

# Eric Pitman Summer Workshop in Computational Science

Intro to



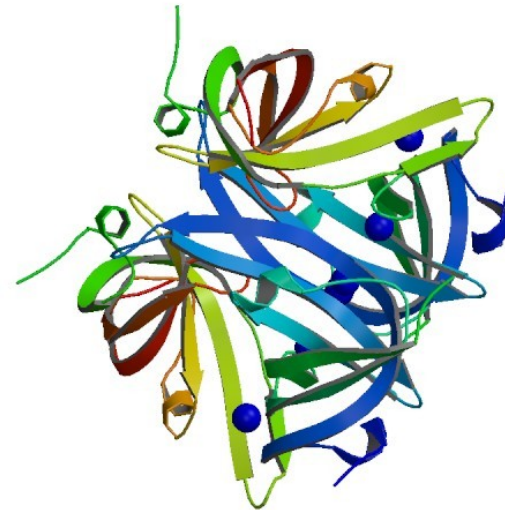
## Project Introduction

Jeanette Sperhac & Amanda Ruby

# Introducing the Workshop Project

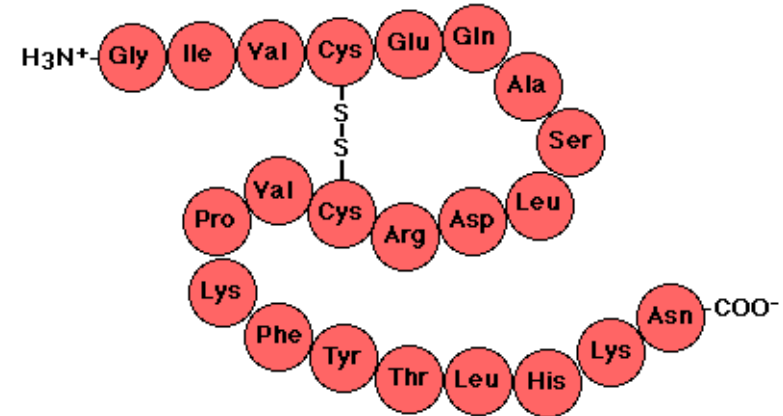
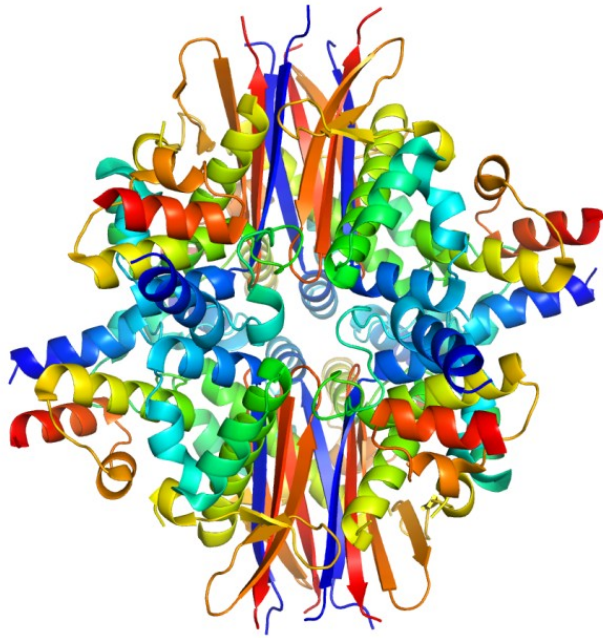
Here's what we'll cover:

- The story of the HWI protein crystallization data
- The Questions
- So what's a classifier?
- Inside the dataset
- The Project in RStudio
- Exploring the Proteins
- What you'll need



