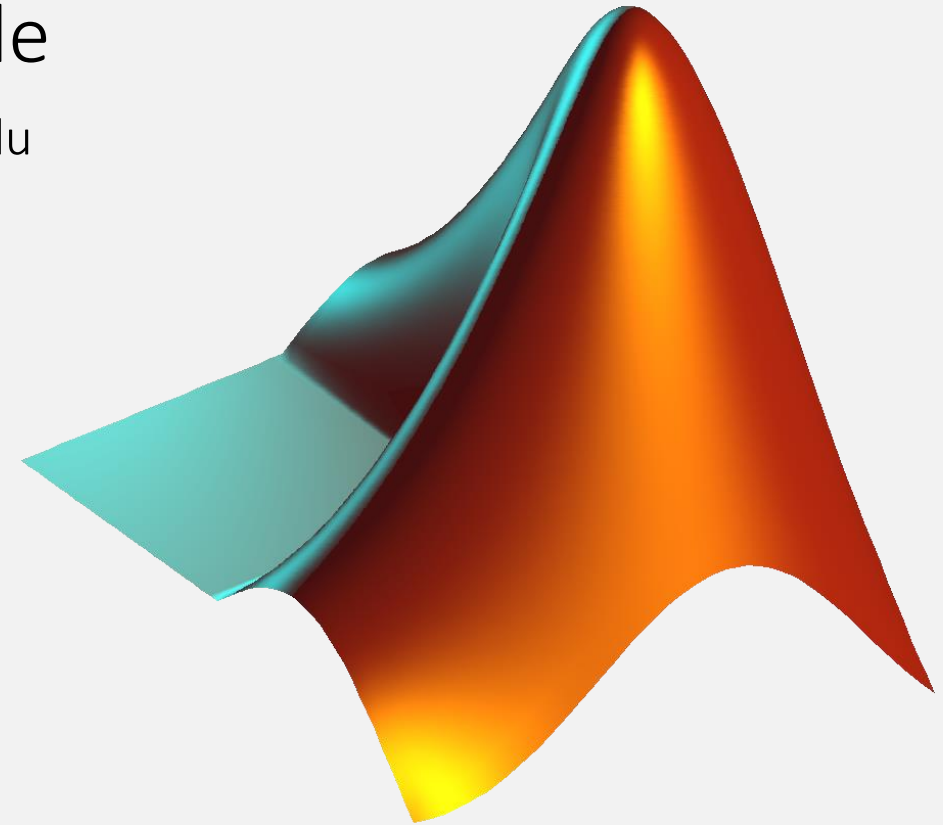


# Intro to MATLAB

## Part 3/3

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# Outline of the workshop

## Day 1

- Interface
- Command lines and basic syntax
- Variables and operations
- Scripts
- `if` statements

## Day 2

- `for` and `while` loops
- More matrices
- Functions
- Files

## Day 3

- Plotting
- Introduction to dynamical systems: ODEs

# Reminders

# Reminders

## if statements

```
exp1 = 400;
exp2 = 500;
% conditional testing
if (exp1 > exp2)
    max = exp1
elseif (exp1 == exp2)
    max = 'both are equal'
else
    max = exp2
end
```

## while loops

```
aa = 10;
% while loop execution
while (aa < 20)
    disp(aa)
    aa = aa + 1;
end
```

- Declare your variables
- Set up the incrementation

## for loops

```
% for loop execution
for (bb = 10:19)
    disp(bb)
end
```

## Functions

```
function infoSeq = describeSeq(seq)
    seqLength = length(seq);
    infoSeq = sprintf('The sequence %s has %d nucleotides', seq, seqLength);
```

```
describeSeq('TATCCGCG')
```

- Start the script with the function definition
- Name the file with the function name

# Reminders

## Read files

```
data = importdata(inputFile, delimiter, headerLines);
```

```
data = importdata('inputFile.txt', '\t', 1);
```

## Write files

```
fid = fopen('outputFile.txt', 'w');  
fprintf(fid, 'Value I want to save %d\n', exp1Genes{ii}, exp1Results(ii));  
fclose(fid);
```

```
fid = fopen(outputFile, 'w');  
fprintf(fid, 'Value I want to save %d\n', exp1Genes{ii}, exp1Results(ii));  
fclose(fid);
```

# Practice

Transform this script into a set of functions we can apply to the larger gene expression dataset, and saving data in .csv

```
exp1Genes = {'1L1A', 'NFKBIA', 'BCL2'};
exp1Results = [120, 446, 653];
threshold = 200;
for (ii = 1:length(exp1Results))
    if (exp1Results(ii) > threshold)
        fprintf('Genes %s expression %d\n', exp1Genes{ii}, exp1Results(ii))
    end
end
```

## Files you need

- Mitchell\_gene\_data.txt dataset

## Models

- printGenesAboveThreshold.m script
- F\_printGeneExpression function
- F\_printGeneExpressionFromFile function

1. Import file
2. Extract data of interest
3. Compare each gene expression level to the threshold
4. If it is above, save its name and expression level on a file

# Practice

## F\_printGenesAboveThreshold

```
function out = F_printGenesAboveThreshold(exp1Genes, exp1Results, threshold,
outputFile)
    % Function returns the expression value from a gene of interest
    fid = fopen(outputFile, 'w');
    out = 'No gene found';
    for (ii = 1:length(exp1Results))
        if (exp1Results(ii) > threshold)
            fprintf(fid, '%s, %d\n', exp1Genes{ii}, exp1Results(ii));
            out = exp1Results(ii);
        end
    end
    fclose(fid);
```

# Practice

## F\_printGenesAboveThresholdFromFile

```
function out = F_printGenesAboveThresholdFromFile(inputFile, outputFile, threshold)
    % Function returns the expression value from a gene of interest
    delimiter = '\t'; % tab delimited
    headerLines = 1; % column headers are on line 1

    A = importdata(inputFile, delimiter, headerLines);
    exp1Genes = A.textdata(2:end, 1);
    exp1Results = A.data;

    fprintf('%s loaded. %d genes\n', inputFile, length(A.data));

    % call function to print gene information
    out = F_printGenesAboveThreshold(exp1Genes, exp1Results, threshold,
    outputFile);
```

```
F_printGenesAboveThresholdFromFile('Mitchell_gene_data.txt',
'output_GenesAboveThreshold.txt', 30);
```



