





Introduction to data exploration using Deedle

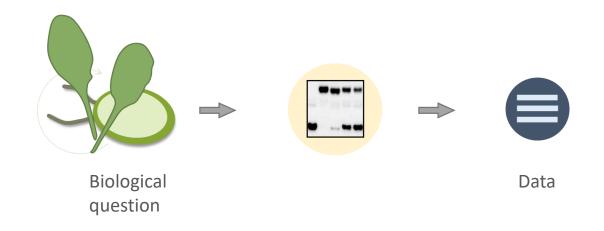


David Zimmer

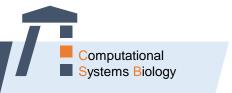
Computational Systems Biology Kaiserslautern University of Technology

Big Data in Biology



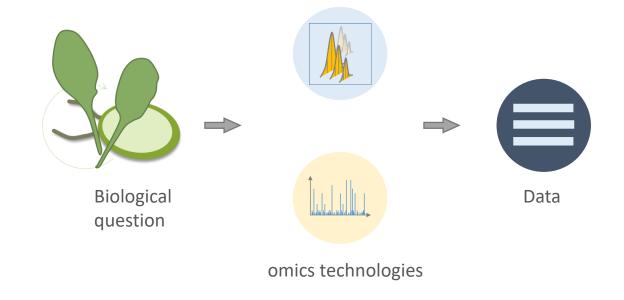


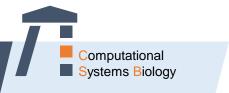
molecular biological technologies



Big Data in Biology







Data can be stored in various formats





DSVs:

delimiter separated values

Peptides.csv

Peptides.tab

Peptides.tab

Markup language

Peptides.xml

model.xml

Data bases

Peptides.SQLite

Proteins.SQL



Delimiter separated formats



Columns

Records
Record
Record
Record
• • •
• • •
• • •
•••

Rows

Name	Wt1	Wt2	Mut1	Mut2	Sig
RBCS	10.1	11.1	5.5	6.1	true
RBCL	2.9	3.0	RBCL	3.6	false
D1	5.2	5.1	D1	5.5	false
	• • •				
0 0 0	• • •			0 0 0	• • •

Delimiter separated formats store:

- Series of individual Records (e.g. Genes), each stored in a individual row.
- Each Record can have multiple fields, the field name is commonly given by the first line of the file (the header)
- Each Column stores the value of one individual field with a given type.



Delimiter separated formats



Columns

Records	
Record	
Record	
Record	
• • •	
• • •	
• • •	
• • •	

Rows

Name	Wt1	Wt2	Mut1	Mut2	Sig
RBCS	10.1	11.1	5.5	6.1	true
RBCL	2.9	3.0	RBCL	3.6	false
D1	5.2	5.1	D1	5.5	false
0 0 0					• • •
0 0 0	• • •	• • •	• • •	• • •	•••
	• • •	• • •	• • •	• • •	•••

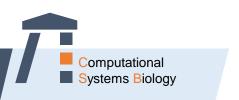
Advantage of Delimiter separated formats:

 Each Column stores the value of one individual field with a given type

Disadvantage of Delimiter separated formats:

• Each Column stores the value of one individual field with a given type.

One Record can contain fields of multiple types



The solution: abstract rows as types

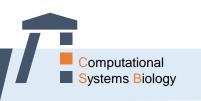


Columns

Records
Record
Record
Record
• • •
• • •

Rows

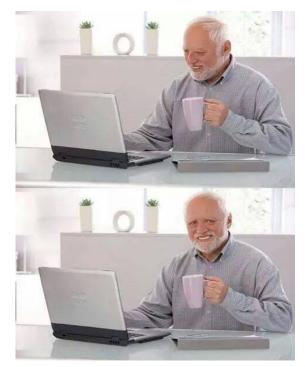
Name	Wt1	Wt2	Mut1	Mut2	Sig
RBCS	10.1	11.1	5.5	6.1	true
RBCL	2.9	3.0	RBCL	3.6	false
D1	5.2	5.1	D1	5.5	false
	• • •	• • •	• • •		• • •
	•••	•••	• • •	•••	•••
• • •	• • •	• • •	• • •	• • •	



 Obvious downside: Data has to be inspected beforehand and the abstraction to a data structure has to be done manually



