MATLAB & Microarray Data Analysis

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MATLAB in 1 minutes

- A computer language for numerical calculation *faster* than C/C++ and other languages
- **A VERY fancy calculator**
- A simple and user friendly programming language
- A tool for data analysis and statistics
- **A tool to produce plots**

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Statistics Toolbox

Apply statistical algorithms and probability models

Key Features

- Regression techniques, including linear, generalized linear, nonlinear, robust, regularized, ANOVA, and mixed-effects models
- Univariate and multivariate probability distributions
- Random and quasi-random number generators and Markov chain samplers
- Hypothesis tests for distributions, dispersion, and location, and design of experiments (DOE) techniques
- Supervised/Unsupervised machine learning algorithms, including support vector machines (SVMs), k-means and hierarchical clustering, Gaussian mixtures, and hidden Markov models

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Bioinformatics Toolbox

Read, analyze, and visualize genomic, proteomic, and high throughput profiling data

Key Features

- **Next Generation Sequencing** analysis and browser
- Sequence alignment analysis and visualization
- **Microarray,** including reading, filtering, normalizing, and visualization
- **Mass spectrometry**, preprocessing, classification, and marker identification
- **Phylogenetic tree analysis**
- Graph theory functions, including interaction maps, hierarchy plots, and pathways
- Data import from genomic, proteomic, and gene expression files, including SAM, FASTA, CEL, and CDF, and from databases such as NCBI and GenBank

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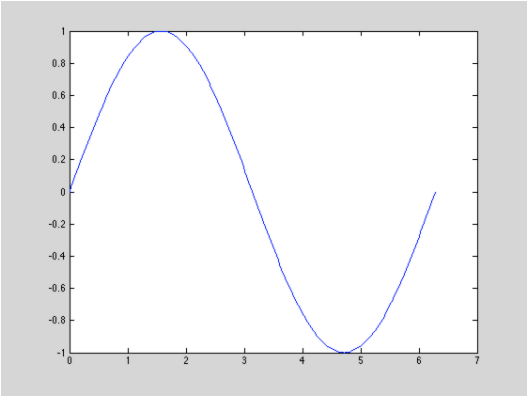
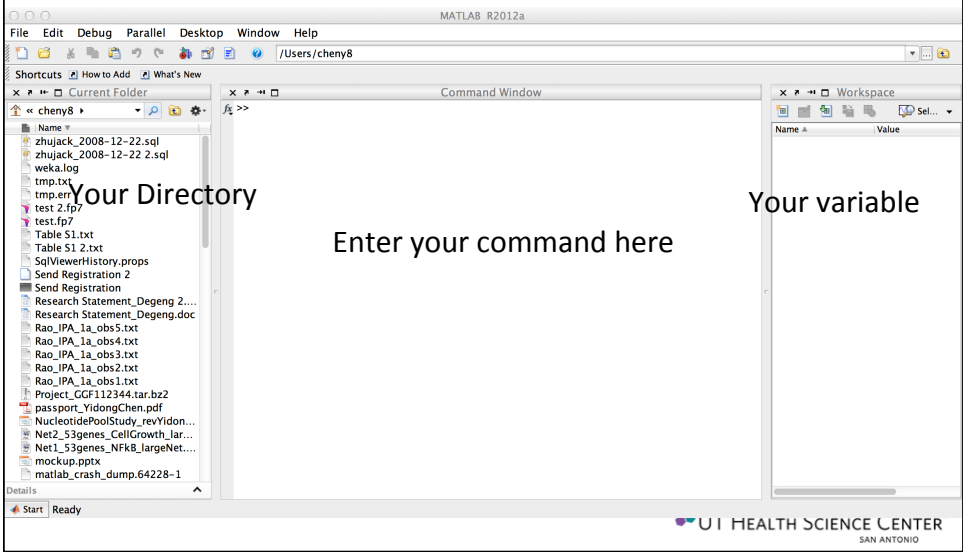
What does MATLAB code look like?

```
t = 0:pi/100:2*pi;
y = sin(t);
plot(t,y)
```



MATLAB Desktop (Mac, R2012a)



Some simple functions

```
>> A = [1 3 2 1; 5 10 11 8; 9 6 7 1; 4 15 14 1]
MATLAB displays the matrix you just entered.
A =     1  3  2  1
        5 10 11 8
        9  6  7  1
        4 15 14 1
>> sum(A)
ans =

   19   34   34   11

>> B = sum(A')
B =

    7   34   23   34
```

```
>> mean( A )
ans =

    4.7500    8.5000    8.5000    2.7500

>> sigma = std( A )
sigma =

    3.3040    5.1962    5.1962    3.5000
```

