



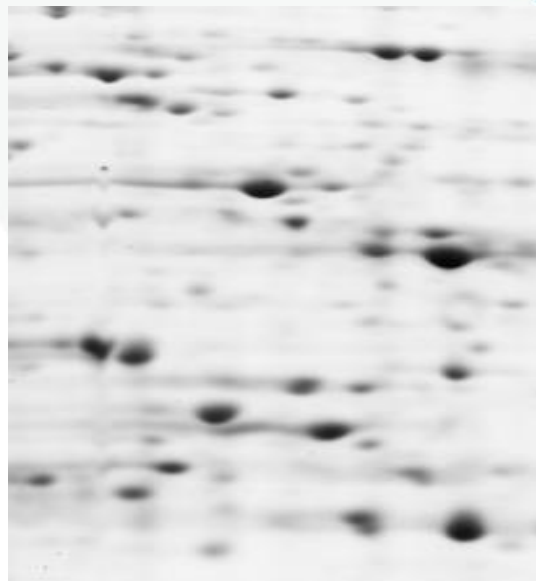
CEITEC

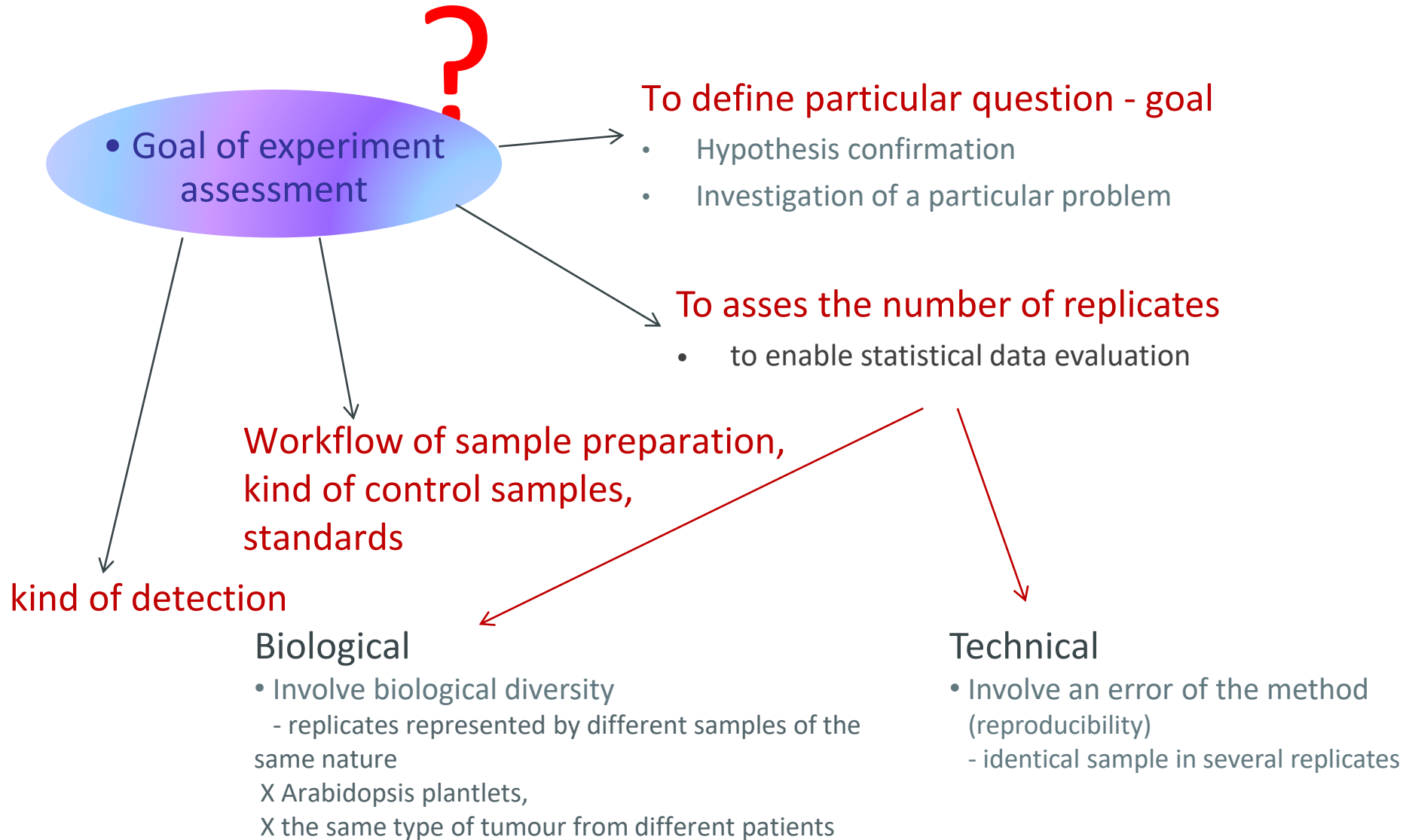
Central European Institute of Technology  
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MUNI