# Plots

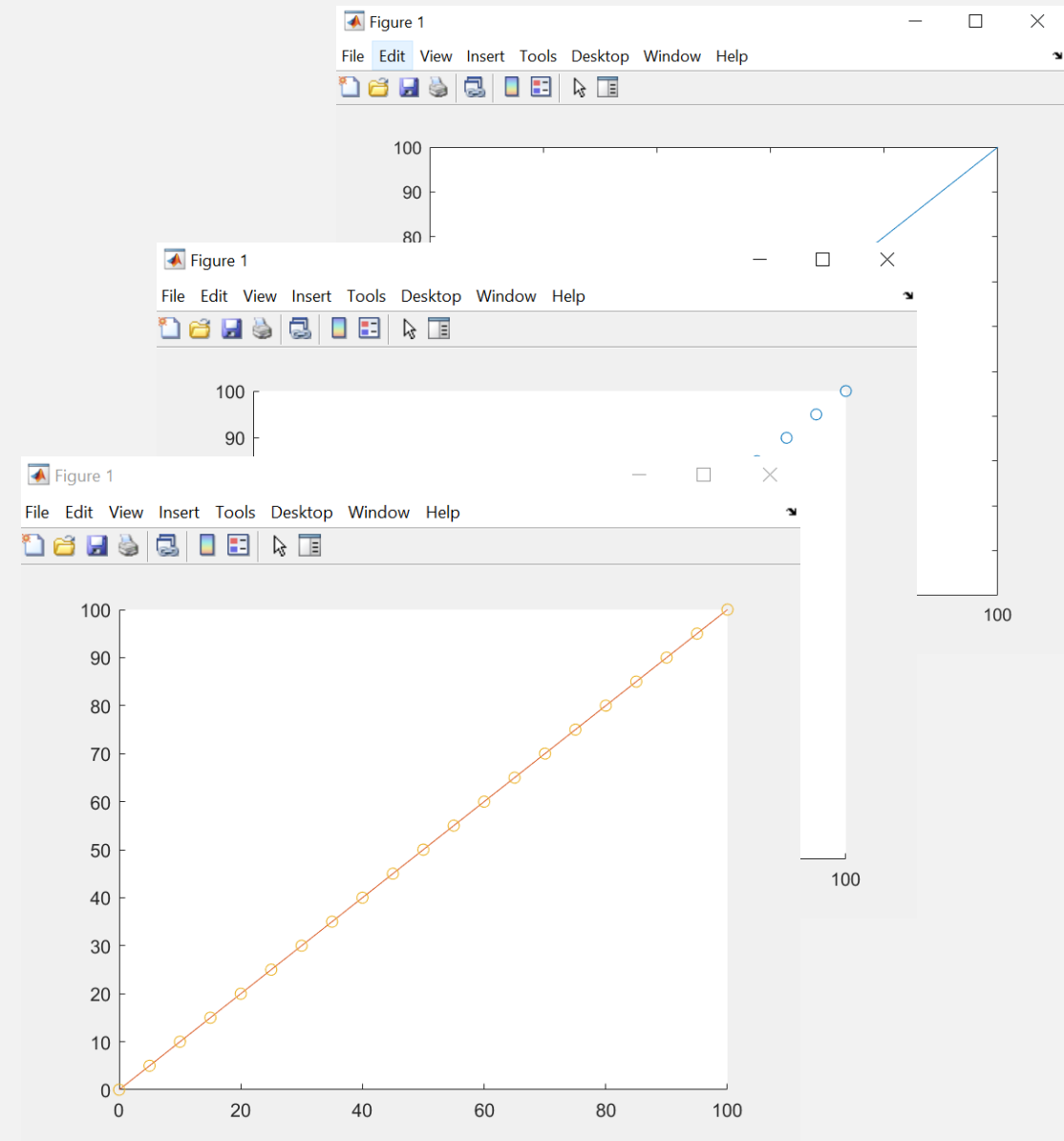
# Our first plots

- Create a plot with the function `plot`
- And others...

```
x = [0:5:100];  
y = x;  
plot(x, y);
```

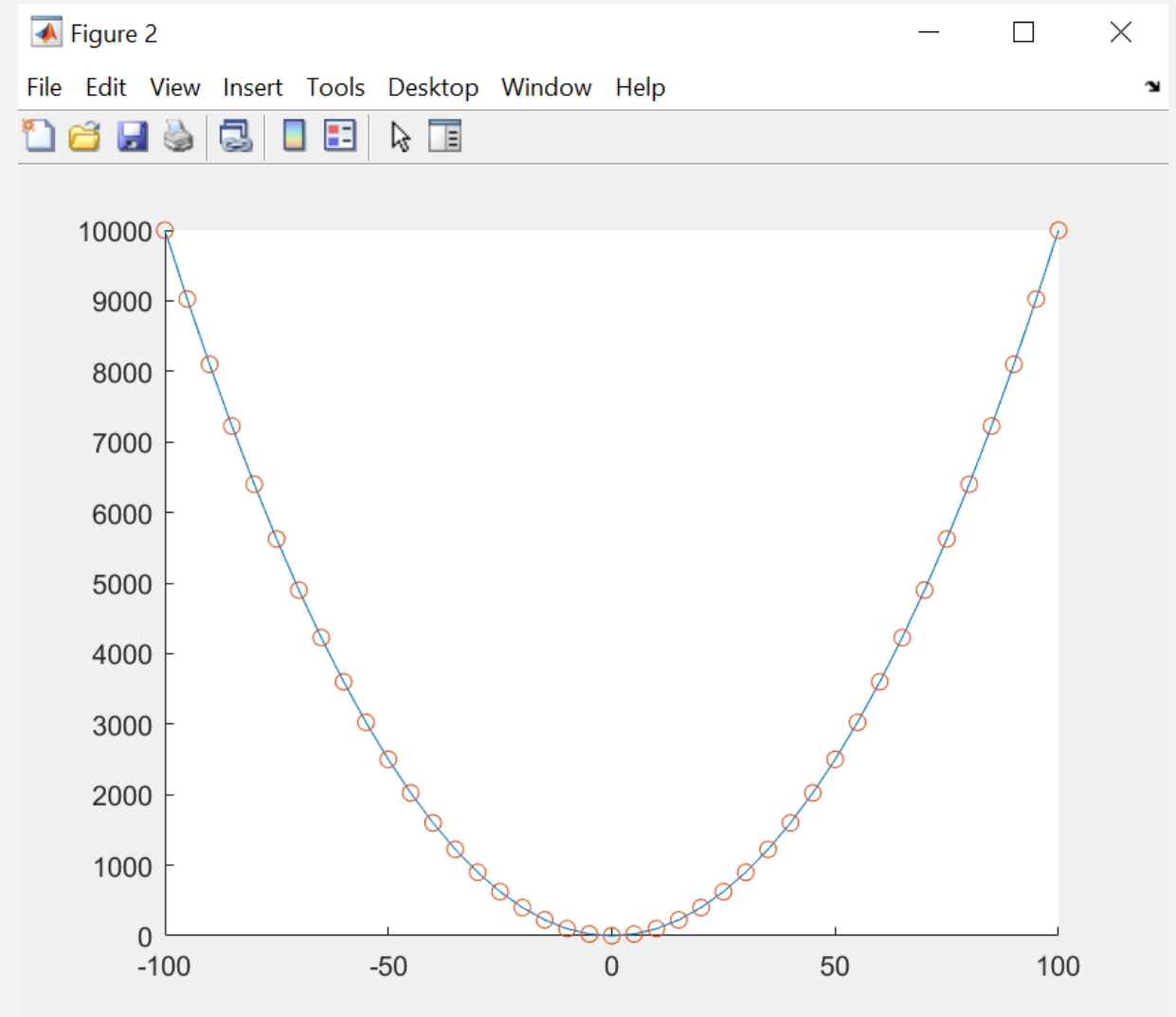
```
x = [0:5:100];  
y = x;  
plot(x, y);  
scatter(x, y);
```

```
x = [0:5:100];  
y = x;  
hold on;  
plot(x, y);  
scatter(x, y);
```