# Proteins

Proteins are large biological molecules, composed of long chains of amino acids

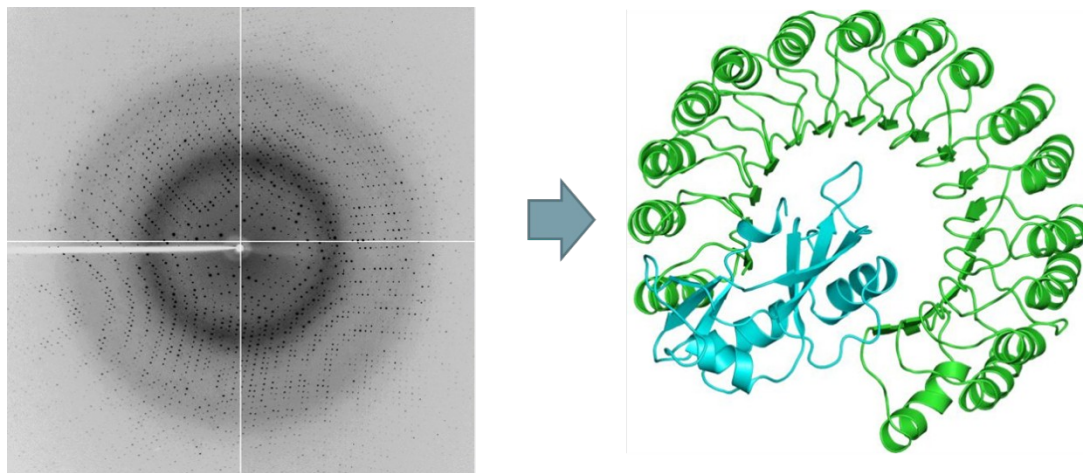


These chains fold into complex structures, allowing the protein to perform biological tasks

STRUCTURE AND  
FUNCTION ARE VERY  
CLOSELY RELATED

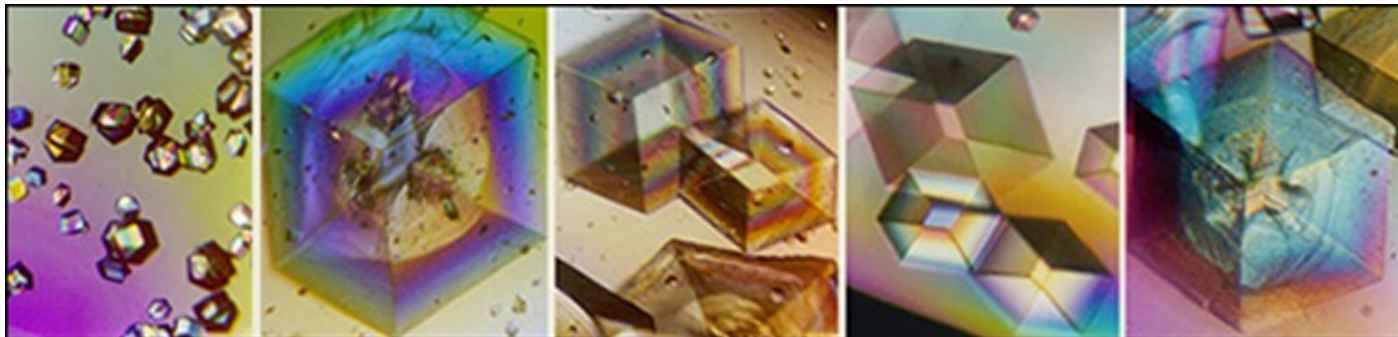
# X-Ray Crystallography

- Protein crystals are bombarded with x-rays. The x-rays are diffracted, giving structural biologists a way to determine structure
- Herbert A. Hauptman developed the mathematical model to convert reflections to molecular structures
- The process requires *protein crystals*



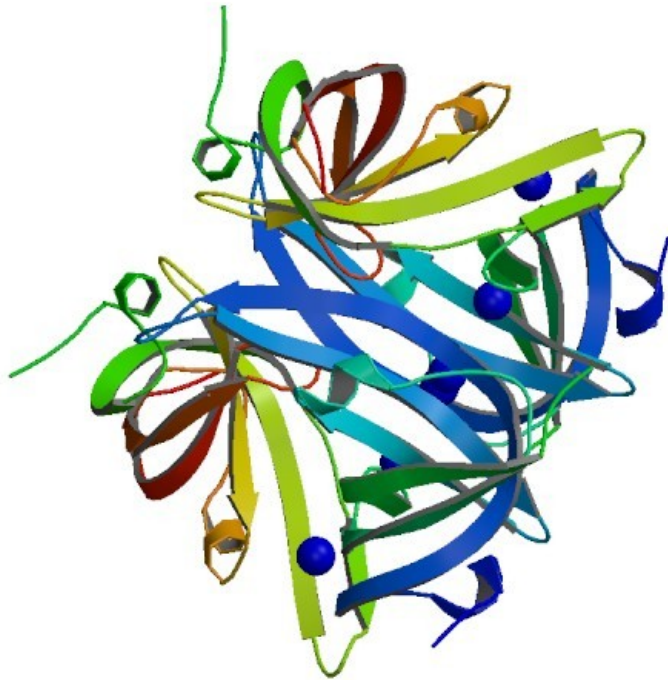
# Crystallization

- Trying to get a protein to “crash out” of solution, in an orderly fashion
- Requires a precise set of conditions, which vary from protein to protein
- Included in this precise set of conditions: a chemical cocktail
- Cocktails are combined into screens (==generations)