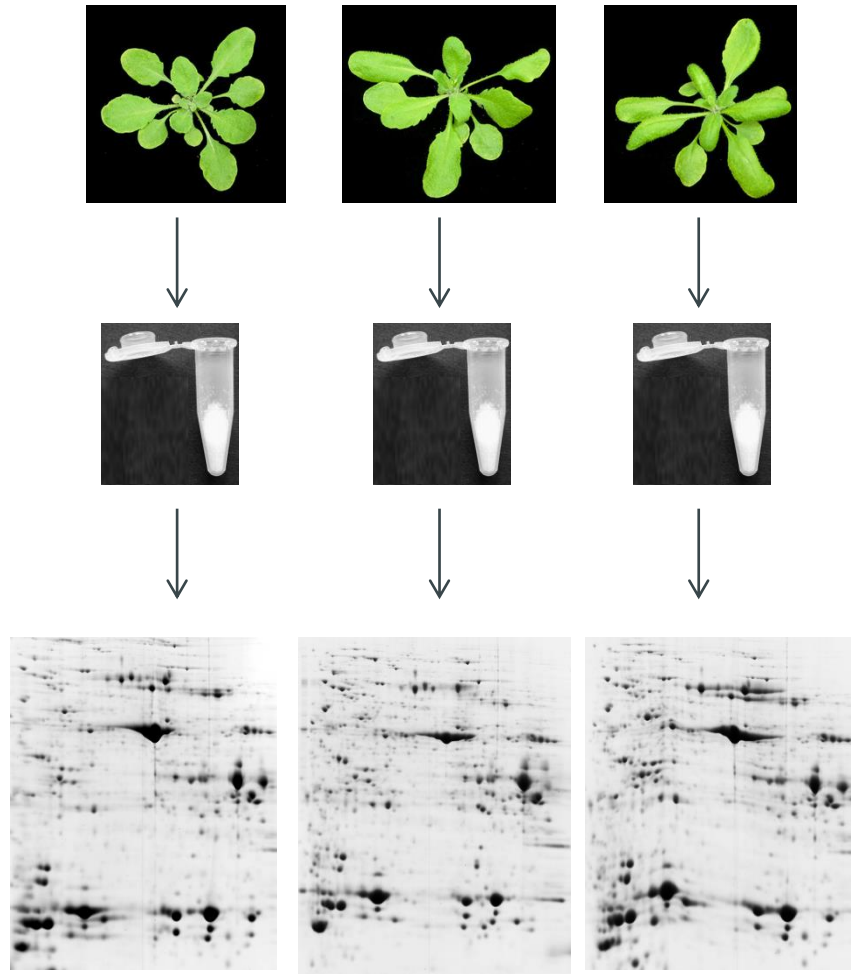
# Image analysis

Gabriela Lochmanová

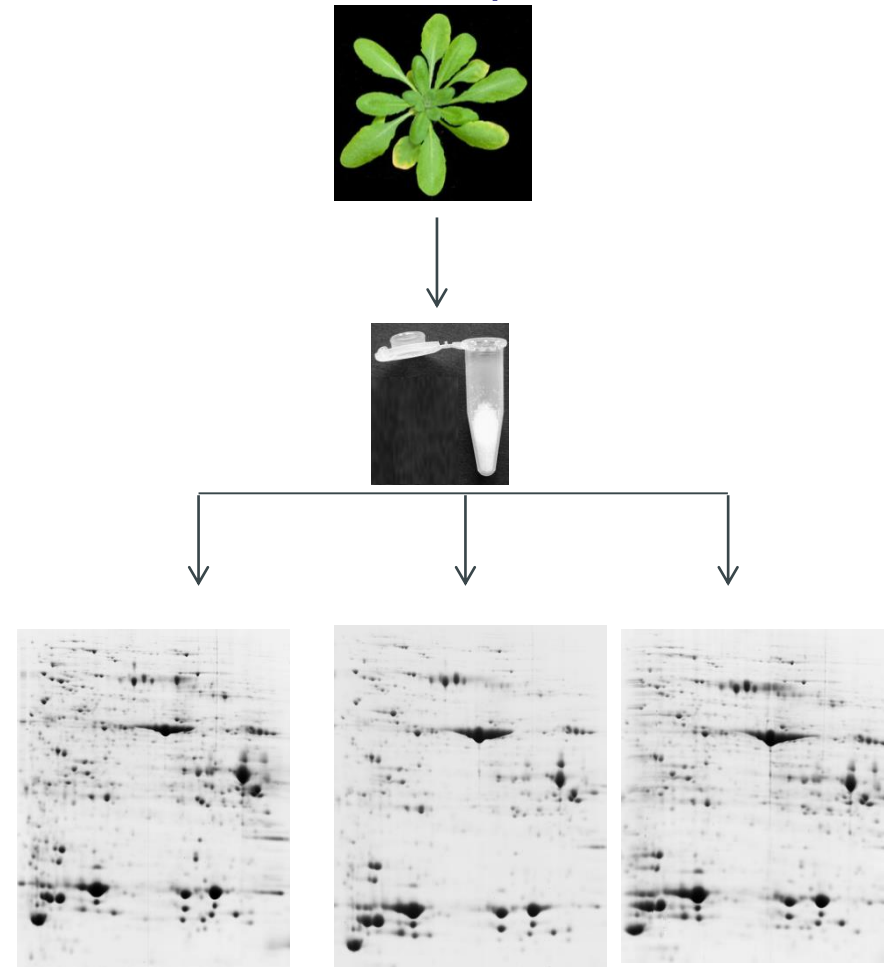




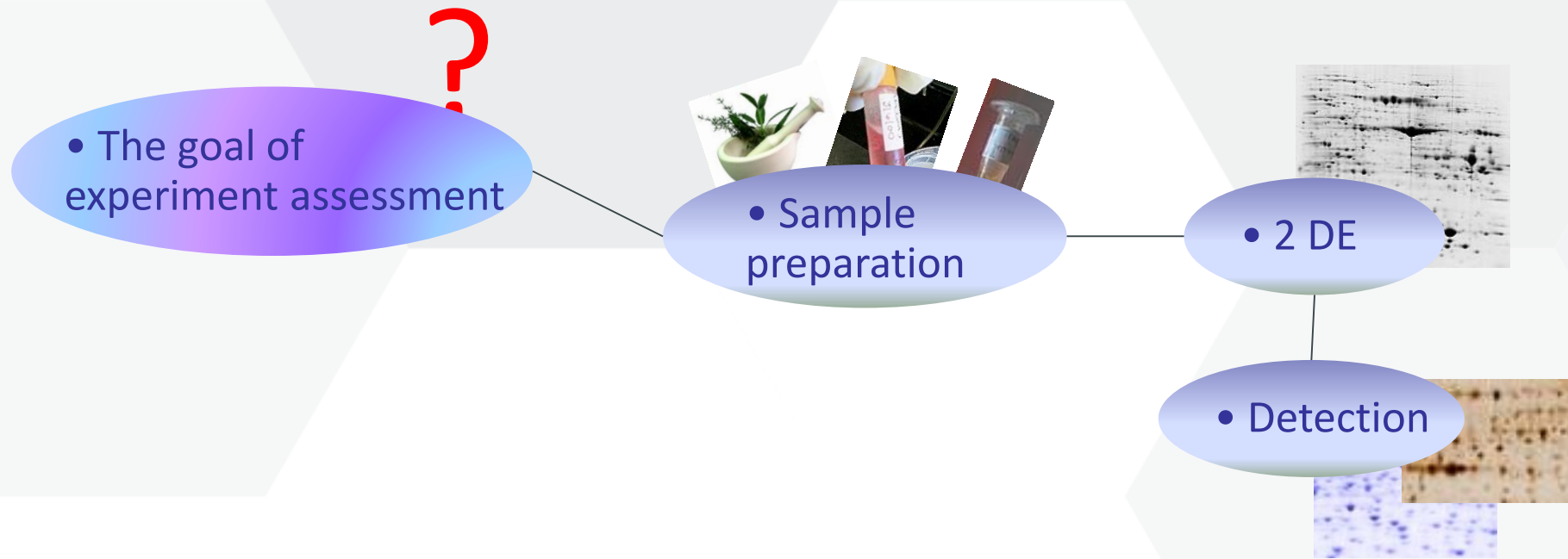
## Biological replicates



## Technical replicates



# Experiment



# General requirements on protein visualization

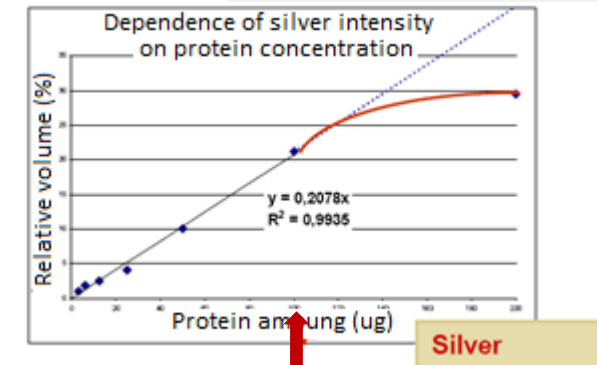
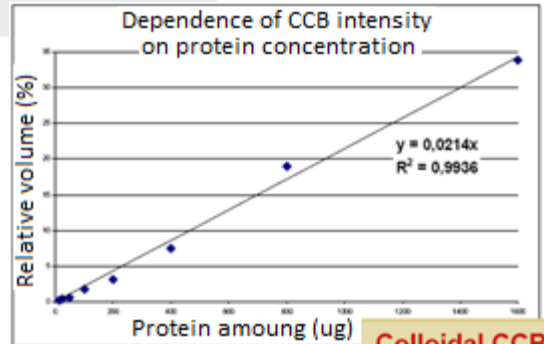
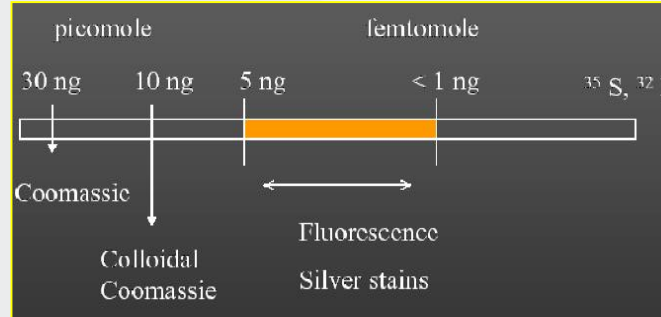
## Detection

- High sensitivity
- Quantitative staining
- Broad linear range of dye intensity dependence on protein amount in the gel

### Dynamical range

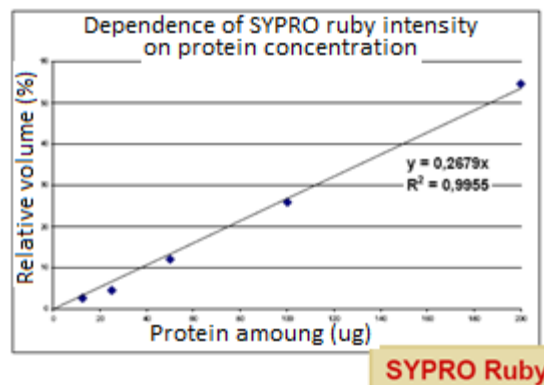
= graph of dye intensity dependence (y axis) on protein concentration (x axis)

- end-point
- lifetime  
(e.g. quenching of fluorescent dyes!)
- Compatibility with following procedures  
(e.g. silver - glutaraldehyde!)



### Silver staining

– limited linearity - only upto 100 ng of protein.



## • Detection

### Kind of detection

Labelling before analysis (DIGE – CyDye, radioactive labelling)

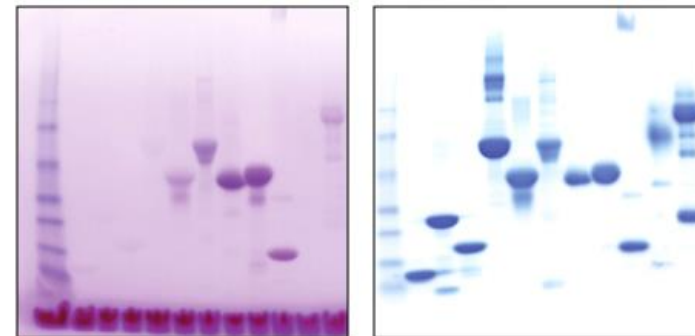
Staining after analysis

**Unspecific staining:** all proteins

- **Visible staining:** Coomassie brilliant blue (R250, G250), silver (acid x ammoniacal variant)
- **Fluorescent staining:** Sypro Ruby (Ex/Em = 280, 450/610 nm), Lucy (Ex/Em = 506/520 nm), Flamingo Pink (Ex/Em = 512/535 nm), Oriole (Ex/Em = 270/604 nm), Krypton (Ex/Em = 520/580), Deep Purple (Ex/Em = 365, 520/610 nm), Lumitein (Ex/Em = 280, 450/610 nm)

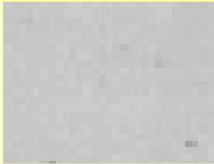
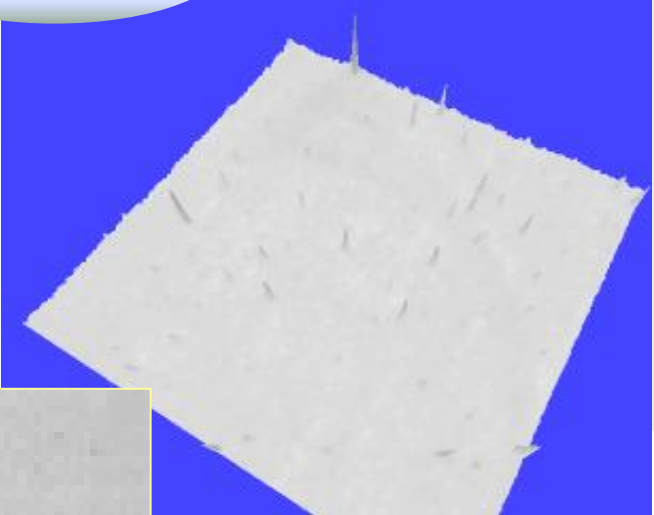
**Specific staining:** post-translational modifications (PTM)

- phosphorylation: Pro-Q Diamond (pSer, pThr, pTyr), Pierce phosphoprotein staining kit (pSer, pThr)
- glycosylation: Pro-Q Emerald, Pierce glycoprotein staining kit
- Radioactive labelling

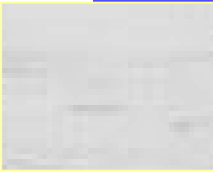
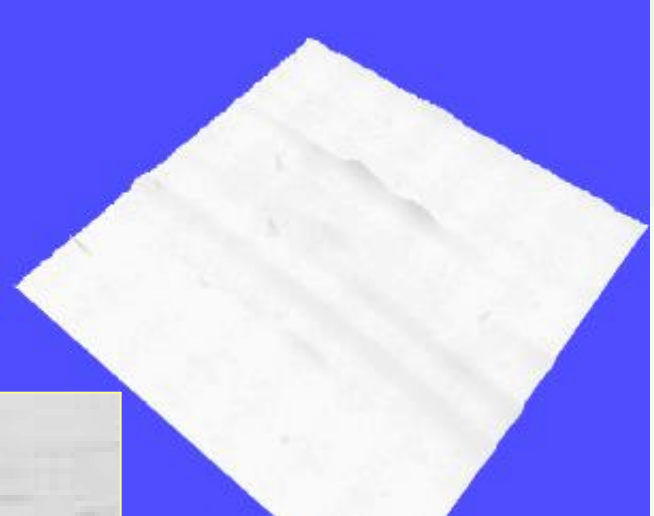