# Our first plots

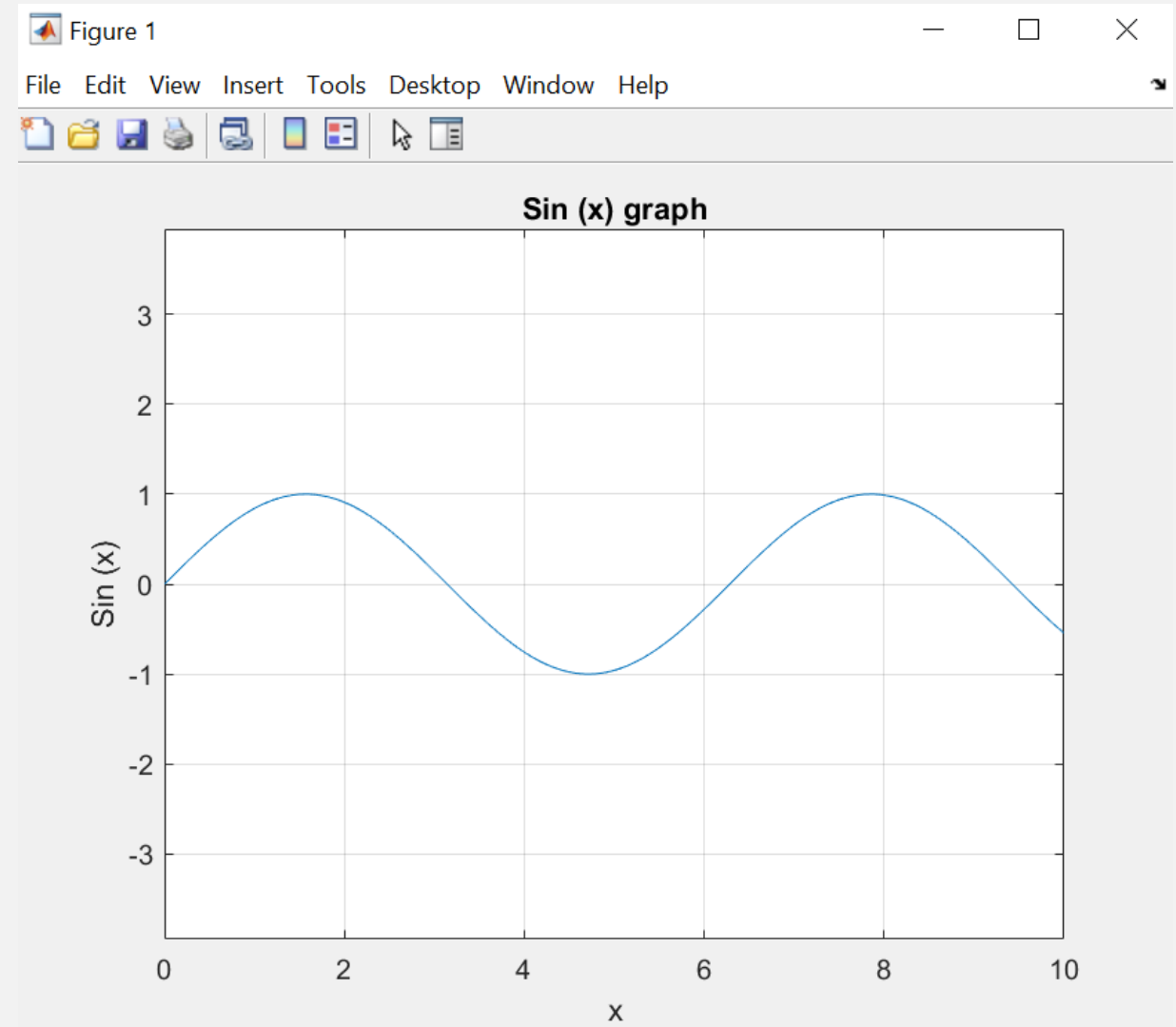
```
figure;  
x = [-100:5:100];  
y = x.^2;  
hold on;  
plot(x, y);  
scatter(x, y);
```



# Our first plots

- Customization

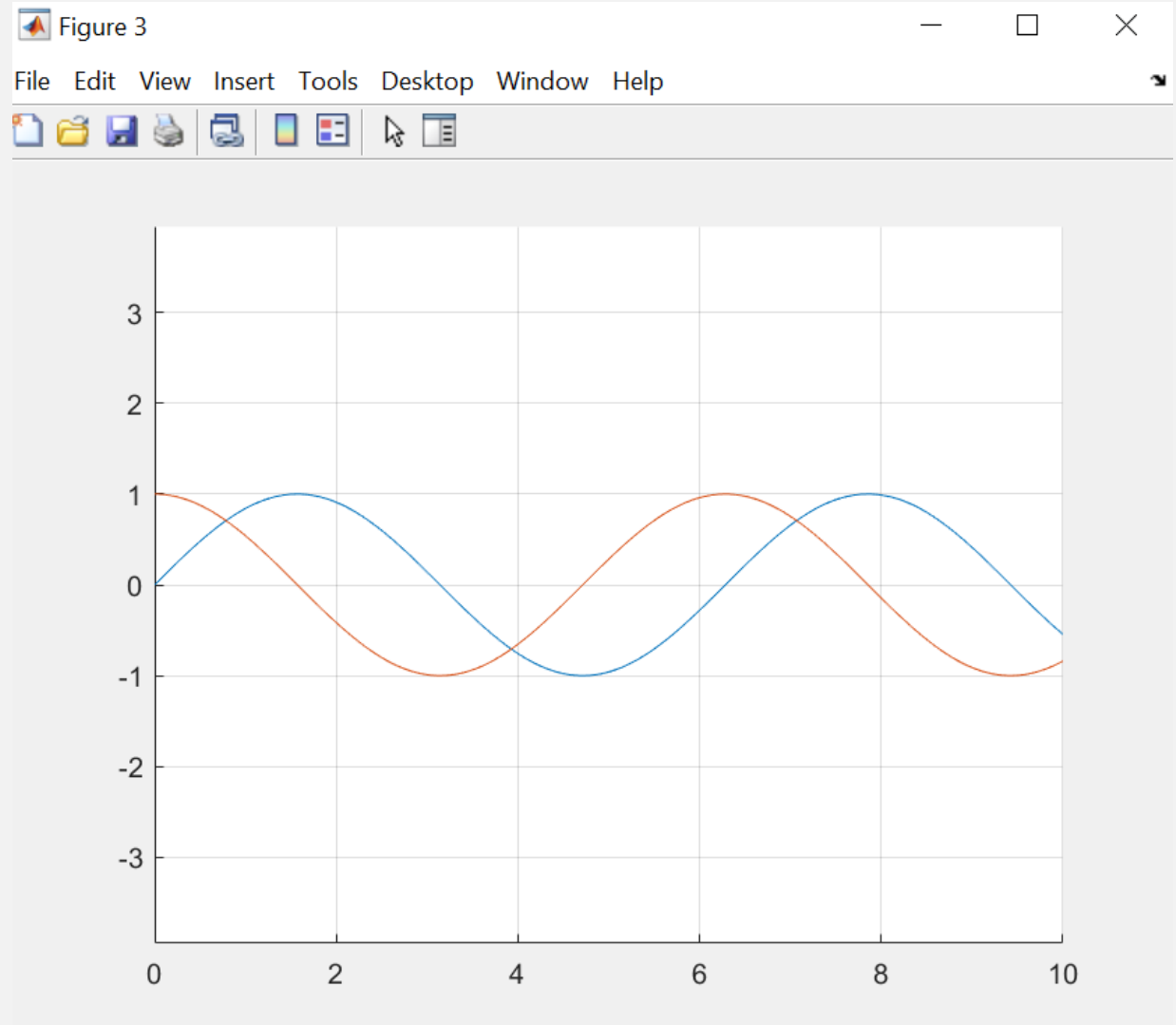
```
figure;  
x = [0:0.01:10];  
y = sin(x);  
plot(x, y);  
xlabel('x');  
ylabel('Sin (x)');  
title('Sin (x) graph');  
grid on, axis equal;
```



# Our first plots

- Customization

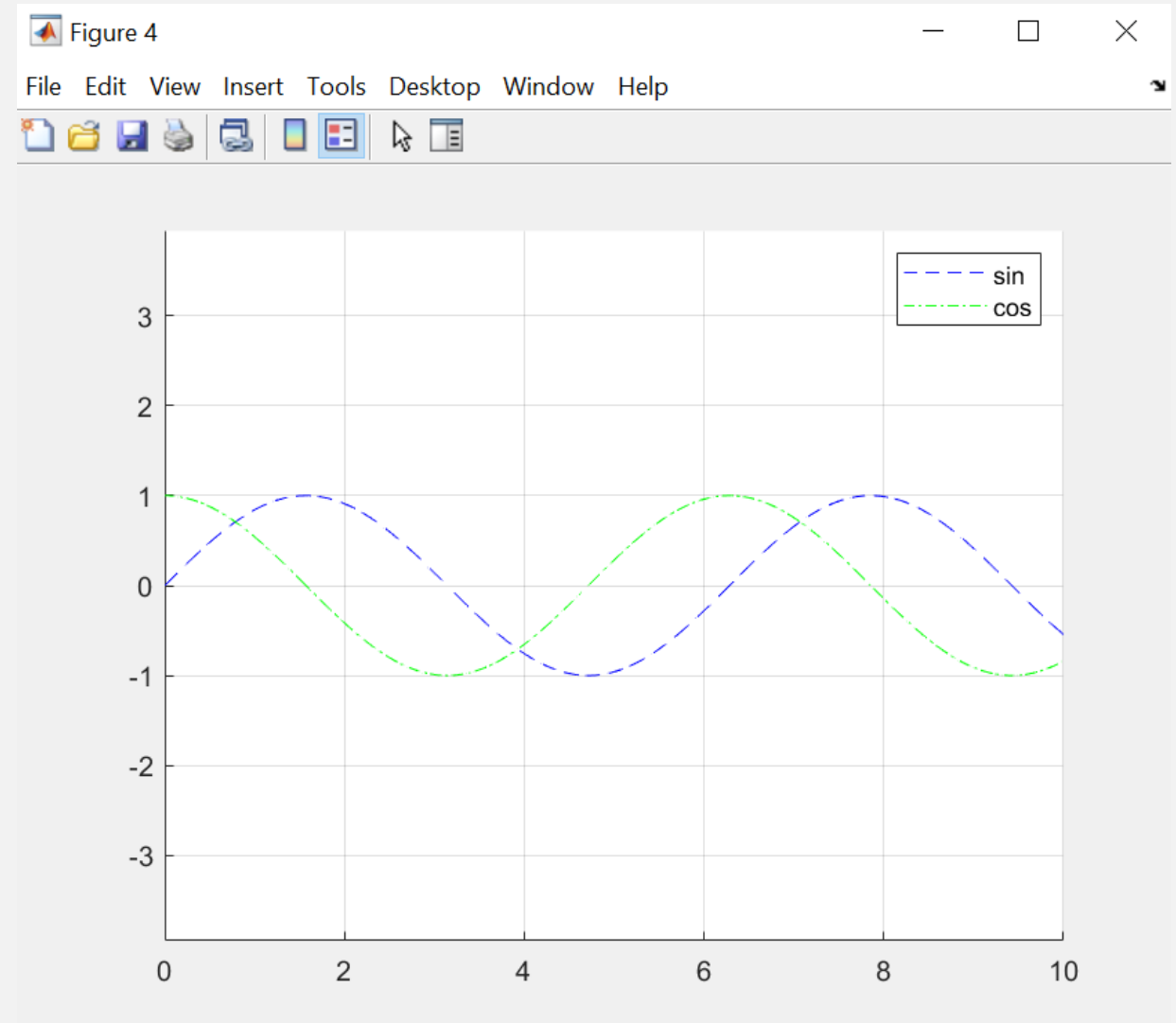
```
figure;  
x = [0:0.01:10];  
y1 = sin(x);  
y2 = cos(x);  
hold on;  
plot(x, y1);  
plot(x, y2);  
grid on, axis equal;
```