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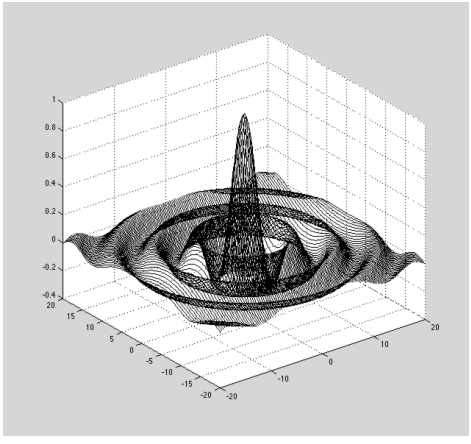
Fancy plots

```
x1 = -20:0.3:20;
y1 = -20:0.3:20;
[x, y] = meshgrid(x1,y1);
r = sqrt( x.^2 + y.^2 );
s = sin(r)./r;
s(find(r==0)) = 1;
plot3( x, y, s );
grid on;

Try these:
plot3( x, y, s, 'k' );
mesh( s );
surf( s );
shading interp
```



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Loading Microarray Data

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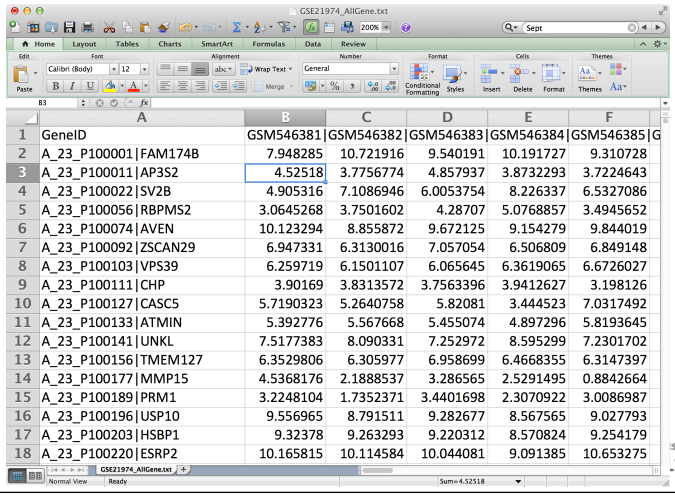
Reading generic text, tab-delimited file

- GSE21974_AllGene.txt – Using excel.



	A	B	C	D	E	F
1	GeneID	GSM546381	GSM546382	GSM546383	GSM546384	GSM546385	G
2	A_23_P100001|FAM174B	7.948285	10.721916	9.540191	10.191727	9.310728	
3	A_23_P100011|AP3S2	4.52518	3.7756774	4.857937	3.8732293	3.7224643	
4	A_23_P100022|SV2B	4.905316	7.1086946	6.0053754	8.226337	6.5327086	
5	A_23_P100056|RBPMS2	3.0645268	3.7501602	4.28707	5.0768857	3.4945652	
6	A_23_P100074|AVEN	10.123294	8.855872	9.672125	9.154279	9.844019	
7	A_23_P100092|ZSCAN29	6.947331	6.3130016	7.057054	6.506809	6.849148	
8	A_23_P100103|VPS39	6.259719	6.1501107	6.065645	6.3619065	6.6726027	
9	A_23_P100111|CHP	3.90169	3.8313572	3.7563396	3.9412627	3.198126	
10	A_23_P100127|CASC5	5.7190323	5.2640758	5.82081	3.444523	7.0317492	
11	A_23_P100133|ATMIN	5.392776	5.567668	5.455074	4.897296	5.8193645	
12	A_23_P100141|UNKL	7.5177383	8.090331	7.252972	8.595299	7.2301702	
13	A_23_P100156|TMEM127	6.3529806	6.305977	6.958699	6.4668355	6.3147397	
14	A_23_P100177|MMP15	4.5368176	2.1888537	3.286565	2.5291495	0.8842664	
15	A_23_P100189|PRM1	3.2248104	1.7352371	3.4401698	2.3070922	3.0086987	
16	A_23_P100196|USP10	9.556965	8.791511	9.282677	8.567565	9.027793	
17	A_23_P100203|HSBP1	9.32378	9.263293	9.220312	8.570824	9.254179	
18	A_23_P100220|ESRP2	10.165815	10.114584	10.044081	9.091385	10.653275	

Importdata, load, textscan, fscanf, xlsread

```
importdata( 'GSE21974_AllGene.txt' );
```

Problem: because the first line is text, this command does not work

```
load 'GSE21974_AllGene.txt'
```

Use textscan:

```
fid = fopen('GSE21974_AllGene.txt' , 'r' );
A = textscan( fid, '%s', 58 );
fclose( fid );
```