- Detection

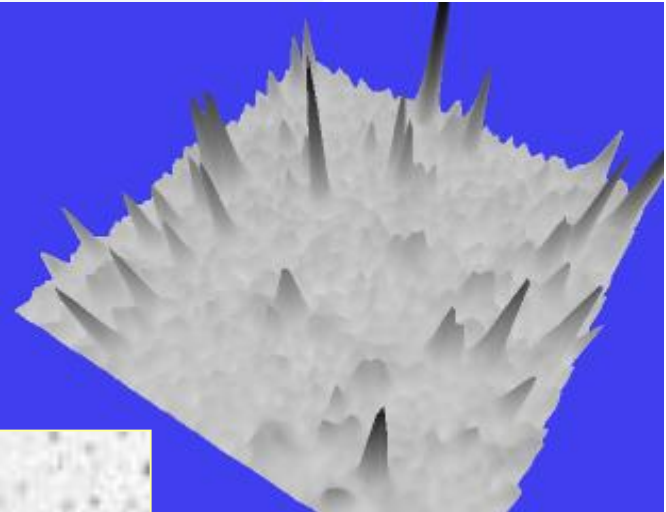
Background – 3D view



Colloidal CCB



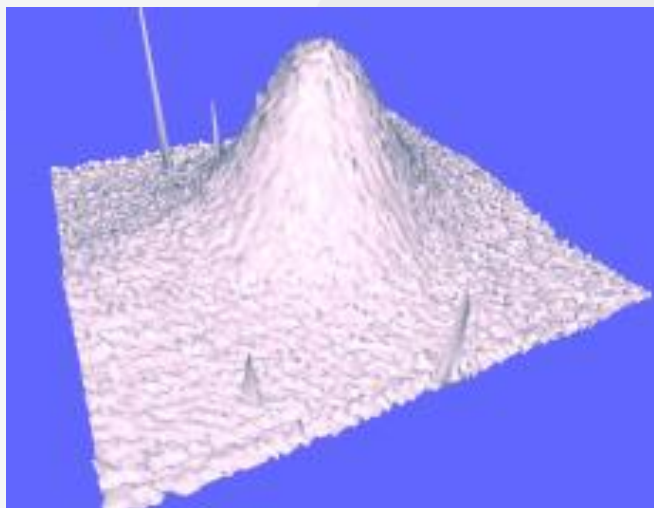
Silver



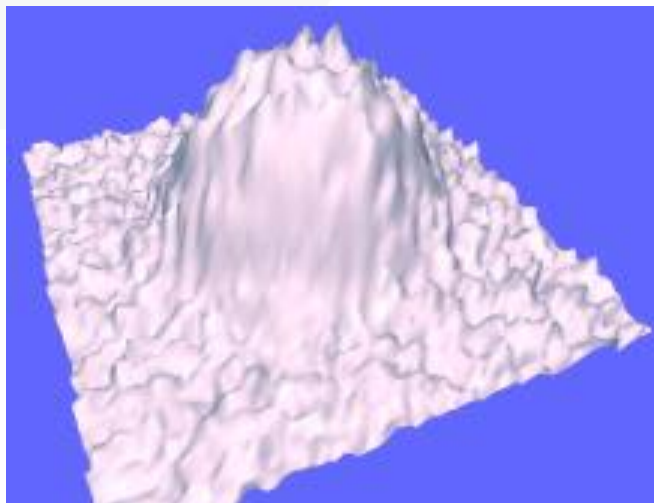
SYPRO Ruby

- Detection

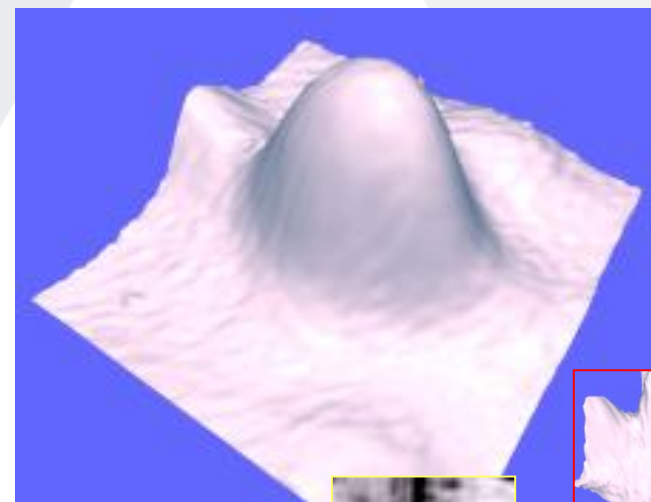
### Protein spot – 3D view



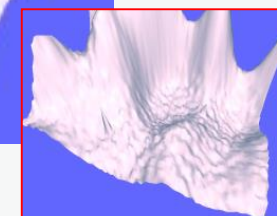
Colloidal CCB



SYPRO Ruby



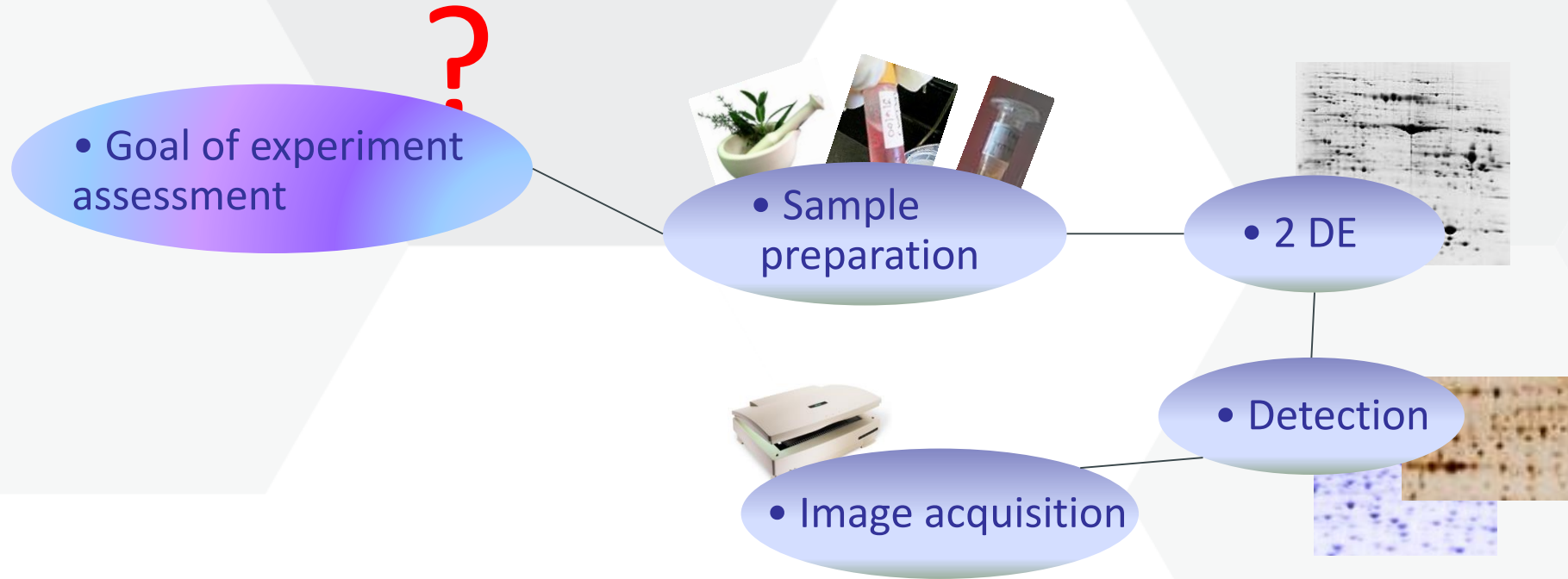
Silver



During image analysis we are working with density of the dye.



# Experiment



Signals from biological samples are converted into the digital data in black and white

• Image acquisition

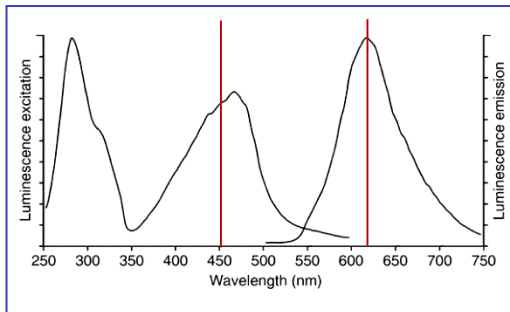
- TIFF format, high resolution

Instrumentation for image acquisition

Instrument choice according to type of detection used

- Visible stains : densitometers
- Fluorescent stains: fluorescence scanners, cameras  
Ex/Em spectrum has to correlate with Ex/Em characteristics of the instrument