# Our first plots

- Customization

```
figure;  
x = [0:0.01:10];  
y1 = sin(x);  
y2 = cos(x);  
hold on;  
plot(x, y1, '--b');  
plot(x, y2, '-.g');  
legend({'sin', 'cos'});  
ylim([-3, 3]);  
grid on, axis equal;
```

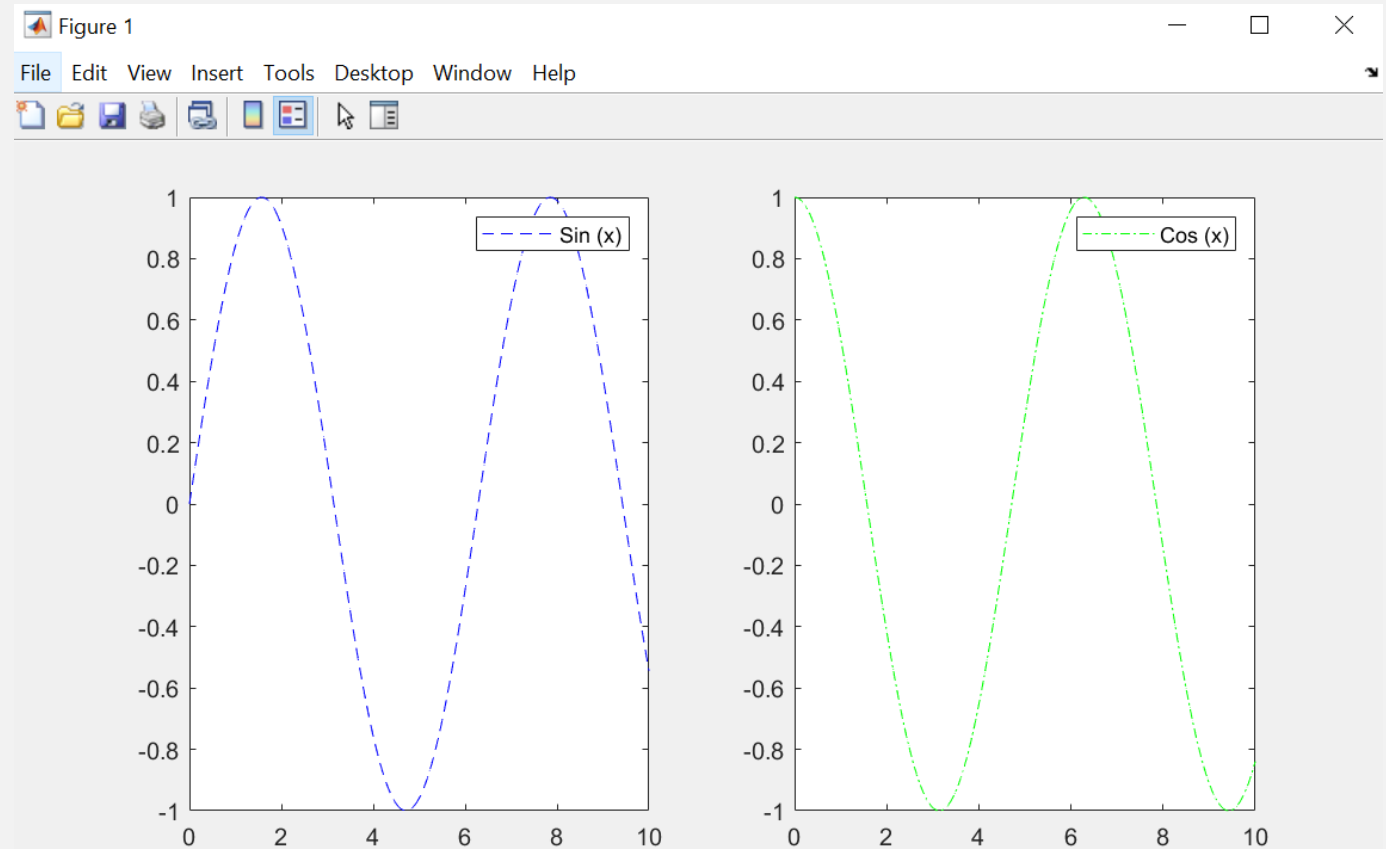


# Our first plots

- Subplots

```
figure;  
x = [0:0.01:10];  
y1 = sin(x);  
y2 = cos(x);  
subplot(1, 2, 1);  
plot(x, y1, '--b');  
legend({'Sin (x)'});  
subplot(1, 2, 2);  
plot(x, y2, '-.g');  
legend({'Cos (x)'});
```

```
>> close all
```



