5964    0.026447   0.0032727      189.22     0.99904
    1.9219    0.021416    0.001918      116.67     0.99613
    3.7174    0.016389    0.002222       270.8     0.99782
    19.037    0.039097   0.0047966      162.95      0.9988
    6.8283    0.028461   0.0034783      230.31     0.99714
----------------------------------------------------------
```

```
R_geweke = store(:,5);
R_geweke(24) = [];
```

```
subplot(2,1,2)
b = bar(R_geweke,'FaceColor','flat');

for i = 1:5
b.CData(i,:) = [211,23,24]./255;
end

for i = 6:14
b.CData(i,:) = [15,104,82]./255;
end

for i = 15:23
b.CData(i,:) = [211,119,46]./255;
end

for i=24:32
b.CData(i,:) = [62,137,168]./255;
end



b.CData(33,:) = [217,76,33]./255;
set(gca,'XTickLabel','');
hold on;
line([0.2, 38], [0.9, 0.9],'Color', [0.1,0.1,0.1],'LineStyle','--',LineWidth=2  );
set(gca,'FontSize',20);
xlim([0 35])
ylabel('R_{geweke}')
yticks([0 0.2 0.4 0.6 0.8 0.9 1]);


set(gca, 'XTick', [3 10 19 28 33]);
set(gca, 'XTickLabel', {'r_i' '\beta_{ij} ' '\phi_{ij}' '\tau_{ij}' 'D_c'});
```



Now showing the traceplots for all the parameters inferred from the SEIVD model

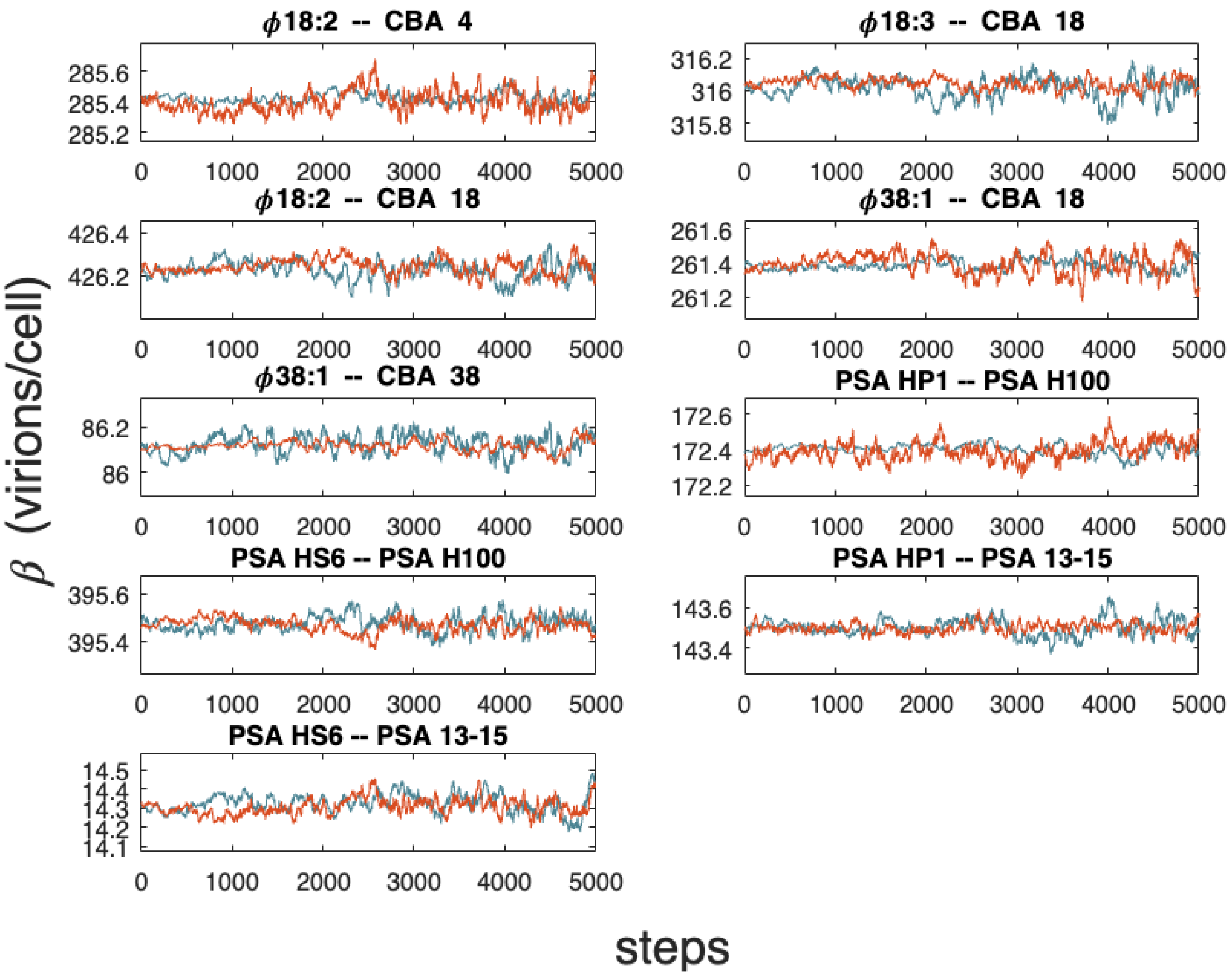
Firstly for burst sizes