S. Ruby: Ex/Em: 280, 450/610 nm



Molecular Imager GS-800



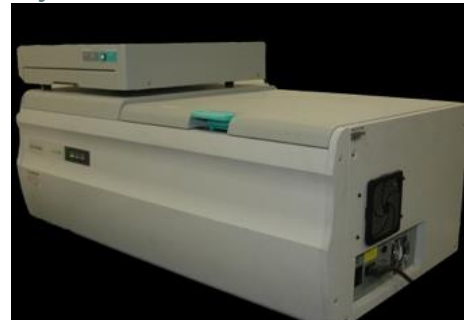
Image Scanner III



Typhoon 9200 Imager



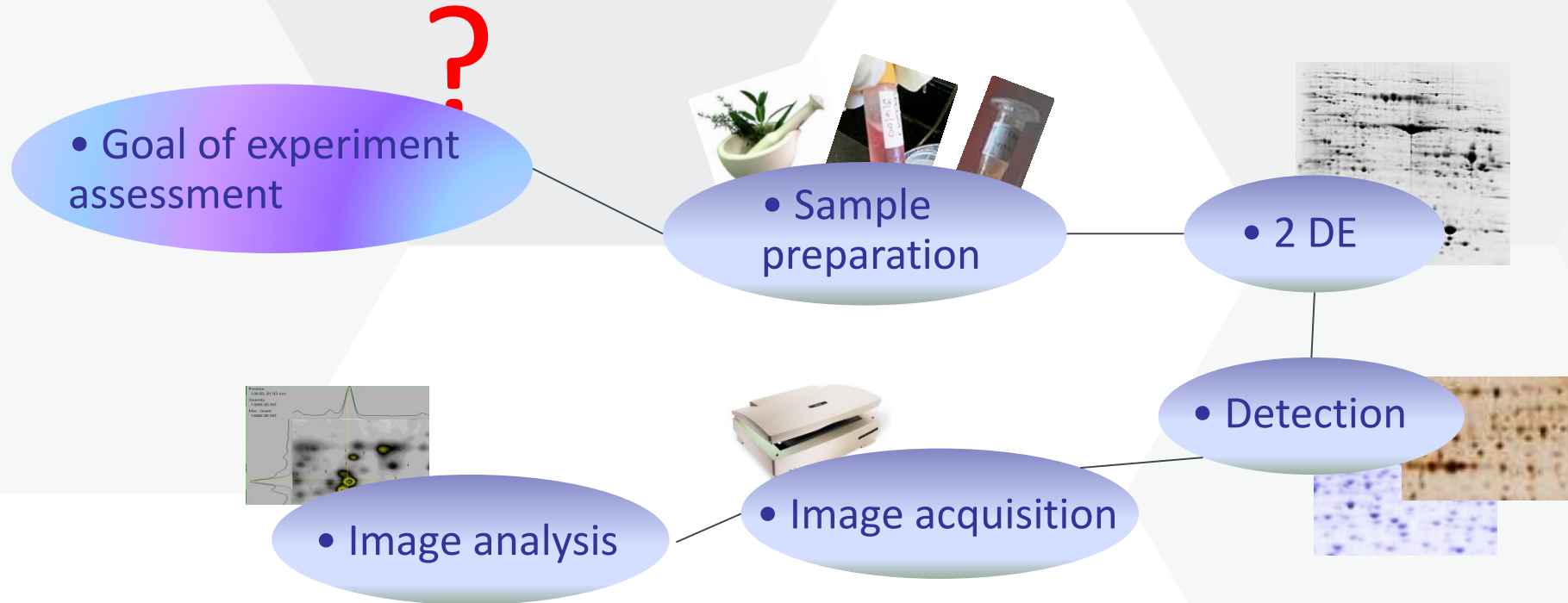
Fuji FLA-3000



PharosFX™ and PharosFX Plus Systems



# Experiment



- Image analysis



- Human eye distinguishes

**500 shades of grey**  
**10 million colours**

Visible light only at **wave length of 380–760 nm**

**Almost ½ of human brain participates on sight control.**

### Analysis using a specialized SW

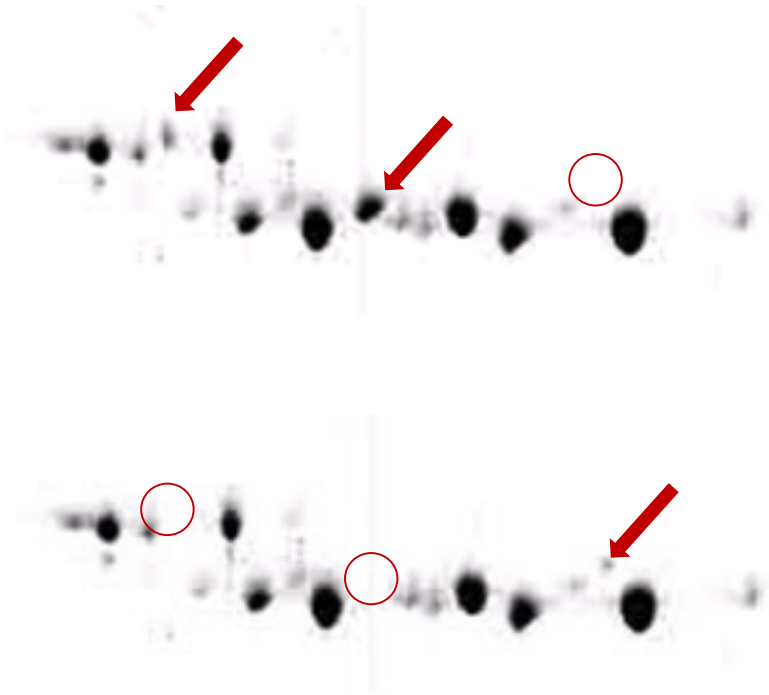
- Comparison and evaluation of 2D gels  
(visual evaluation of 2D gels is not possible)



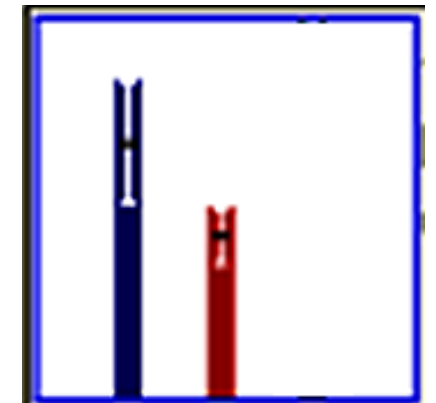
• Image analysis

→ Analysis using a specialized SW

Qualitative evaluation



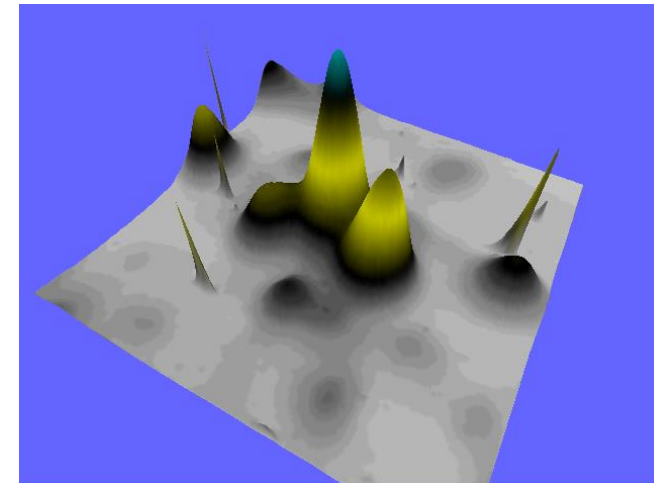
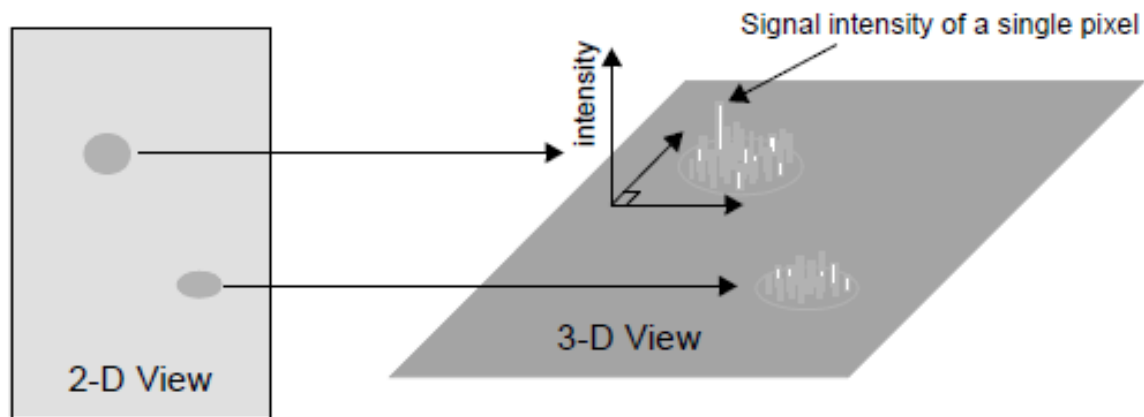
Quantitative evaluation / Statistical analysis



- Image analysis

- **Spot quantity**  
**= total intensity of a defined spot**  
**(for evaluation gaussian visualization is used)**

- corresponds with protein amount in a particular spot



- Image analysis

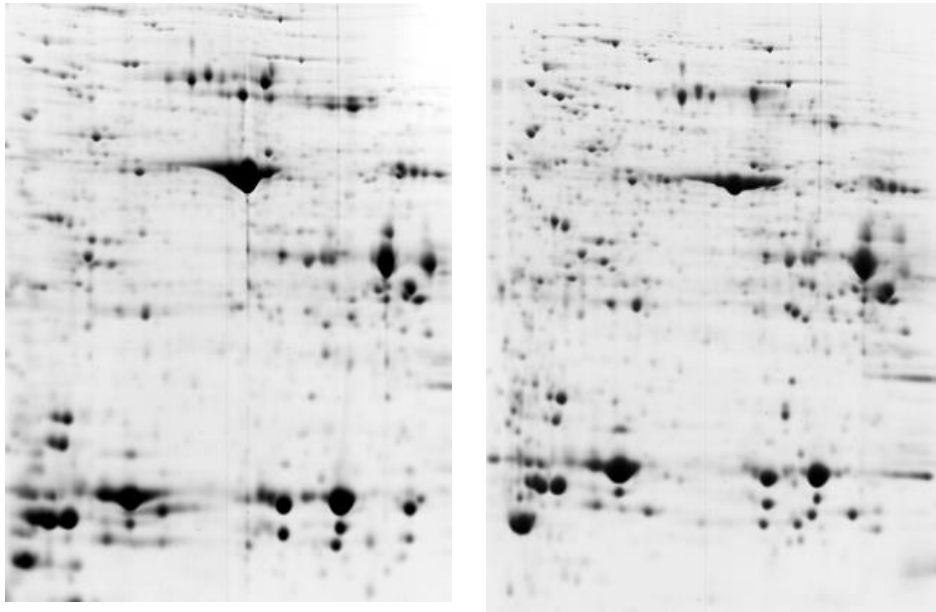
→ Strategy according to defined goal

- treated sample x control
- time-dependent treatment

The quality of image analysis corresponds to the quality of protein separation.