# Bar plots

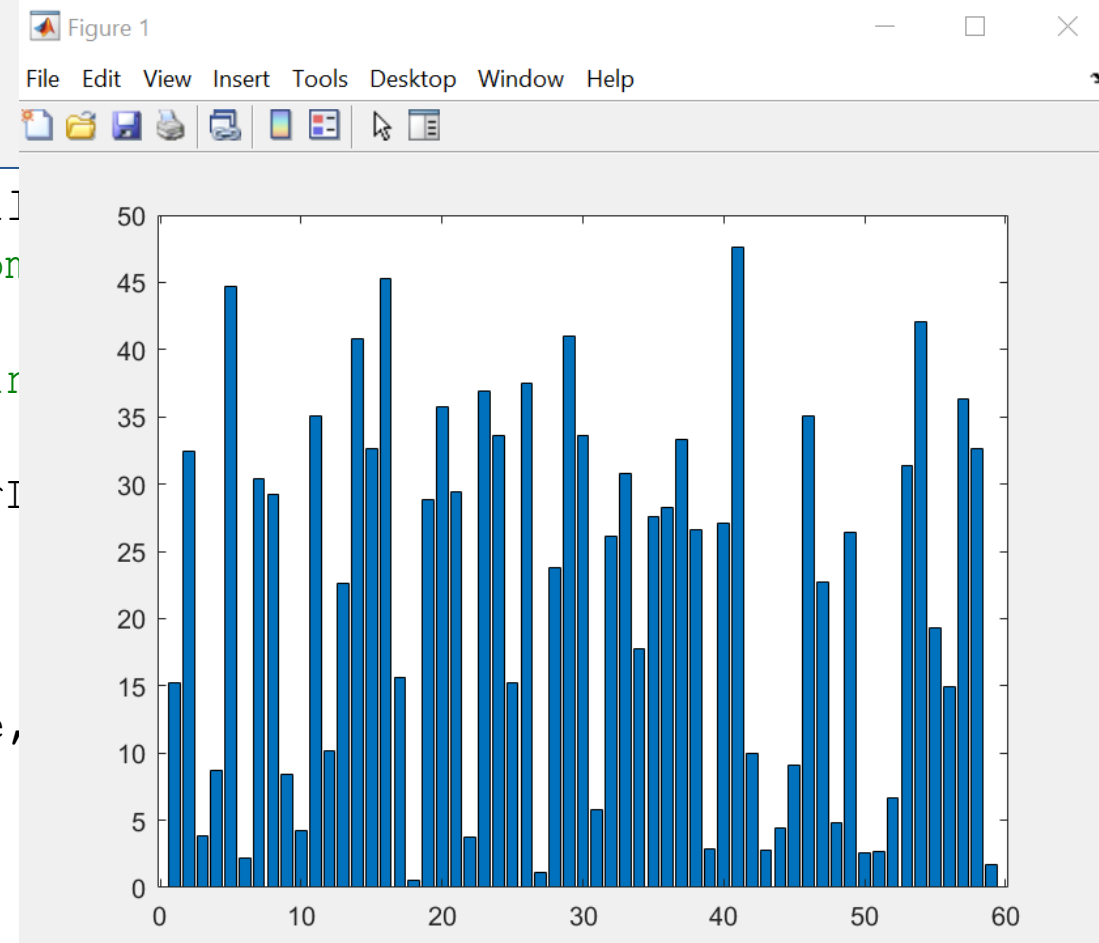
```
function out = F_printGenesAboveThresholdFromFile(inputFile, outputFile, threshold)
% Function returns the expression value from a file
delimiter = '\t'; % tab delimited
headerLines = 1; % column headers are on line 1

A = importdata(inputFile, delimiter, headerLines);
exp1Genes = A.textdata(2:end, 1);
exp1Results = A.data;

fprintf('%s loaded. %d genes\n', inputFile, size(exp1Genes, 1));

% call function to print gene information
out = F_printGenesAboveThreshold(exp1Genes, outputFile, threshold);

% plot data
bar(exp1Results);
```





# Bar plots

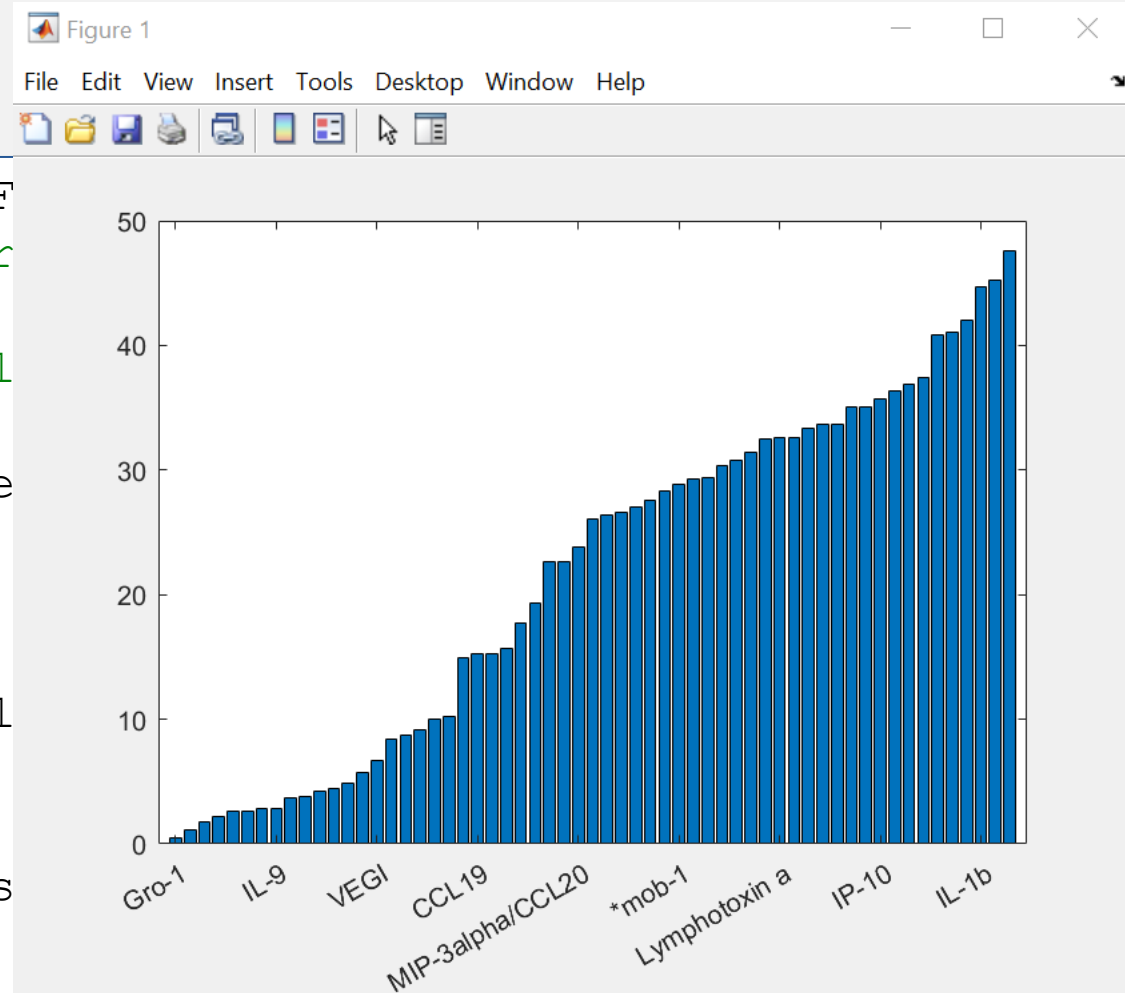
```
function out = F_printGenesAboveThresholdFromF
% Function returns the expression value for
delimiter = '\t'; % tab delimited
headerLines = 1; % column headers are on line 1

A = importdata(inputFile, delimiter, headerLines);
exp1Genes = A.textdata(2:end, 1);
exp1Results = A.data;

fprintf('%s loaded. %d genes\n', inputFile, length(exp1Genes));

% call function to print gene information
out = F_printGenesAboveThreshold(exp1Genes, exp1Results,
outputFile);

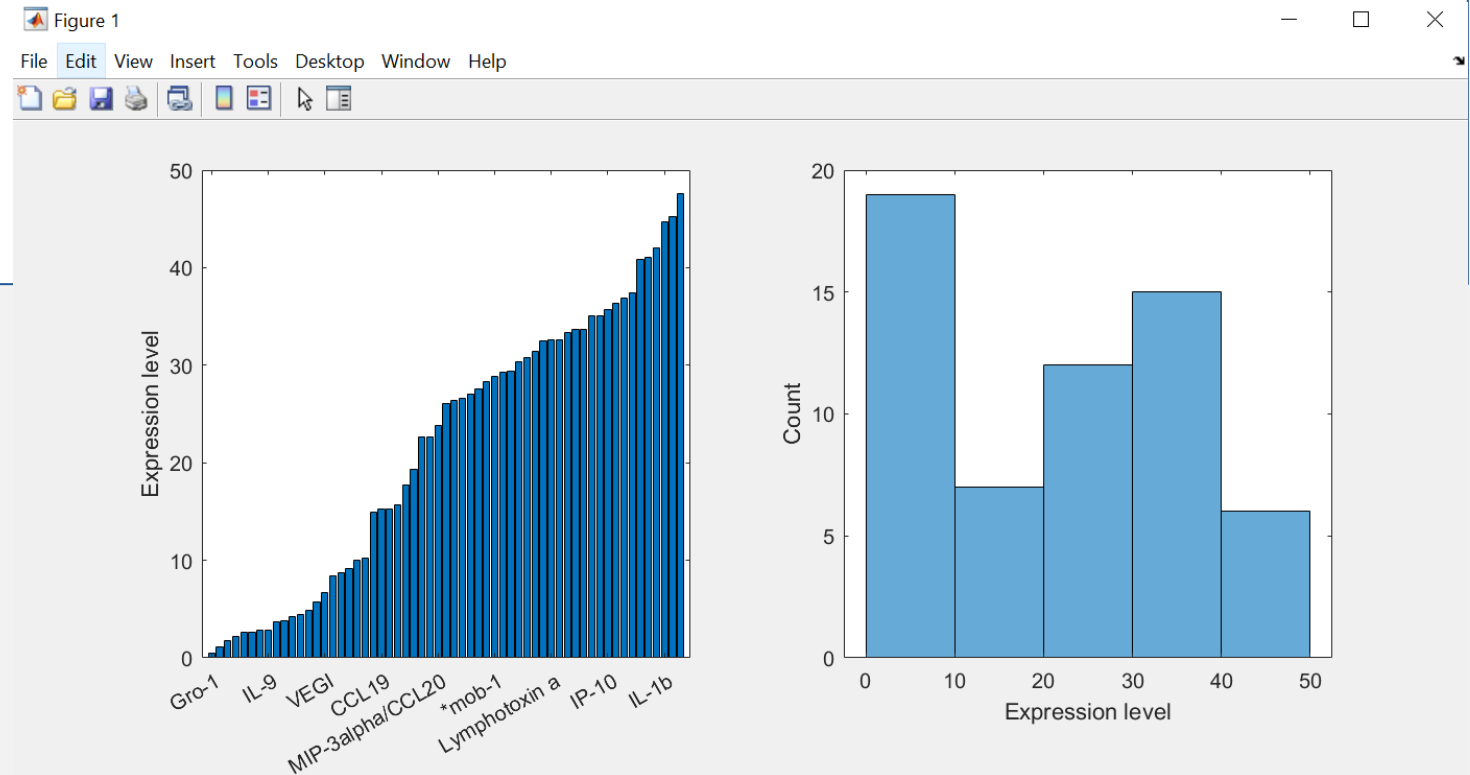
% plot data
[exp1ResultsSorted, kk] = sort(exp1Results);
namesSorted = exp1Genes(kk);
bar(exp1ResultsSorted);
set(gca, 'XTick', 1:7:length(exp1Genes), 'XTickLabel', namesSorted);
```