Read Microarray data

- Affyread: affymetrix CEL file
- Agferead: agilent feature extraction
- Ilmnbsread: illumina beadStudio output file (text file)

We use custom code

- For generic text
  - `ReadTextWithoutHeader()`

  e.g.

```
data = ReadTextWithHeader( 'GSE21974_AllGene.txt', 3 );
```

- For agilent microarray
  - `ReadAgilentResult()`

  e.g.

```
data = ReadAgilentResult(
'GSM546381_US91803681_251485049822_S01_GE1_105_Dec08_1_1.txt' );
```

  Request source code @ CBBI

Examination of Raw Agilent Microarray Data

- Download one of example Agilent gene expression data
  - http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM546381

TYPE	FEPARAMS	DATA *	TYPE	STATS	DATA *	TYPE	FEATURES
text	Protocol_Name	GE1_105_Dec08 (Read Only)	float	gDarkOffsetAverage	6.16137	integer	FeatureNum
text	Protocol_date	11/21/08 12:35	float	gDarkOffsetMedian	6.16137	integer	Row
text	Scan_Date	9/16/09 11:06	float	gDarkOffsetStdDev	1.39298	integer	Col
text	Scan_ScannerName	Agilent Technologies Scanner G2505(	integer	gDarkOffsetNumPts	0	text	accessions
integer	Scan_NumChannels	1	integer	gSaturationValue	779631	text	chr_coord
float	Scan_MicronsPerPixelX	5	float	gAvgSig2BkgeQC	589.932	integer	SubTypeMask
float	Scan_MicronsPerPixelY	5	float	gAvgSig2BkgNegCtrl	1.47761	text	SubTypeName
text	Scan_OriginalGUID	d7cf9523-ff83-43d3-bc16-4c98d5173	float	gRatioSig2BkgeQC_NegCtrl	399.247	integer	Start
text	Grid_Name	014850_D_F_20090416	integer	gNumSatFeat	0	text	Sequence
text	Grid_Date	4/16/09 0:00	float	gLocalBGInlierNetAve	12.7466	integer	ProbeUID
integer	Grid_NumSubGridRows	1	float	gLocalBGInlierAve	18.908	integer	ControlType
integer	Grid_NumSubGridCols	1	float	gLocalBGInlierSDev	1.73806	text	ProbeName
integer	Grid_NumRows	532	integer	gLocalBGInlierNum	44645	text	GeneName
integer	Grid_NumCols	85	float	gGlobalBGInlierAve	18.908	text	SystematicName
float	Grid_RowSpacing	73.3235	float	gGlobalBGInlierSDev	1.73806	text	Description
float	Grid_ColSpacing	63.5	integer	gGlobalBGInlierNum	44645	float	PositionX
float	Grid_OffsetX	0	integer	gNumFeatureNonUnifOL	1	float	PositionY
float	Grid_OffsetY	36.6617	integer	gNumPopnOL	138	float	gSurrogateUsed
float	Grid_NomSpotWidth	65	integer	gNumNonUnifBGOL	0	boolean	gIsFound
float	Grid_NomSpotHeight	65	integer	gNumPopnBGOL	370	float	gProcessedSignal
text	Grid_GenomicBuild	hg18:NCBI36:Mar2006	float	gOffsetUsed	6.16137	float	gProcessedSigError
text	FeatureExtractor_Barcode	251485049822_1_1	float	gGlobalFeatInlierAve	2228.19	integer	gNumPixOLHi
text	FeatureExtractor_Sample		float	gGlobalFeatInlierSDev	11292.8	integer	gNumPixOLLo
text	FeatureExtractor_ScanFileName	D:\Daten_Agilent_Rechner\ScanData	integer	gGlobalFeatInlierNum	44876	integer	gNumPix
text	FeatureExtractor_ArrayName	US91803681_251485049822_S01	float	AnyColorPrcntFeatNonUnifOL	0.00222148	float	gMeanSignal
text	FeatureExtractor_DesignFileName	014850_D_F_20090416.xml	float	AnyColorPrcntBGNonUnifOL	0	float	gMedianSignal
text	FeatureExtractor_PrintingFileName		float	AnyColorPrcntFeatPopnOL	0.306564	float	gPixSDev
text	FeatureExtractor_PatternName	Agilent-014850	float	AnyColorPrcntBGPopnOL	0.821948	float	gPixNormIQR
text	FeatureExtractor_ExtractionTime	9/16/09 12:07	float	TotalPrcntFeatOL	0.00230542	integer	gBGNumPix
text	FeatureExtractor_UserName	sa_agilent	integer	gNumNegBGSubFeat	4210	float	gBGMeanSignal
text	FeatureExtractor_ComputerName	AGILENT02	integer	gNonCtrlNumNegFeatBGSubSig	3344	float	gBGMedianSignal
text	FeatureExtractor_ScanFileGUID	957a1497-1aa5-4f45-ba2e-2ab8537d	float	gSpatialDetrendRMSFit	1.17339	float	gBGPixSDev