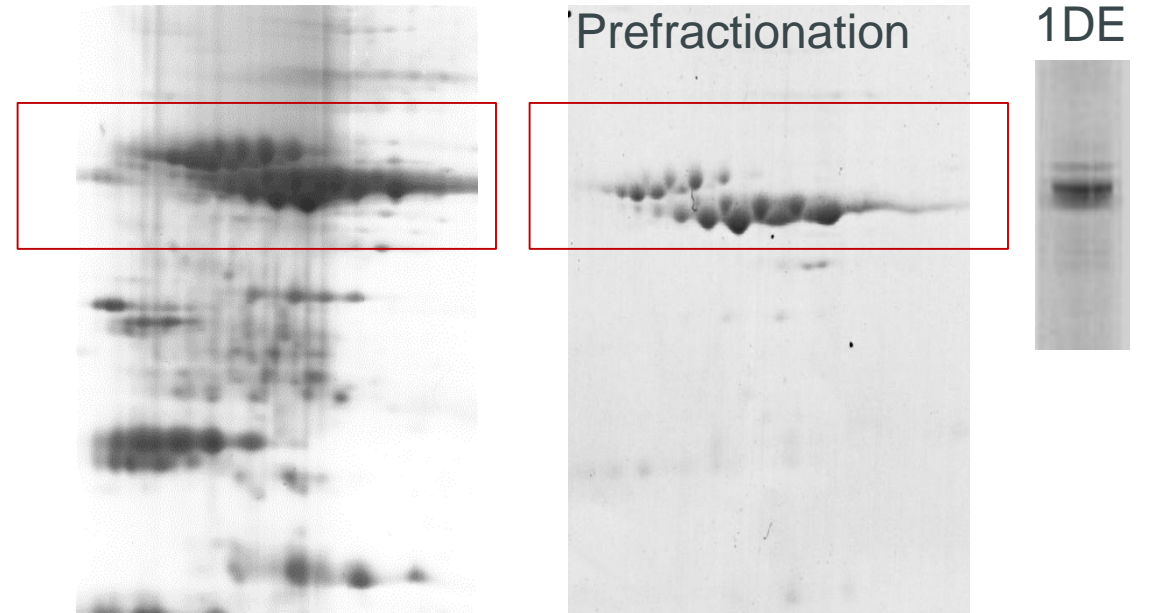
- Selection of spots which significantly differ based on certain design of experiment

– detection up- and down-regulated proteins



- Selection of limited number of significant spots
  - Protein isoforms
  - Post-translational modifications

– quantitative changes in the profile of certain spots



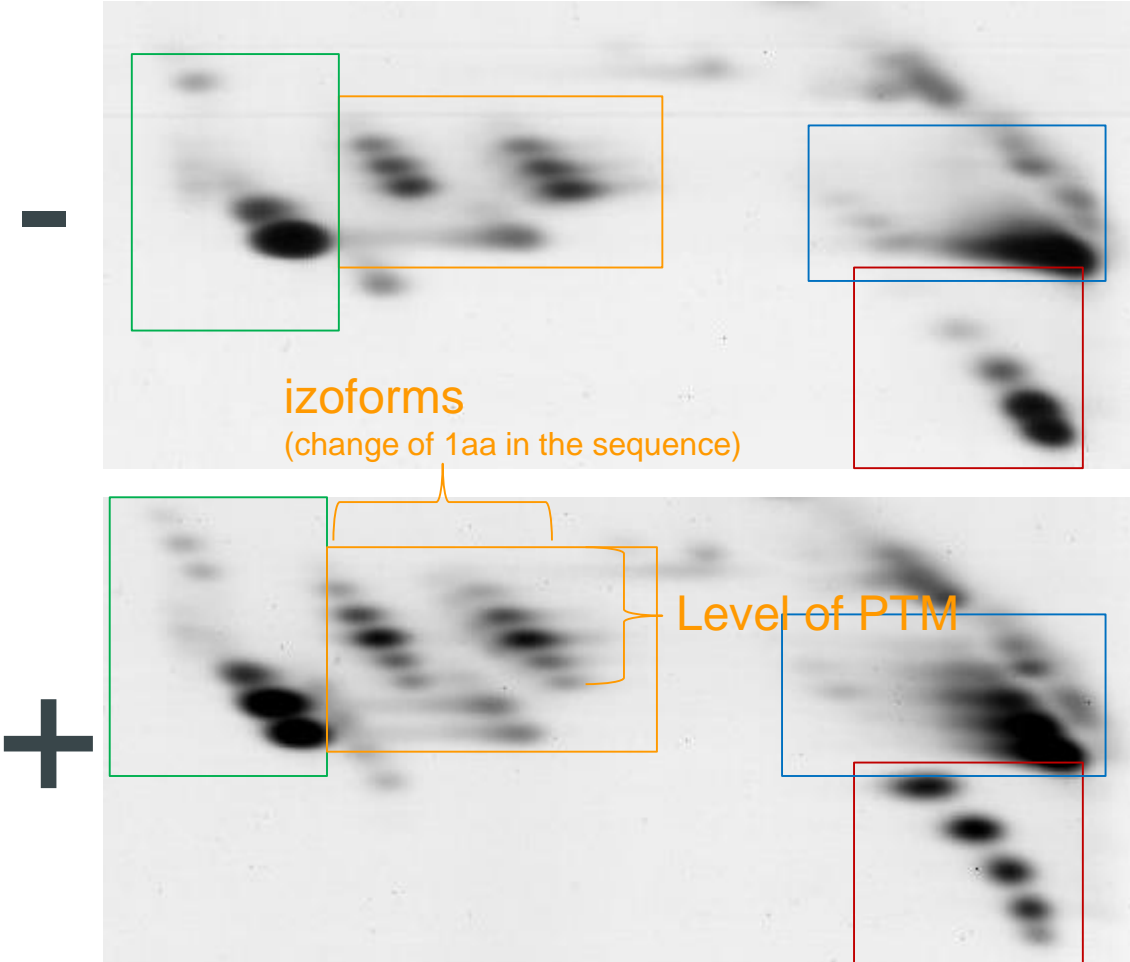
- Image analysis

Strategy according to defined goal

1-DE



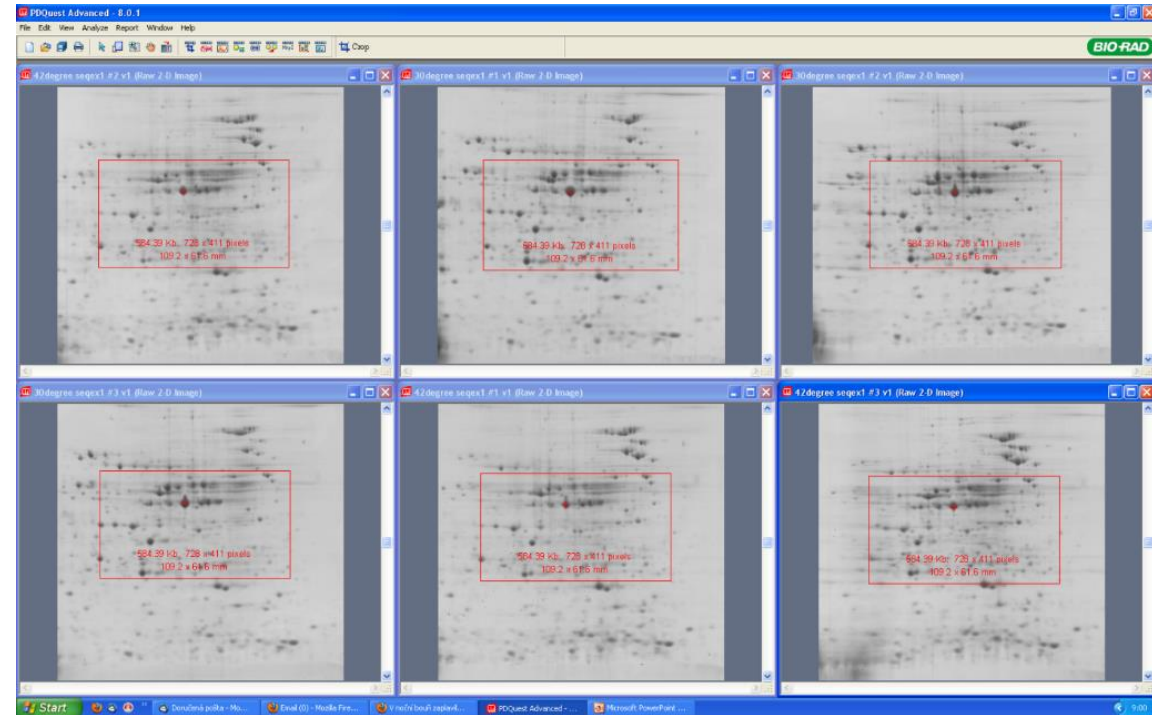
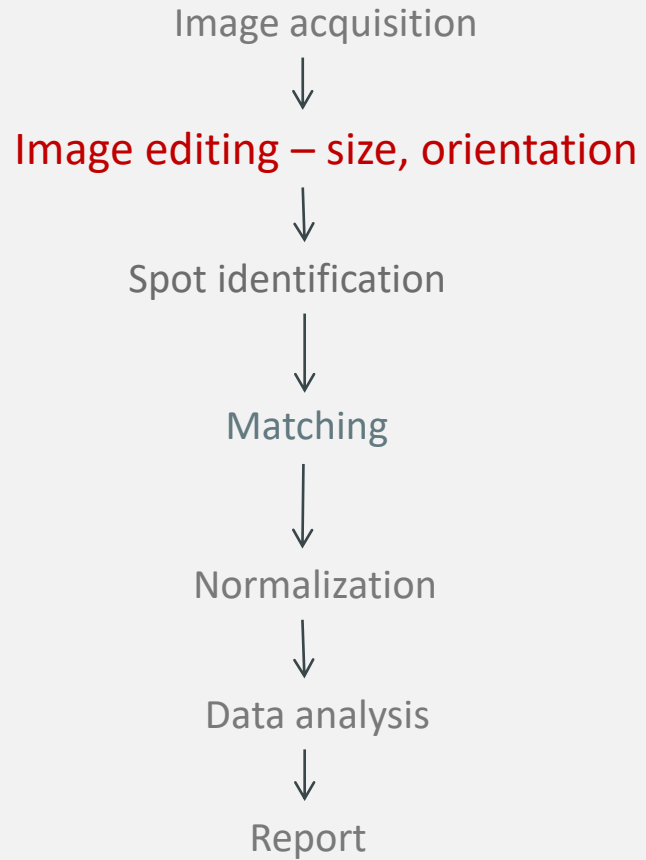
2-DE