# Bar plots

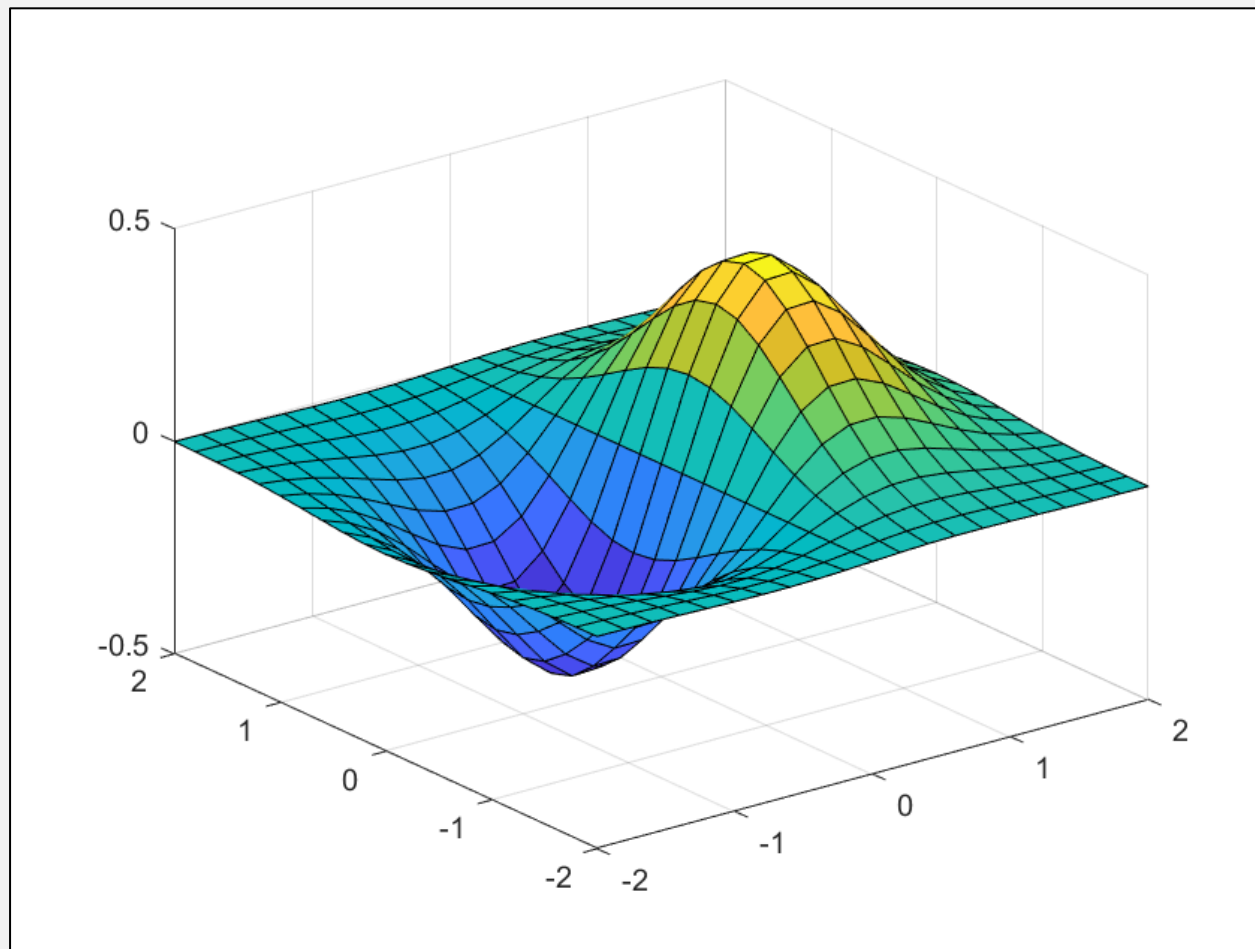
```
% plot data
```

```
[exp1ResultsSorted, kk] = sort(exp1Results);  
namesSorted = exp1Genes(kk);  
subplot(1,2,1);  
bar(exp1ResultsSorted);  
set(gca, 'XTick', 1:7:length(exp1Genes), 'XTickLabel', namesSorted);  
ylabel('Expression level');  
subplot(1,2,2);  
histogram(exp1Results);  
xlabel('Expression level');  
ylabel('Count');
```



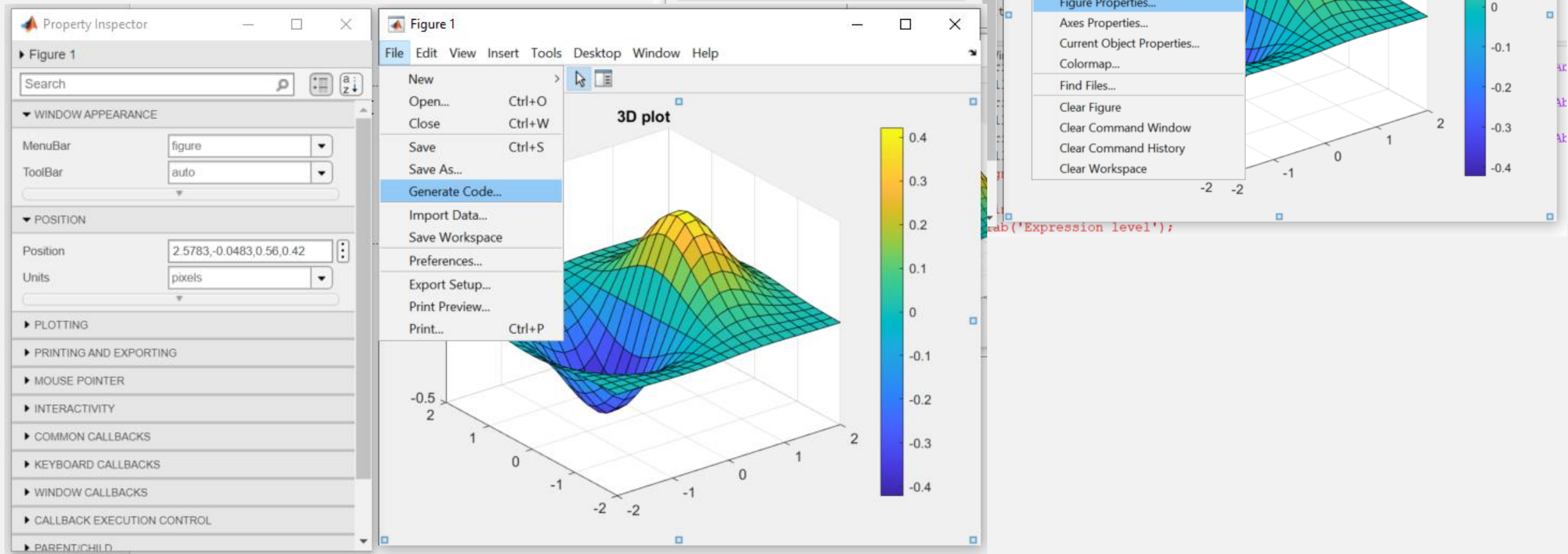
# 3D plots

```
% generate x and y coordinates  
[x, y] = meshgrid(-2:.2:2);  
  
% set z as a function of x and y  
z = x.*exp(-x.^2 - y.^2);  
  
% plot  
surf(x, y, z);
```