Presenting Results









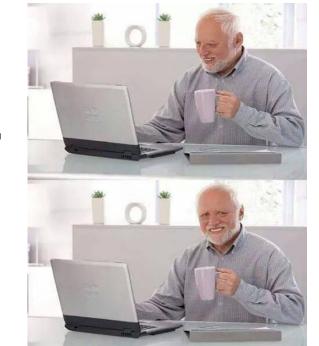
Presenting Results

```
type QuantifiedProtein = {
                                 : string
    Name
    WT1
                                 : float
    WT2
                                 : float
                                 : float
    Mut1
    Mut2
                                 : float
    isSignificant
                                 : bool
    Wt1VsMut1
                                 : float
                                 : float
    Wt1VsMut2
```





Presenting Results

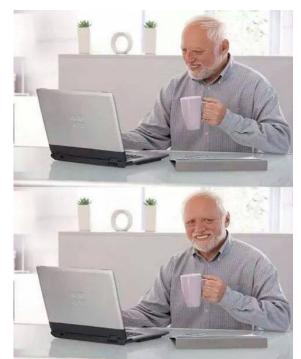


```
type QuantifiedProtein = {
                                 : string
    Name
    WT1
                                 : float
    WT2
                                 : float
                                 : float
    Mut1
    Mut2
                                 : float
    isSignificant
                                 : bool
    Wt1VsMut1
                                 : float
                                 : float
    Wt1VsMut2
    Wt2VsMut1
                                 : float
    Wt2VsMut2
                                 : float
```





Presenting Results



```
type QuantifiedProtein = {
                                                          : string
                           Name
                           WT1
                                                           float
                           WT2
                                                         : float
                                                         : float
                           Mut1
                           Mut2
                                                          : float
                                                         : bool
                           isSignificant
                           Wt1VsMut1
                                                         : float
                           Wt1VsMut2
                                                          : float
                           Wt2VsMut1
                                                         : float
                                                         : float
                           Wt2VsMut2
                                                          : float
                           WtMeans
                           MutMeans
                                                         : float
                           WtStdev
                                                         : float
                           MutStdev
                                                           float
                                                         : float
                           PearsonCorrWt1VsMut1
Incorporating Input / changing rear son Corr Wt1 Vs Mut2
                                                         : float
```

float

PearsonCorrWt2VsMut1



The solution: Data Frame programming



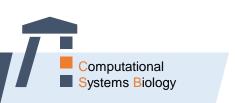
	1
	2
dows	3
(0 00	• • •
	• • •

Records

Name	Wt1	Wt2	Mut1	Mut2	Sig
RBCS	10.1	11.1	5.5	6.1	true
RBCL	2.9	3.0	RBCL	3.6	false
D1	5.2	5.1	D1	5.5	false
0 0 0	• • •	• • •	• • •		• • •
0 0 0					
0 0 0					• • •
			0 0 0		• • •

let rawData :Frame<int,string> =
 Frame.ReadCsv(rawDataPath,separators="\t",)

- Data Frames represent type structures that abstract tabular organized data in memory
- Data Frame objects can be seemlesly extended, reorderd, aggegated and also merged



The solution: Data Frame programming



Data Frame

Series 1 Series 2 Series 2 Series 3 Series 4 Series 4

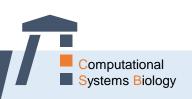
	Records
	1
	2
	3
l	•••

Rows

Name	Wt1	Wt2	Mut1	Mut2	Sig
RBCS	10.1	11.1	5.5	6.1	true
RBCL	2.9	3.0	RBCL	3.6	false
D1	5.2	5.1	D1	5.5	false
		• • •			
			0 0 0		
					0 0 0

let rawData :Frame<int,string> =
 Frame.ReadCsv(rawDataPath,separators="\t",)

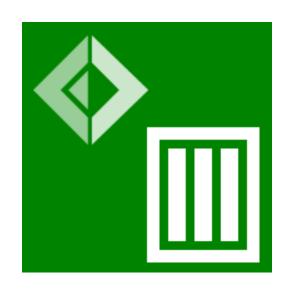
 Most Data Frames API abstract a tables as a collection of Series of same length, but different types



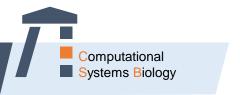
• "Data Frame programming is fast becoming the "standard" way of doing multi-dimensional and statistical data processing in systems such as R, Python and now .NET. "

Deedle: .Net Data Frame library





- Deedle is an easy to use library for data and time series manipulation and for scientific programming in .Net.
- Deedle relies on two basic data structures, the Series and the Frame
- A Frame can be viewed as a list of Series, with each Series being a Column of the Frame. If possible: use the data frame in a column-wise way



Working with Deedle Data Series



```
let firstNames = Series.ofValues ["Kevin";"Lukas";"Benedikt";"Michael"]
```

1 Kevin2 Lukas3 Bene.4 Micha.

Working with Deedle Data Series



```
let firstNames = Series.ofValues ["Kevin";"Lukas";"Benedikt";"Michael"]
let coffeesPerWeek = Series.ofValues [15;12;10;11]
```

Kevin
Lukas
Bene.
Micha.