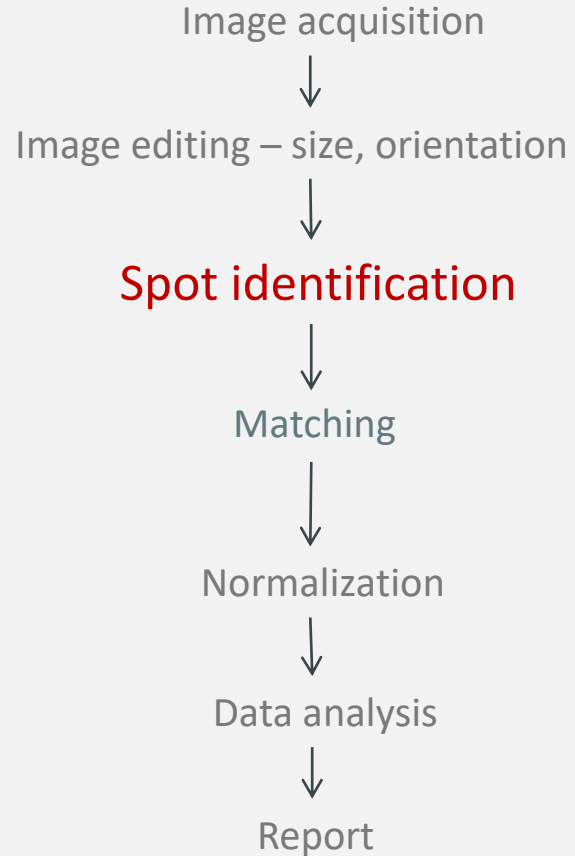


- Analýza obrazu

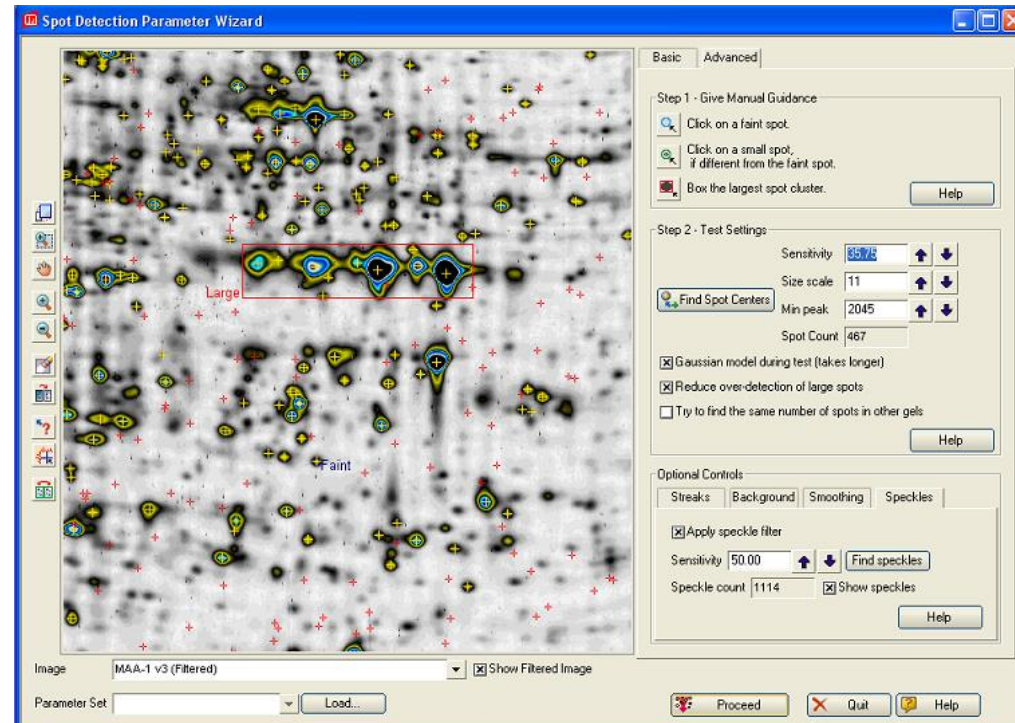
## Evaluation using PDQuest



# Evaluation using PDQuest

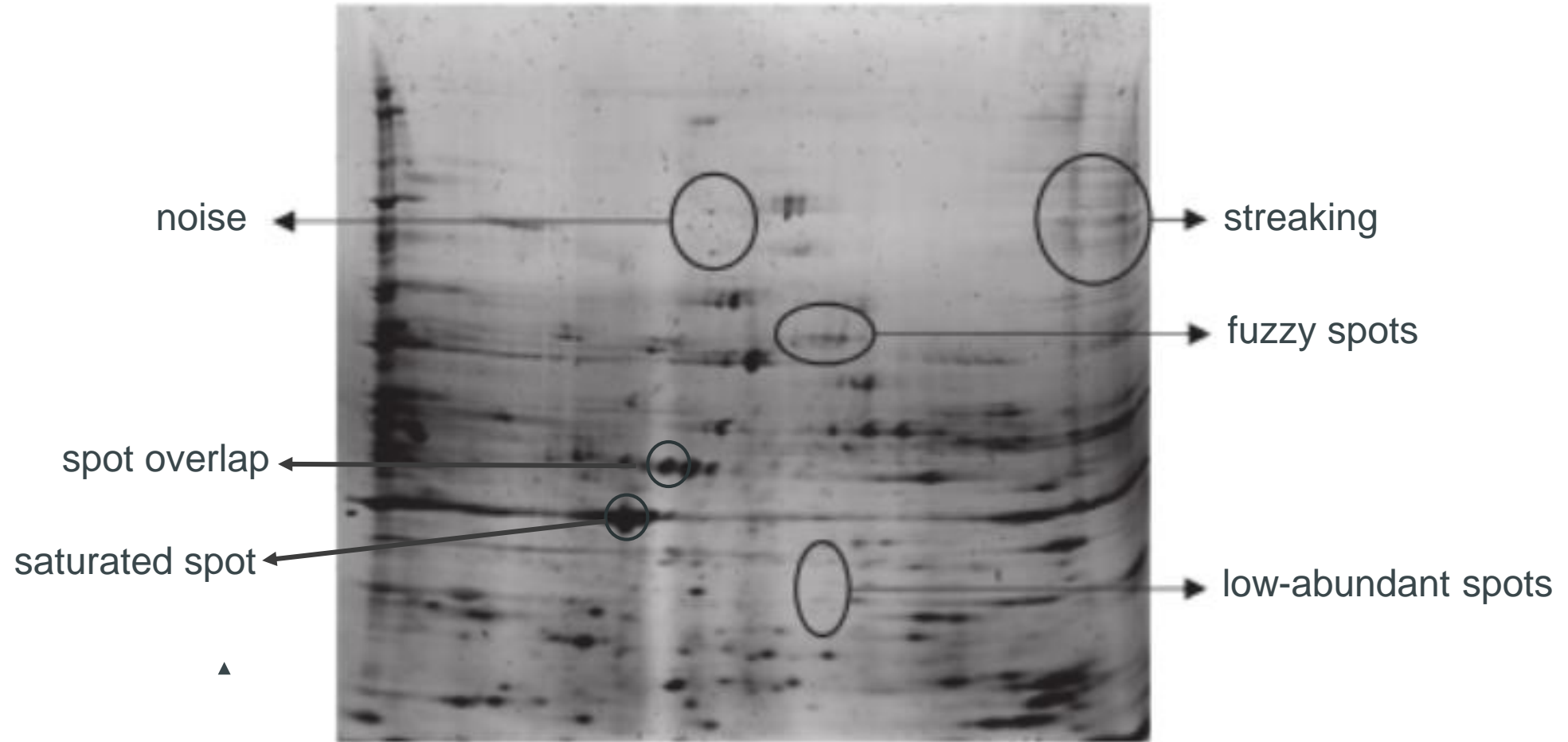


- Spot detection wizard
  - to select the parameters for detecting spots and background filtration in gel scans
- Different gels – different parameters needed



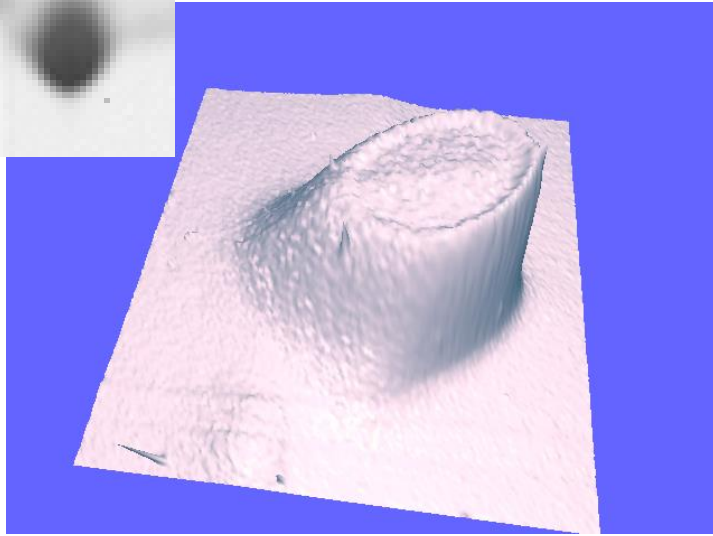
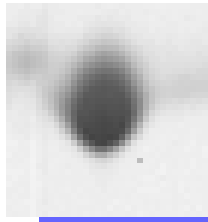
- Image analysis

Common anomalies present in 2D image

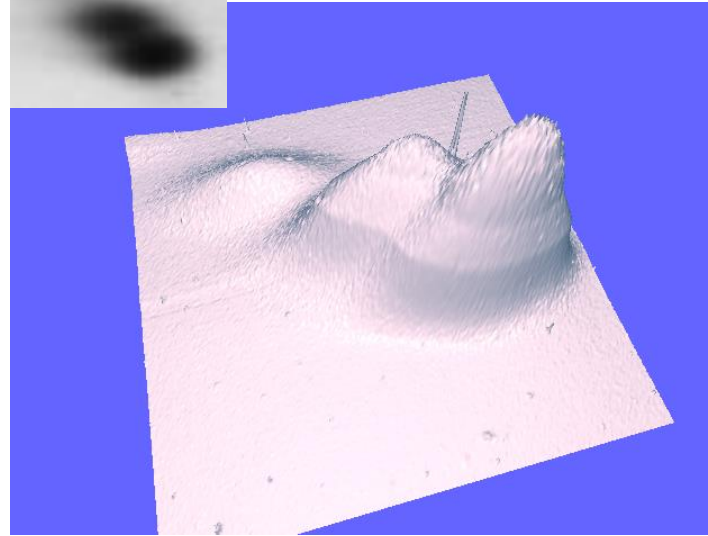
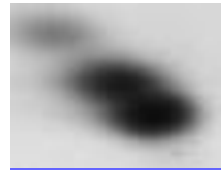


Goez et al. 2018 (modified)

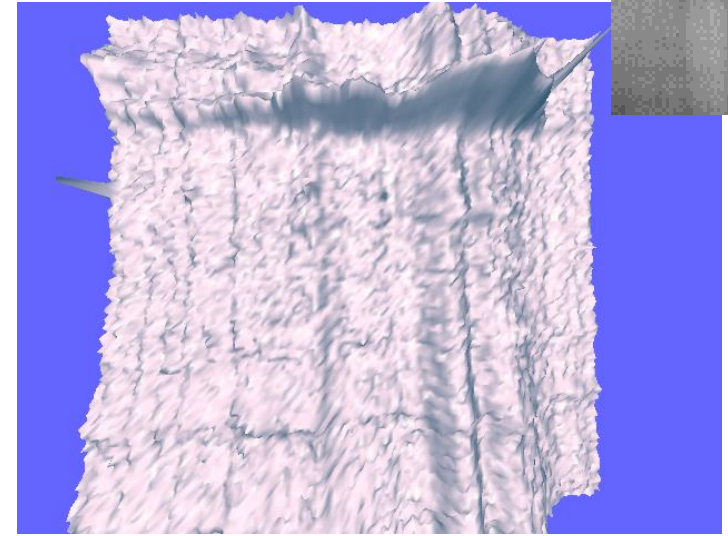
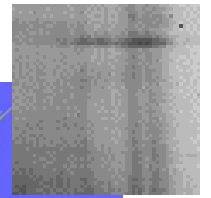
**Saturated spot**