# Plot editor

- Customize your plot
- Generate a function to recreate it



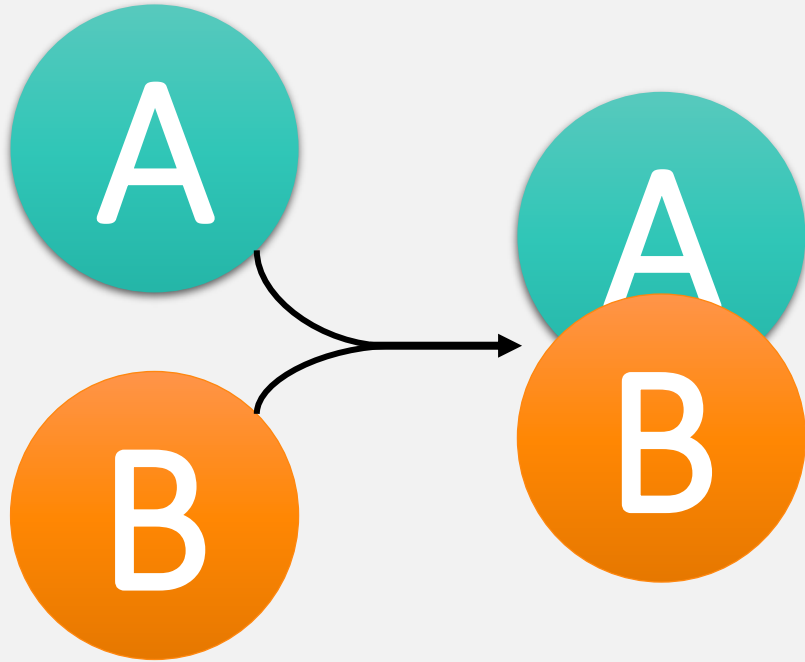
# Introduction to dynamical systems: ODEs

# Modeling dynamical systems

- Modeling biological processes with equations
- Ordinary differential equations for temporal dynamics
  - Test or generate hypotheses
  - Mechanistic explanation of the results
  - Visualization
  - ...

# Modeling dynamical systems

- Case study: 2 metabolites (A & B) forming an (hetero)polymer (AB)



How do the concentrations  $[A]$ ,  $[B]$ , and  $[AB]$  vary over time?

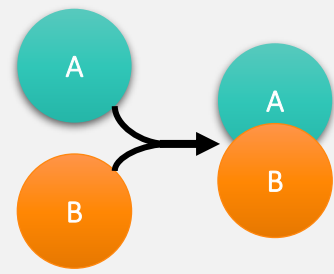
$$\frac{d[A]}{dt} \propto [A][B] \longrightarrow \frac{d[A]}{dt} = -k[A][B]$$

$$\frac{d[B]}{dt} \propto [A][B] \longrightarrow \frac{d[B]}{dt} = -k[A][B]$$

$$\frac{d[AB]}{dt} \propto [A][B] \longrightarrow \frac{d[AB]}{dt} = k[A][B]$$

# Modeling dynamical systems

- Case study: 2 metabolites (A & B) forming an (hetero)polymer (AB)



## ODE function, defining the rates of changes

```
function delta = F_odeFile(t, x)
% ODE function for a system of differential equations
% t = vector of time points
% x = vector of metabolites

% parameters
k = 7;

% rate = k[A][B]
bindingRate = k * x(1) * x(2);

% store the rate of change for each metabolite
delta = zeros(length(x), 1);

% d[A]/dt = - rate
delta(1) = -bindingRate;
% d[B]/dt = - rate
delta(2) = -bindingRate;
% d[AB]/dt = - rate
delta(3) = bindingRate;

end
```

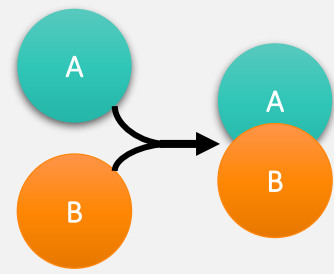
System of differential equations

$$\left\{ \begin{array}{l} \frac{d[A]}{dt} = -k[A][B] \\ \frac{d[B]}{dt} = -k[A][B] \\ \frac{d[AB]}{dt} = k[A][B] \end{array} \right.$$



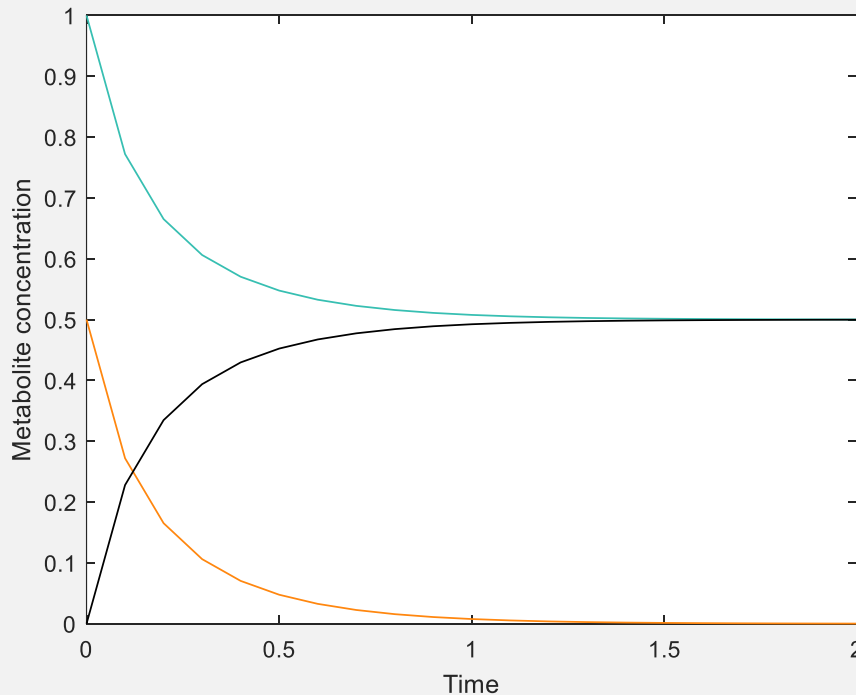
# Modeling dynamical systems

- Case study: 2 metabolites (A & B) forming an (hetero)polymer (AB)



## ODE solver

```
% ODE solver: ode15s(ODE function, time span, initial  
conditions)  
[t, y] = ode15s(@F_odeFile, [0:0.1:2], [1,0.5,0]);  
plot(t, y);
```