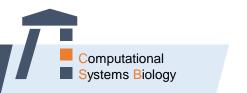
1 15 2 12 3 10 4 11

Working with Deedle Data Series



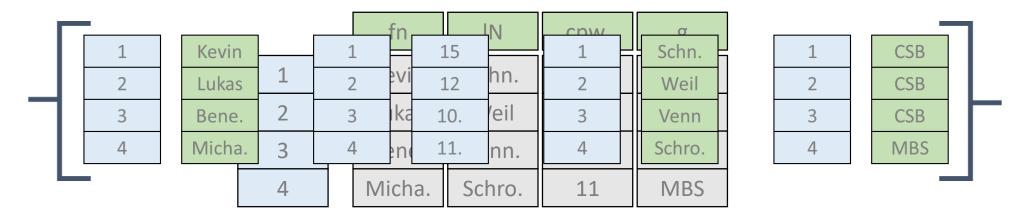
```
let firstNames
                     = Series.ofValues ["Kevin";"Lukas";"Benedikt";"Michael"]
let coffeesPerWeek = Series.ofValues [15;12;10;11]
                     = Series.ofValues ["Schneider";"Weil";"Venn";"Schroda"]
let lastNames
                     = Series.ofValues ["CSB";"CSB";"CSB";"MBS"]
let group
                                     15
                                                          Schn.
                                                                                 CSB
              Kevin
              Lukas
                                     12
                                                          Weil
                                                                                 CSB
                                     10
                                                                                 CSB
              Bene.
                                                          Venn
              Micha.
                                     11
                                                          Schro.
                                                                                MBS
```

Interactive Output: ...





```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
```



```
Interactive Output:
                     val persons : Frame<int,string> =
                           fΝ
                                    1N
                                              cpw g
                     0 -> Kevin Schneider 15 CSB
                     1 -> Lukas
                                    Weil
                                                 CSB
                                              12
                     2 -> Benedikt Venn 10
                                                 CSB
     Computational
                     3 -> Michael Schroda
                                                  MBS
    Systems Biology
```



```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
```

1	
2	
3	
4	

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS



```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
let coffeePerWeek' :Series<int,string> = persons |> Frame.getCol ("cpw")
```

1	
2	
3	
4	

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

1	
2	
3	
4	





```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
let coffeePerWeek' :Series<int,int> = persons |> Frame.getCol ("cpw")
```

1
2
3
4

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

1	15
2	12
3	10
4	11





```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
let coffeePerWeek' :Series<int,int> = persons |> Frame.getCol ("cpw")
```

1
2
3
4

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

1	15
2	12
3	10
4	11



Grouping Rows of a Deedle Data Frame



```
let persons = Frame(["fN";"lN";"cpw";"g"],[firstNames;lastNames;coffeesPerWeek;group])
let groupedByG :Frame<string*int,_> = persons |> Frame.groupRowsBy "g"
```

CSB 1 2 3 MBS 4

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

Slicing columns of a Deedle Data Frame



```
let groupedByG :Frame<string*int,_> = persons |> Frame.groupRowsBy "g"
let withOutG :Frame<string*int,_> = groupedByG |> Frame.sliceCols ["fN";"lN";"cpw"]
```

```
CSB 1 2 3 MBS 4
```

fn	IN	cpw.
Kevin	Schn.	15
Lukas	Weil	12
Bene.	Venn.	10
Micha.	Schro.	11

Aggregating By index



```
let groupedByG :Frame<string*int,_> = persons |> Frame.groupRowsBy "g"
let coffeePerWeek'' :Series<string*int,int>= groupedByG |> Frame.getCol ("cpw")
```

CSB MBS

CSB 0 -> 15

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

CSB		1	15
		2	12
		3	10
MBS		4	11

Interactive Output: val coffeePerWeek'' : Series<(string * int),int> =





Aggregating By index



```
let coffeePerWeek'' :Series<string*int,int>= groupedByG |> Frame.getCol ("cpw")
let coffeePerWeekPerGroup =
    Series.applyLevel Pair.get10f2 (Series.values >> Seq.sum) coffeePerWeek''
```

CSB 1 2 3 MBS 4

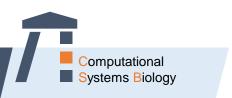
fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

CSB		1	15
		2	12
		3	10
MBS		4	11

Interactive Output: val it : Series<string,int> =

CSB -> 37

MBS -> 11



Aggregating By index



```
let coffeePerWeek'' :Series<string*int,int>= groupedByG |> Frame.getCol ("cpw")
let coffeePerWeekPerGroup =
    Series.applyLevel Pair.get10f2 (Series.values >> Seq.sum) coffeePerWeek''
```