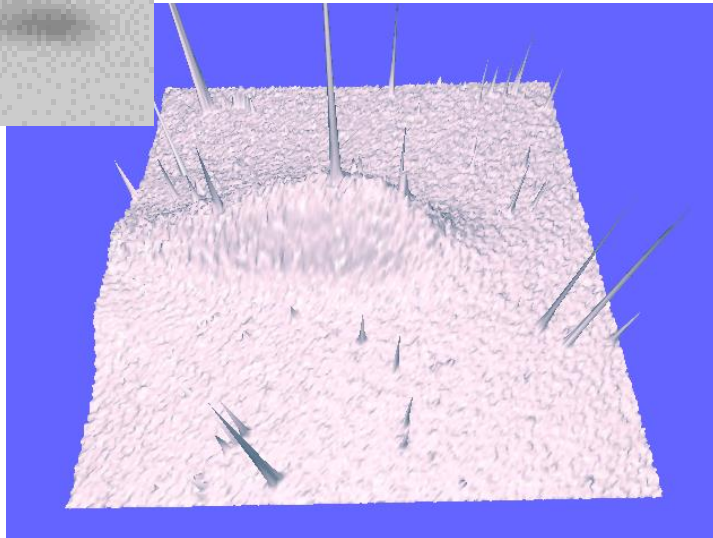
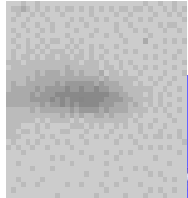
**Spot overlap**



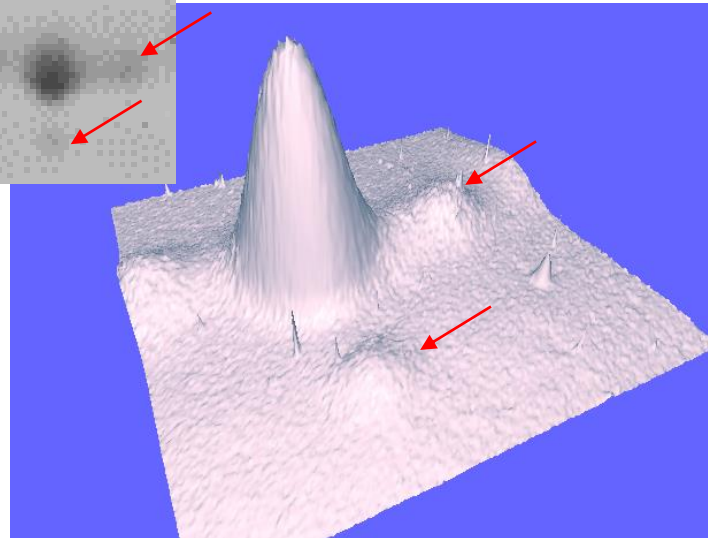
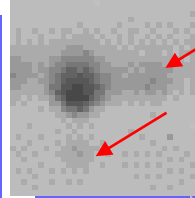
**Streaking**



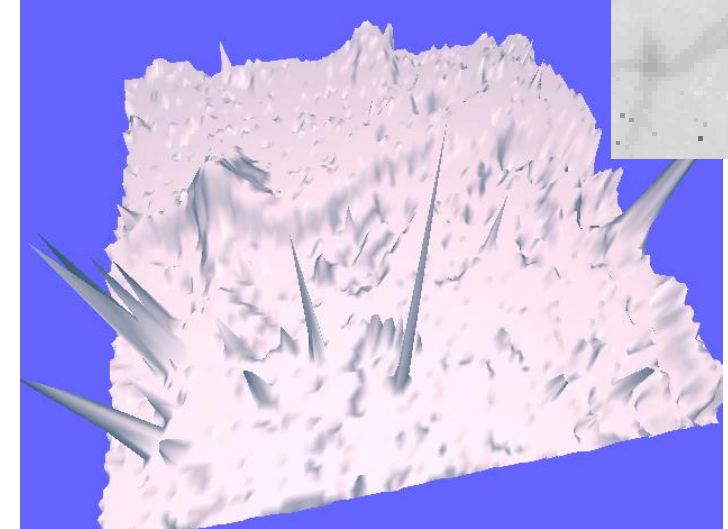
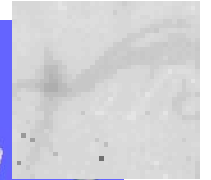
**Fuzzy spot**



**Low-abundant spot**



**Noise**



# Evaluation using PDQuest

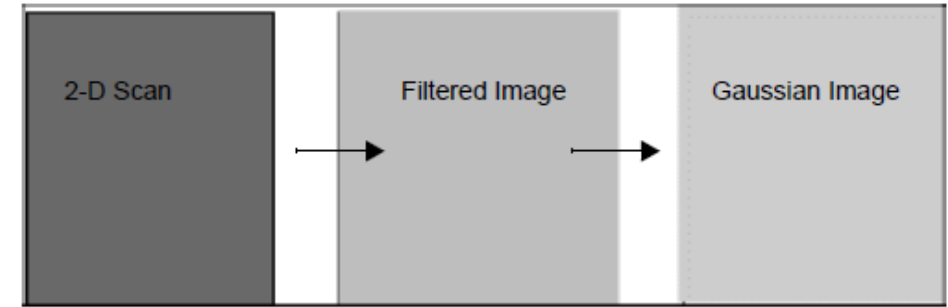
## Spot detection and background filtration

Local changes in the background based on the intensity of present protein spots (higher intense spots ~ higher background)

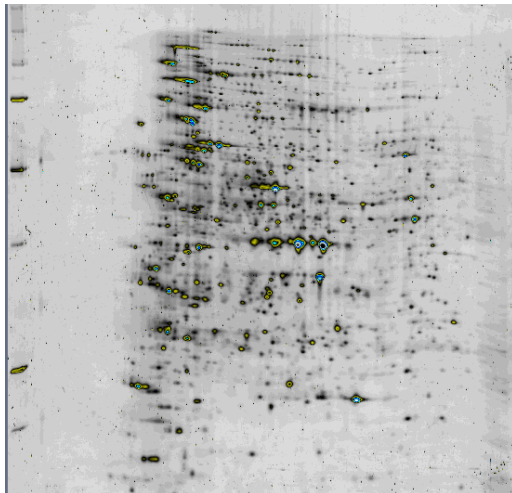
→ detection errors.

- **Scanset**

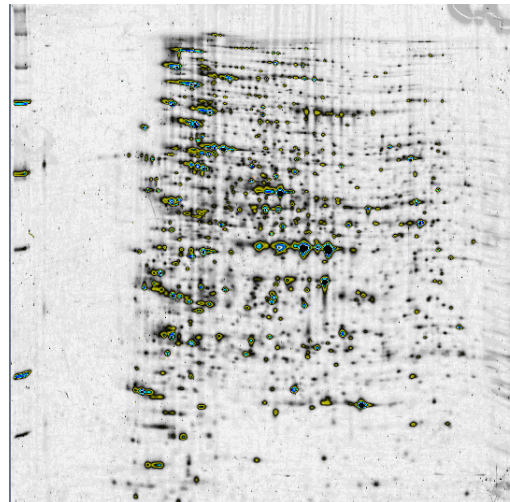
= set of images originating from a single gel (3 visualization of each gel)