System of differential equations

$$\frac{d[A]}{dt} = -k[A][B]$$

$$\frac{d[B]}{dt} = -k[A][B]$$

$$\frac{d[AB]}{dt} = k[A][B]$$

# Modeling dynamical systems

- Case study: fancier version

## ODE function, defining the rates of changes

```
function delta = F_odeFile2(t, x)
% ODE function for a system of differential equations
% t = vector of time points
% x = vector of metabolites

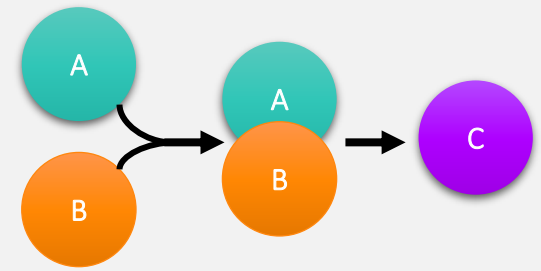
% parameters
k = 7;
k2 = 0.7;

% rate = k[A][B]
bindingRate = k * x(1) * x(2);
conversionRate = k2 * x(3);

% store the rate of change for each metabolite
delta = zeros(length(x), 1);

% d[A]/dt = - rate
delta(1) = -bindingRate;
% d[B]/dt = - rate
delta(2) = -bindingRate;
% d[AB]/dt = - rate
delta(3) = bindingRate - conversionRate;
% d[C]/dt = - rate
delta(4) = conversionRate;

end
```



System of differential equations

$$\frac{d[A]}{dt} = -k[A][B]$$

$$\frac{d[B]}{dt} = -k[A][B]$$

$$\frac{d[AB]}{dt} = k[A][B] - k_2[AB]$$

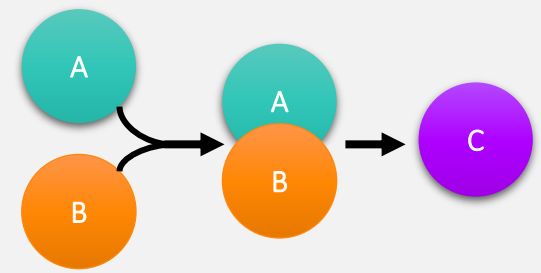
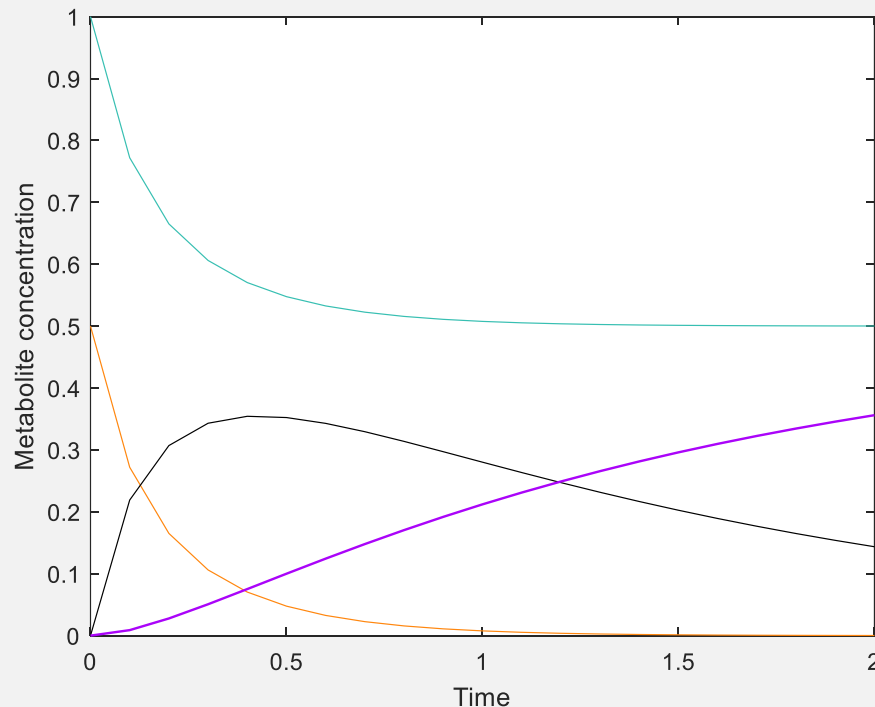
$$\frac{d[C]}{dt} = k_2[AB]$$

# Modeling dynamical systems

- Case study: fancier version

## ODE solver

```
% ODE solver: ode15s(ODE function, time span, initial  
conditions)  
[t, y] = ode15s(@F_odeFile2, [0:0.1:2], [1,0.5,0,0]);  
plot(t, y);
```



System of differential equations

$$\frac{d[A]}{dt} = -k[A][B]$$

$$\frac{d[B]}{dt} = -k[A][B]$$

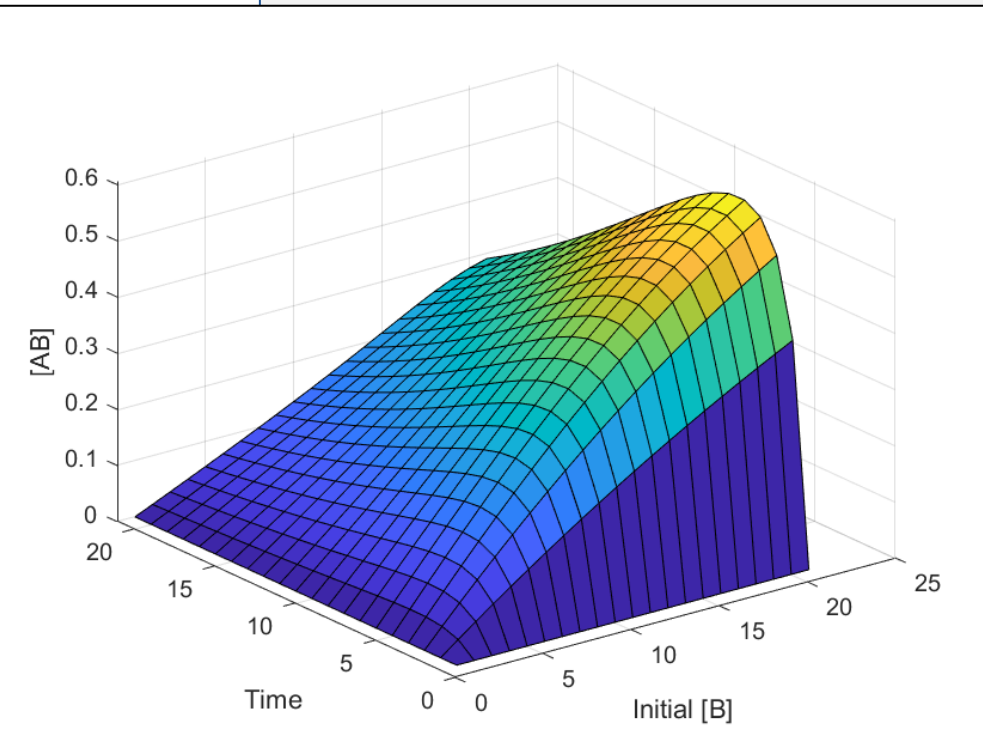
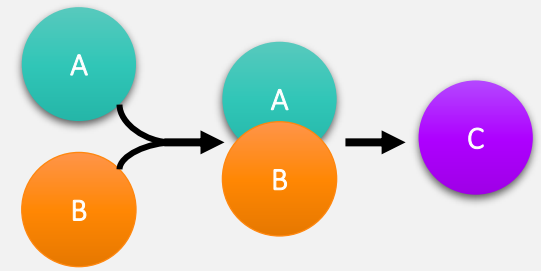
$$\frac{d[AB]}{dt} = k[A][B] - k_2[AB]$$

$$\frac{d[C]}{dt} = k_2[AB]$$

# Modeling dynamical systems

- Exploring the parameter space

```
matrixOfTimeCourses = zeros(length([0:0.1:2]),  
length([0:0.05:1]));  
currentIndex = 1;  
for (ii = [0:0.05:1])  
    [t, y] = ode15s(@F_odeFile2, [0:0.1:2], [1,ii,0,0]);  
  
    matrixOfTimeCourses(:,currentIndex) = y(:,3);  
    currentIndex = currentIndex + 1;  
  
    %figure;  
    %plot(t, y);  
end  
  
figure;  
surf(matrixOfTimeCourses);  
xlabel('Initial [B]')  
ylabel('Time')  
zlabel('[AB]');
```



Take home, questions?

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- More matrices
- Functions
- Files

## Day 3

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- Introduction to dynamical systems: ODEs