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```
function M2M_report(m2m_result)

%UNTITLED3 Summary of this function goes here
% Detailed explanation goes here
```

Data generation

```
mydata = m2m_result.data_gen.mydata;
mydata = M2M_purge(mydata);
errordata = m2m_result.data_gen.errordata;
statenames = m2m_result.data_gen.statenames;

for i = 1:size(mydata,1)
    rect = [20 20 1024 768];
    fh = figure('Color','w','Position',rect);
    figure(fh)
    grid on
    scatter(mydata(28,:),mydata(i,:))
    hold on
    scatter(errordata(28,:),errordata(i,:))
    title(statenames(i))
    xlabel(statenames(28))
    ylabel(statenames(i))
end
```

Not enough input arguments.

```
Error in M2M_report (line 6)
mydata = m2m_result.data_gen.mydata;
```

DNA simulation

```
MYDATA = m2m_result.data_gen.MYDATA;
ip = [1,2,3,4,5,6,7,11,12];
a = floor(size(ip,2)^(1/2));
b = ceil(size(ip,2)/a);
sum=0;
rect = [20 20 1024 768];
fig_dna = figure('Color','w','Position',rect);
figure(fig_dna)
while(sum <size(ip,2))
    for i = ip
```

```

        sum = sum + 1;
        hold on
        grid on
        yyaxis left
        subplot(b,a,sum)
        scatter(MYDATA(33,:),normdata(MYDATA(i,:)));
        legend(statenames(i))
        title('DNA duplication')
        xlabel('Time [h]')
        ylabel('Concentration (a.u.)')

        yyaxis right
        scatter(MYDATA(33,:),MYDATA(32,:), '*')
        ylabel('DNA')
        axis([0 max(MYDATA(end,:))+1 1.5 4.5])
    end
end

```

Wanderlust all combinations

```

if doplots % subplot layout % possible combinations of dimensions in 2d C = nchoosek(1:d,2);
%WChooseK ? a = floor(size(C,1)^(1/2)); b = ceil(size(C,1)/a);

rect = [20 20 800 600]; G.fh = figure('Color','w','Position',rect);

for i = 1:size(C,1)

    subplot(a,b,i)
    [~,dens,X,Y] = kde2d(data(:,C(i,:)));
    pcolor(X,Y,dens); shading interp % density
    hold on
    scatter(data(:,C(i,1)),data(:,C(i,2)),1,'w.') % all datapoints
    scatter(data(G.Opts.s,C(i,1)),data(G.Opts.s,C(i,2)),1,'rx') % start po
    plot(ywant(C(i,1,:),:),ywant(C(i,2,:),:),'r','LineWidth',3) % path
    xlabel(dimension_names{C(i,1)})
    ylabel(dimension_names{C(i,2)})

end end

```

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