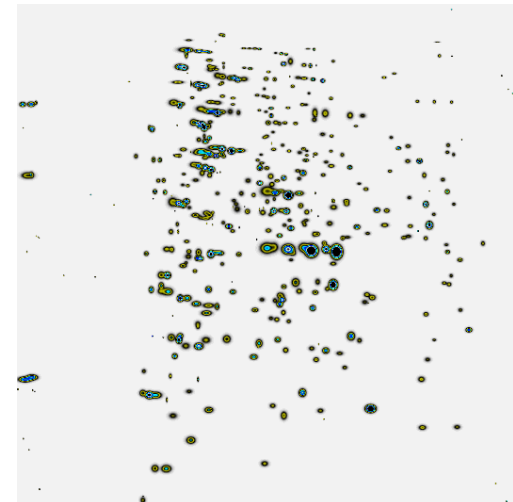
Raw 2D image



Filtered



Gaussian

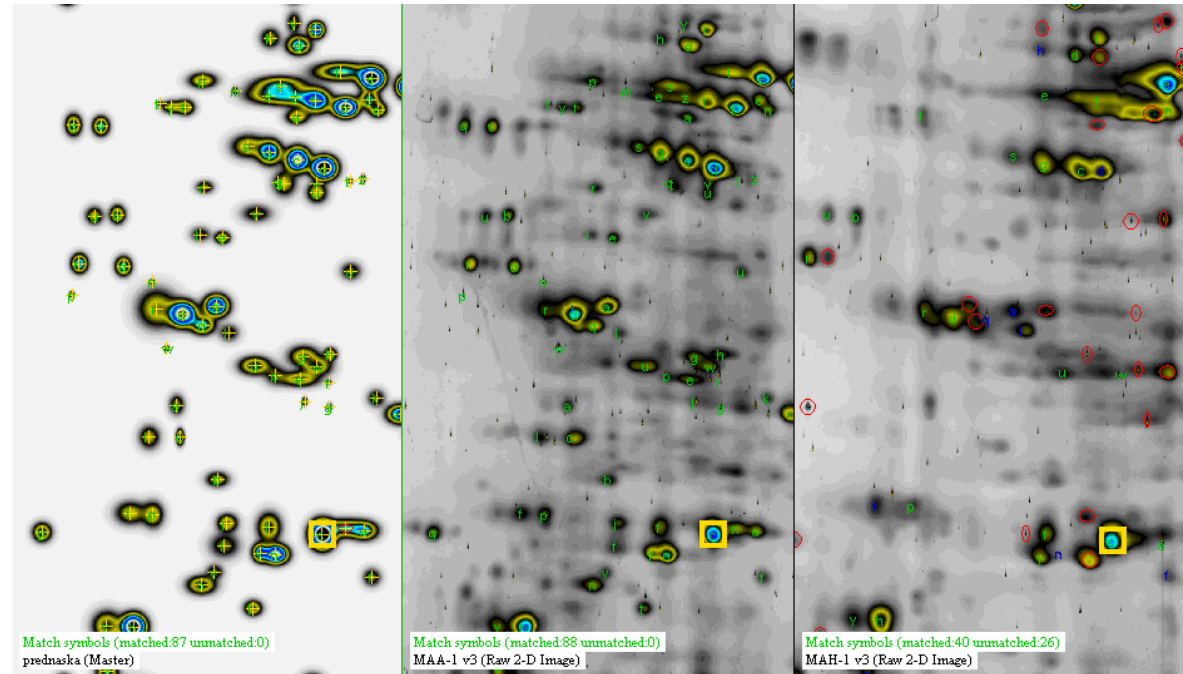
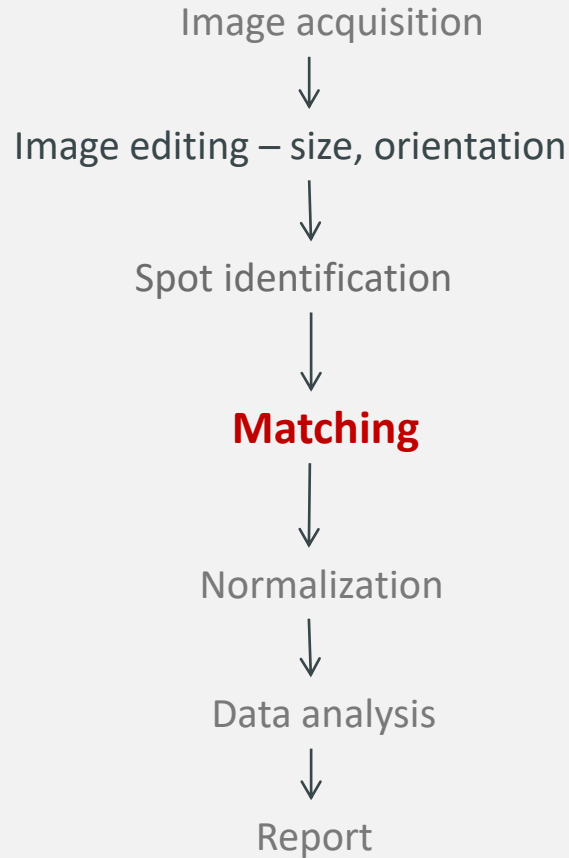


- Image analysis

## Evaluation using PDQuest

- Basic problem of image analysis: the differences in the spot position among gels
  - the necessity to perform an alignment

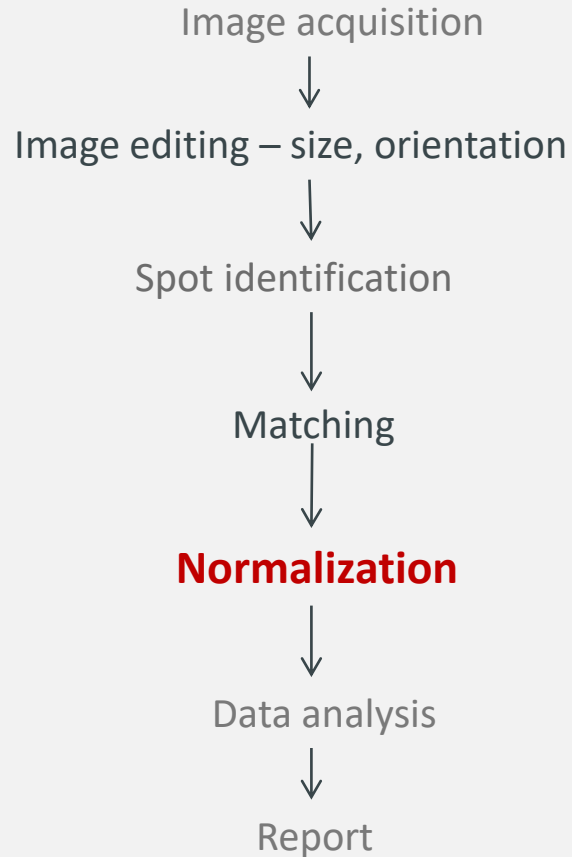
- **Matchset** = set of gels which are compared among each other within a single experiment
  - 
  - Master gel = artificial gel; involves spots from all compared gels



- Image analysis

## Evaluation using PDQuest

- **Normalize** = compensation of variation in spot size and intensity among gels that is not due to differential protein expression
- condition for appropriate spot quantity comparison



- Variance caused by different factors:
  - - pipetting errors during sample prep
  - - handling errors resulting in sample loss during sample prep
  - - sample loss during transfer from strip to gel
  - - inconsistent staining among gels
  - - inconsistent detection energy sources among gels during image acquisition
  - - .....
- **Normalization factor** (according to selected method)
  - Total quantity in analysis set
  - Total quantity in valid spots
  - Total density in gel image
  - Specified value
  - Mean of log ratios
  - Local regression model

- Image analysis

# Evaluation using PDQuest

- Report

## Image report

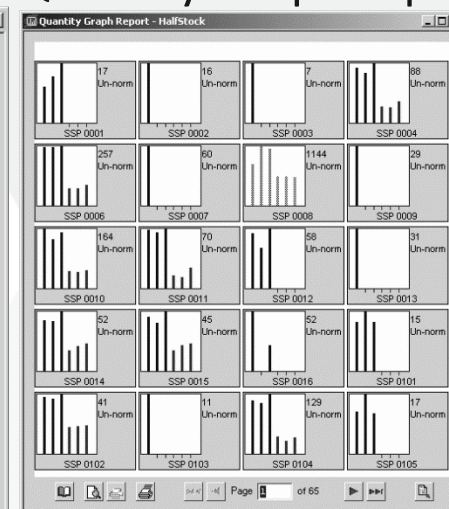
Image Report For: half3 v1 x3 (Raw 2-D Image)

Description N/A  
 Directory C:\PDQuest Data\MatchSets\\_MS00017 2003-07-08 Data  
 Filename half3 v1 x3.gsc  
 Image Date unknown  
 Imager GS-710 Pixel size(um) X: 176.0, Y: 176.0  
 Image Area(mm): X: 178.6, Y: 140.2 Data Range 2.00 OD  
 Image Pixels X: 1015, Y: 797 Memory Size 791.94 Kb  
 Image History  
 11-Nov-1999 10:29 : Power Mean (3X3)  
 Acquisition Parameters  
 Gain Setting: 0.0  
 Size Mode: absolute  
 Ref Bkgd Time: 0.00 sec.  
 PMT Voltage: (0%)

## Quantity Table report

| SSP  | stock1 | stock2 | stock3 | half1 | half2 | half3 |
|------|--------|--------|--------|-------|-------|-------|
| 0001 | 10.2   | 13.4   | 16.9   | 1.3   | 1.3   | 1.3   |
| 0002 | 16.4   | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0003 | 7.2    | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0004 | 82.3   | 75.0   | 88.4   | 24.6  | 22.8  | 31.6  |
| 0006 | 256.4  | 256.5  | 257.2  | 74.1  | 73.9  | 88.9  |
| 0007 | 59.5   | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0008 | 791.7  | 1143.5 | 1100.5 | 569.0 | 565.4 | 544.8 |
| 0009 | 29.3   | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0010 | 163.6  | 135.8  | 155.8  | 45.9  | 44.1  | 48.2  |
| 0011 | 69.5   | 66.3   | 70.2   | 15.2  | 12.7  | 24.6  |
| 0012 | 54.1   | 40.0   | 57.9   | 1.3   | 1.3   | 1.3   |
| 0013 | 30.8   | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0014 | 44.9   | 43.8   | 52.2   | 18.2  | 22.0  | 24.4  |
| 0015 | 40.7   | 36.1   | 44.5   | 15.6  | 19.2  | 20.5  |
| 0016 | 52.5   | 1.3    | 22.8   | 1.3   | 1.3   | 1.3   |
| 0101 | 12.1   | 14.6   | 12.1   | 1.3   | 1.3   | 1.3   |
| 0102 | 39.7   | 38.2   | 40.9   | 18.3  | 18.8  | 19.3  |
| 0103 | 10.8   | 1.3    | 1.3    | 1.3   | 1.3   | 1.3   |
| 0104 | 116.6  | 110.3  | 128.9  | 36.7  | 27.1  | 34.7  |
| 0105 | 12.3   | 17.2   | 11.6   | 1.3   | 1.3   | 1.3   |
| 0106 | 34.8   | 36.2   | 34.3   | 1.3   | 1.3   | 1.3   |

## Quantity Graph report





# Experiment



• Spot cutting

→ **Manually** (scalpel, spot picker)

- Visible stains
- Fluorescent stains
  - transilluminator

OneTouch Plus spot picker



UV-transilluminator  
(Ex: 302, 365 nm)



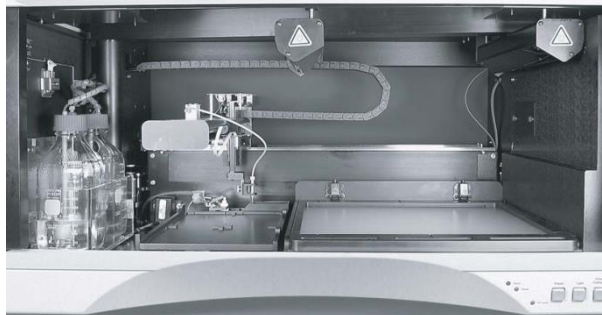
Dark Reader  
(Ex: 490 nm)



**Automation**

- Spot cutter

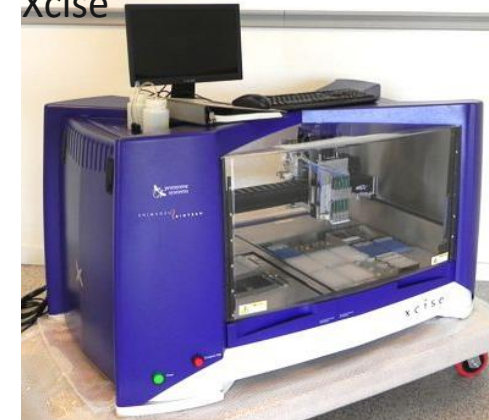
Exquest



Ettan Spot picker



Xcise





## 2-DE

- The best method of protein visualization in the form of protein spot which might be characterized its abundance, localization, presence / absence.
- The most often anomalies influencing image analysis:  
vertical and horizontal streaking, fuzzy spots, saturated spots, low-abundant spots, spot overlap, noise.
- Laborious, time consuming method, limited reproducibility, limited resolution (1 spot  $\neq$  1 protein!).



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Thank you for your attention.

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