```
addpath('./figures/')
```

```
Warning: Name is nonexistent or not a directory: /Users/rdey33/Downloads/VIMIMO/example_notebooks/./
figures
```

```
fig1 = figure;

transient_id = 5000;


color1 = [76,132,147]./255;
```

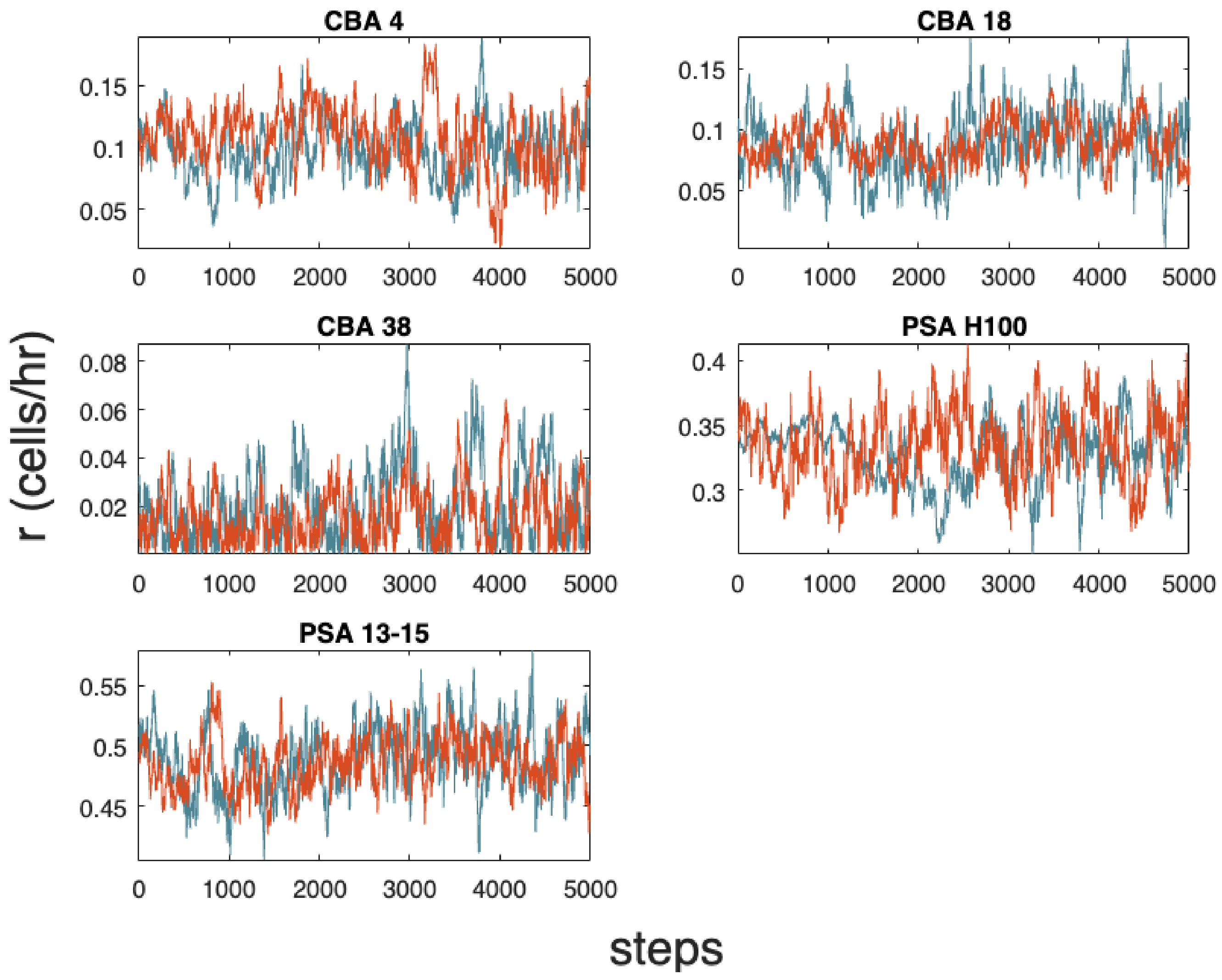
```
color2 = [217,76,33]./255;