CSB 1 2 3 MBS 4

fn	IN	cpw.	g
Kevin	Schn.	15	CSB
Lukas	Weil	12	CSB
Bene.	Venn.	10	CSB
Micha.	Schro.	11	MBS

 CSB
 37

 MBS
 11

Interactive Output: val it : Series<string,int> =

CSB -> 37

MBS -> 11



Back to CSV – Data Frame from file



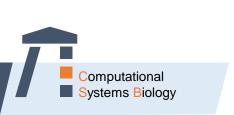
The training data set:

DEQRDLKWRHQHCA

Id>	(ProtId	Peptide	Wt_rep1	Wt_rep2	
0	->	AT1G	MNGHOKWVTRCRUNOT	0.756559369801931	-0.436239204755912	• • •
1	->	AT2G	VGCLFRCRPNLHGWHPCCAL	0.346180296054525	1.12382655833822	• • •
3	->	AT4G	FOWUNPOSSCTLOIEREDPC	2.07291451373885	2.33281672094402	• • •
2	->	AT3G	FCWTENSRCFEEWINFAG	1.94744188867146	1.40618787884551	• • •
4	->	AT5G	GWNHGEHORLA	2.49191364989232	2.55526019285937	• • •
5	->	AT1G	EGEGFKFOSAQGSNSSOKD	0.463247366431074	-0.185142152934379	• • •
6	->	AT2G	FQVOKNGMGEAPTPK	1.35116967991367	1.19087642041569	• • •
7	->	AT3G	AMVQLLKGHHN	1.63563065144294	1.24054827708146	• • •
8	->	AT4G	INWIHOOLHNTQEQHOAA	2.2376101319133	2.03897108568878	• • •

2.32829708747299

2.39682265165475



-> AT5G

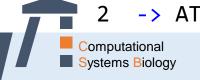
Dealing with CSV – Data Frame from/to file



```
let rawData :Frame<int,string> =
   Frame.ReadCsv(@"C:\Users\david\...\toyData.tab",separators="\t")
```

Interactive Output:

```
ProtId Peptide
Idx
                                 Wt rep1
                                                    Wt rep2
  -> AT1G
            MNGHOKWVTRCRUNOT
                                 0.756559369801931
                                                    -0.436239204755912
  -> AT2G
            VGCLFRCRPNLHGWHPCCAL 0.346180296054525
                                                    1.12382655833822
  -> AT4G
            FOWUNPOSSCTLOIEREDPC 2.07291451373885
                                                    2.33281672094402
   -> AT3G
            FCWTENSRCFEEWINFAG
                                 1.94744188867146
                                                    1,40618787884551
```

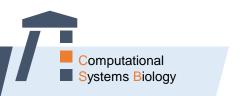


Dealing with CSV – Data Frame from/to file



```
let rawData :Frame<int,string> =
    Frame.ReadCsv(@"C:\Users\david\...\toyData.tab",separators="\t")
rawData.SaveCsv(@"C:\Users\david\...\toyData.tab",separator='\t',includeRowKeys=false)
```

```
Interactive Output:
    val it : unit = ()
```



Your Enemy: The study



MOLECULAR & CELLULAR PROTEOMICS

Published by the American Society for Biochemistry and Molecular Biology

Mol Cell Proteomics. 2014 Dec; 13(12): 3602–3611.

Published online 2014 Oct 2. doi: 10.1074/mcp.M114.039081

PMCID: PMC4256508 PMID: 25277243

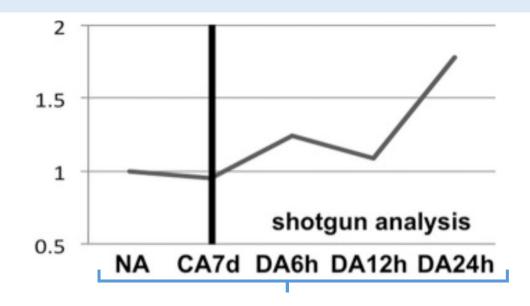
Analysis of Differential Expression Patterns of mRNA and Protein During Coldacclimation and De-acclimation in *Arabidopsis**

- Organism: Arabidopsis thaliana
- Aim : Study proteome dynamics

during Cold-acclimation and

De-acclimation

Method : N14/N15 labled shotgun proteomics

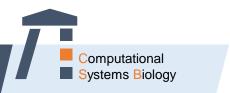


5 timepoints

3 biological replicates

3 technical replicates

45 samples



Interactive programming





The end