FirstLook

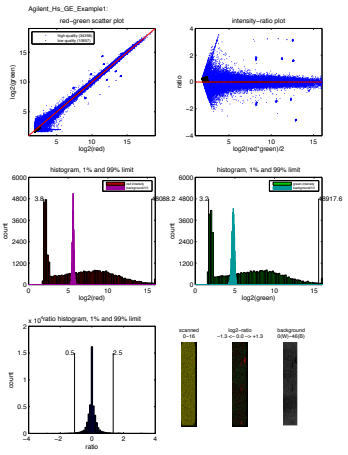
When you use

```
ReadAgilentResult('Agilent_Hs_
GE_Example1.txt'),
```

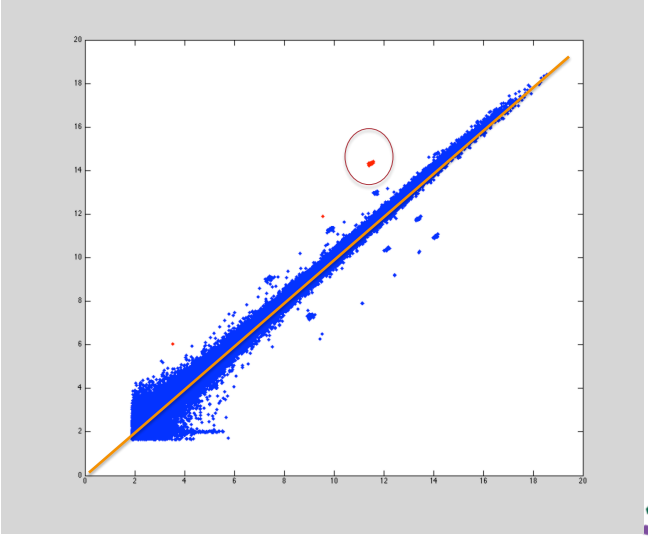
it generate a pdf file,

```
Agilent_Hs_GE_Example1.txt_qFig.p
df
```

It is mainly for quality control purpose.



Control probes, background fluorescent



What are these??

Normalization

- Boxplot, Lowess, quantile

```
>> boxplot( data.value, 'plotstyle', 'compact' );
>> data.normValue = quantilenorm( data.value );
```

(for agilent microarrays, lowess correction is not needed)

```
hold on;
plot( data.value(8698,:), 'r' );
text( 1, data.value(8698,1), data.GeneID(8698), 'interpret',
'none', 'horizontalalignment', 'right');
```


Intensity, median/mean, ratio, etc

- This is single channel data file with data in gProcessedSignal
- For 2 channels, data are in `rProcessedSignal`, and `gProcessedSignal`. With ratio in log10 transformation.
  - http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSM785046

PCA, MDS, etc

- Principal component analysis

```
[coefs, scores, sigma2] = princomp( data.value' );
```

- Multidimensional scaling

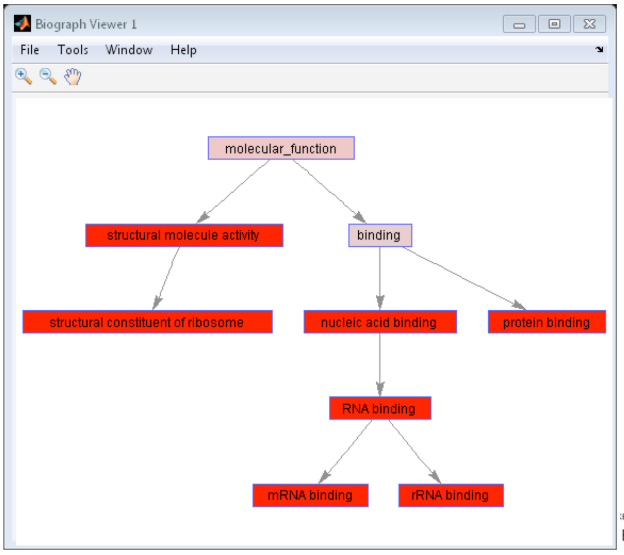
Differential Gene Expression

```
p = mattest( data.value( 1:2:57), data.value(2:2:57) );
adjp = mafdr( p, 'BHFDR', true );

Or

[fdr, q] = mafdr( p );
```

Gene Ontology



Other subjects

- Phylogenetic tree
- Sequence alignment
- Motif search
- Mass Spec data analysis
- And many more…