for i = 1:9

subplot(5,2,i)
plot(chain_1(transient_id:end,5+i),'Color',color1 );
xlim([0 5000])
hold on;

end


for i = 1:9

subplot(5,2,i)
plot(chain_2(transient_id:end,5+i),'Color',color2);
ylim([  min(min(chain_1(transient_id:end,5+i)),min(chain_2(transient_id:end,5+i)))-0.1
xlim([0 5000])
make_title(i);

end

han=axes(fig1,'visible','off');
%han.Title.Visible='on';
han.XLabel.Visible='on';
han.YLabel.Visible='on';
ylabel(han,'\beta (virions/cell)');
xlabel(han,'steps');
%title(han,'yourTitle');
set(gca,'FontSize',18)
```



For host growth rates

```
fig2 = figure;


for i = 1:5

subplot(3,2,i)
plot(chain_1(transient_id:end,i), 'Color',color1 );
xlim([0 5000])
hold on;

end


for i = 1:5

subplot(3,2,i)
plot(chain_2(transient_id:end,i),'Color',color2);
```

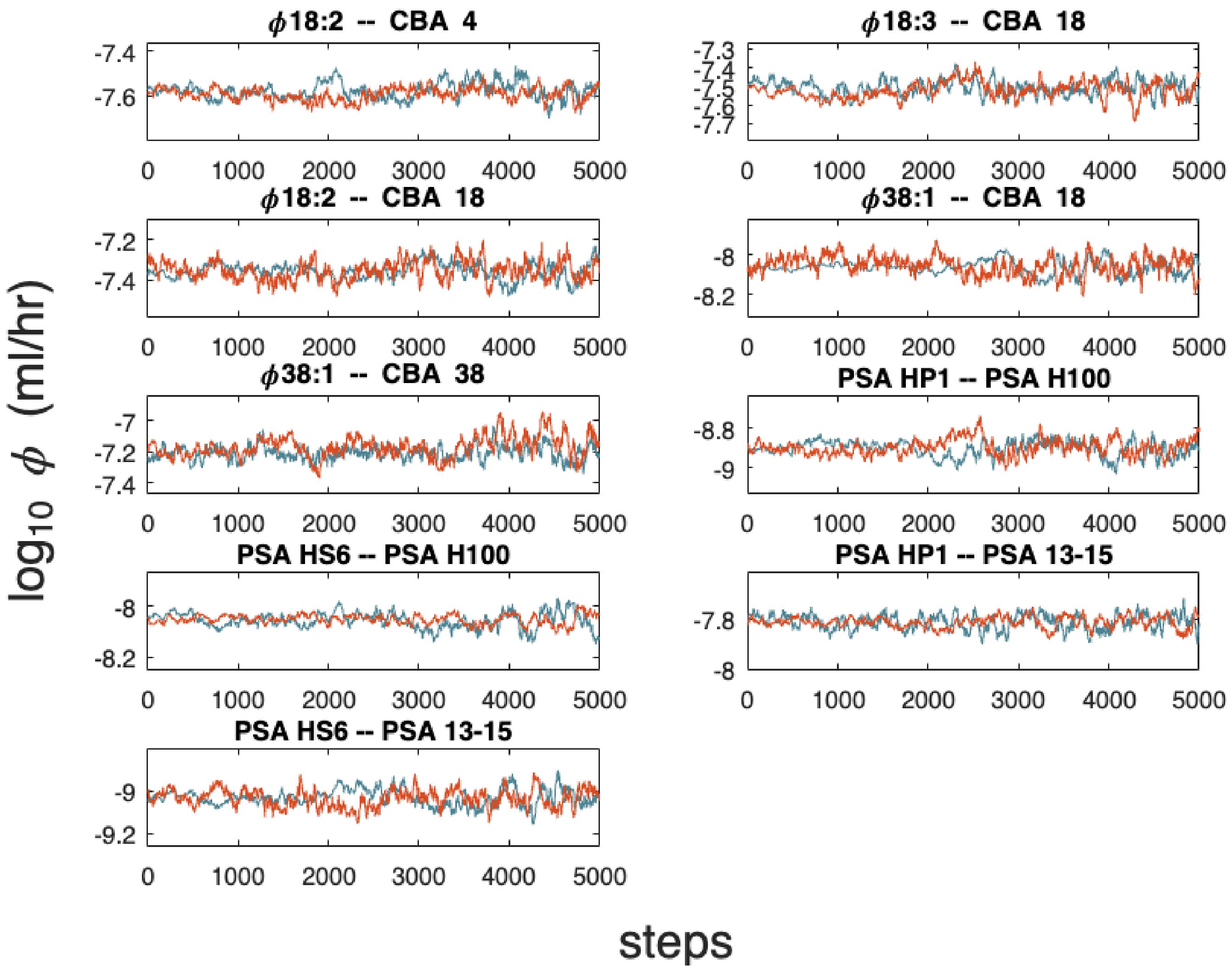
```
ylim([  min(min(chain_1(transient_id:end,i)),min(chain_2(transient_id:end,i))),  max(ma
xlim([0 5000])
make_title_host(i);

end

han=axes(fig2,'visible','off');
%han.Title.Visible='on';
han.XLabel.Visible='on';
han.YLabel.Visible='on';
ylabel(han,'r (cells/hr)');
xlabel(han,'steps');
%title(han,'yourTitle');
set(gca,'FontSize',18)
```



For viral adsoprtion rates

```
fig3 = figure;
```

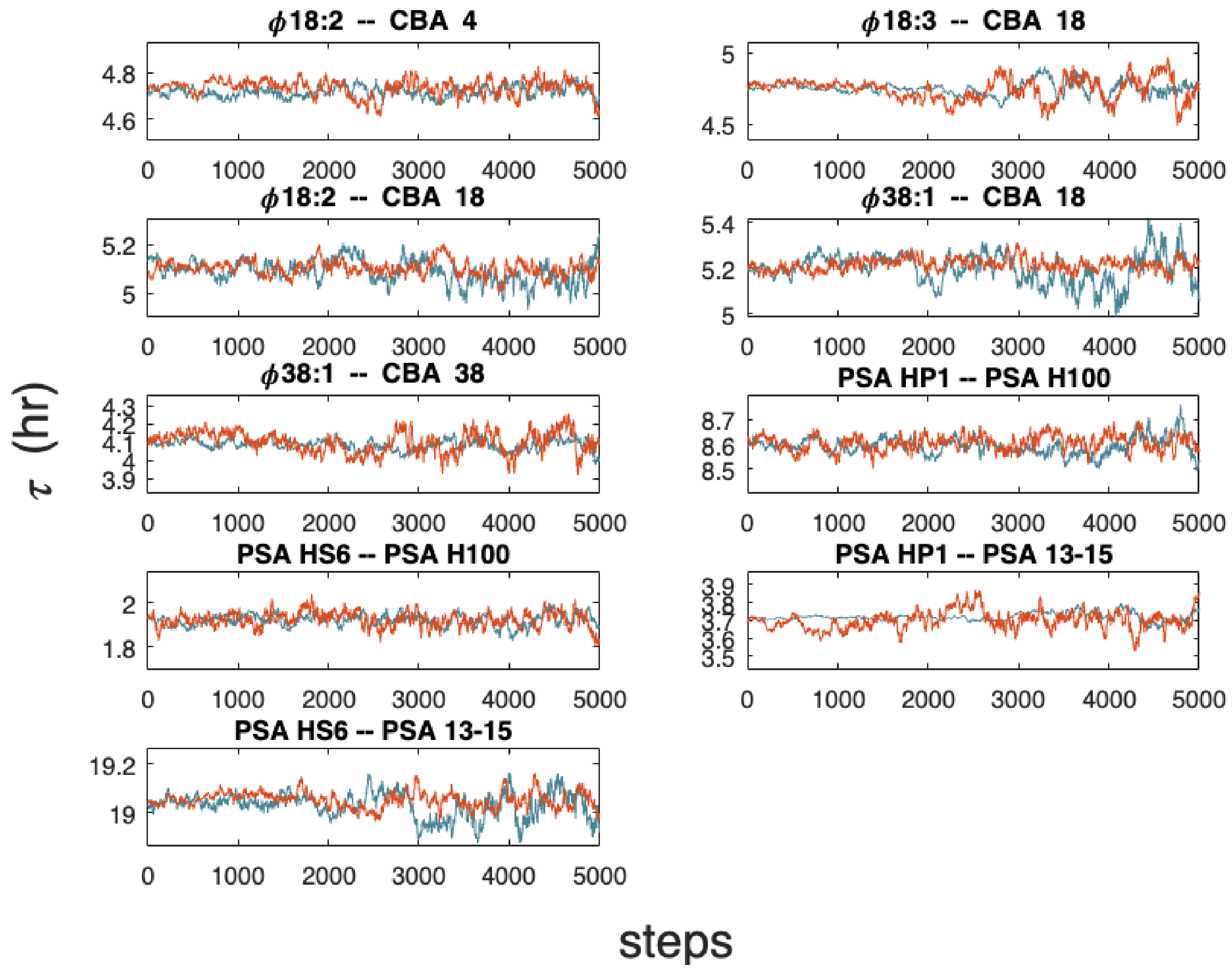
```
for i = 1:9
subplot(5,2,i)
plot(chain_1(transient_id:end,14+i), 'Color',color1 );
xlim([0 5000])
hold on;
end



for i = 1:9
subplot(5,2,i)
plot(chain_2(transient_id:end,14+i),'Color',color2);
ylim([  min(min(chain_1(transient_id:end,14+i)),min(chain_2(transient_id:end,14+i)))-0
xlim([0 5000])
make_title(i);
end

han=axes(fig3,'visible','off');
%han.Title.Visible='on';
han.XLabel.Visible='on';
han.YLabel.Visible='on';
ylabel(han,'log_{10} \phi (ml/hr) ');
xlabel(han,'steps');
%title(han,'yourTitle');
set(gca,'FontSize',18)
```



For viral latent periods

```
fig4 = figure;

for i = 1:9

subplot(5,2,i)
plot(chain_1(transient_id:end,24+i),'Color',color1);
xlim([0 5000])
hold on;

end



for i = 1:9

subplot(5,2,i)
plot(chain_2(transient_id:end,24+i),'Color',color2);
```

```
ylim([  min(min(chain_1(transient_id:end,24+i)),min(chain_2(transient_id:end,24+i)) -0

xlim([0 5000])
make_title(i);
end



han=axes(fig4,'visible','off');
%han.Title.Visible='on';
han.XLabel.Visible='on';
han.YLabel.Visible='on';
ylabel(han,'\tau (hr) ');
xlabel(han,'steps');
%title(han,'yourTitle');
set(gca,'FontSize',18)
```


ϕ18:2 -- CBA 4
ϕ18:3 -- CBA 18
ϕ18:2 -- CBA 18
ϕ38:1 -- CBA 18
ϕ38:1 -- CBA 38
PSA HP1 -- PSA H100
PSA HS6 -- PSA H100
PSA HP1 -- PSA 13-15
PSA HS6 -- PSA 13-15
τ (hr)
steps