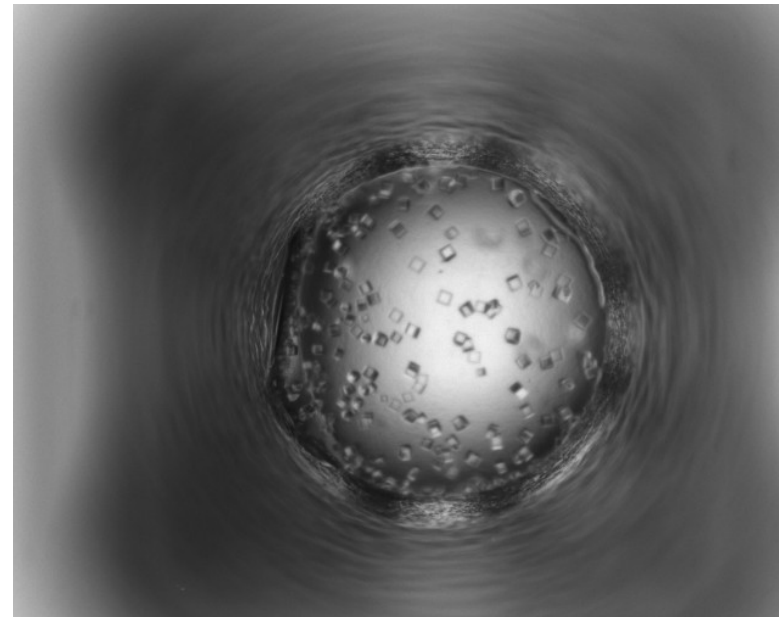
# Introducing the Workshop Project

*To achieve this (protein structure):*



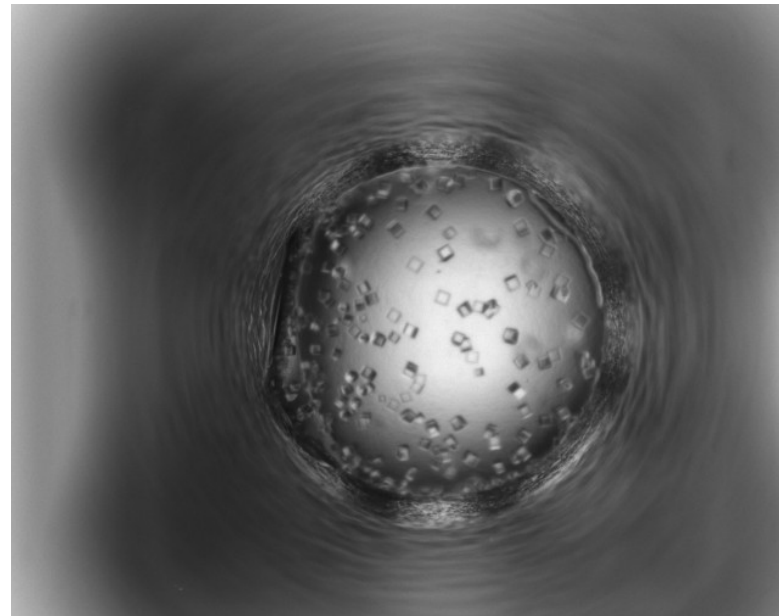
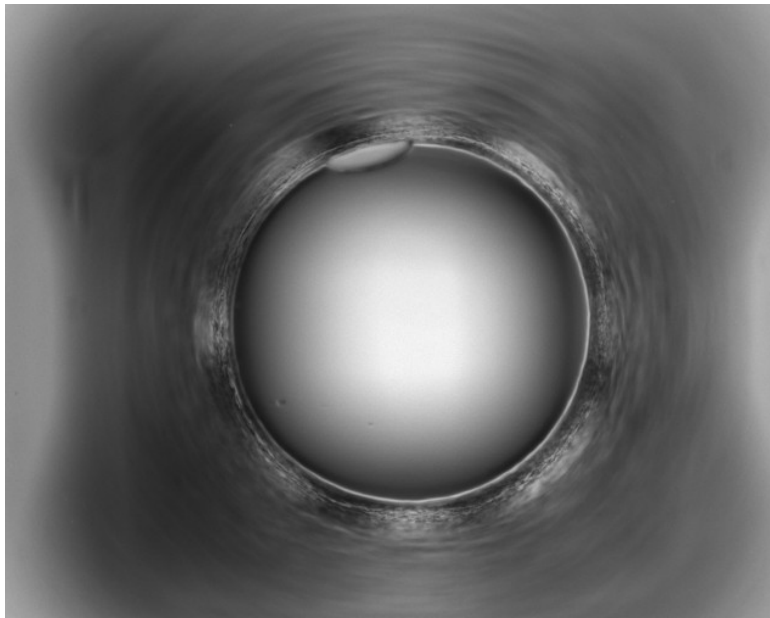
Protein Data Bank ID: 3dm3

*We must get this (pure, crystallized protein):*





# HWI Protein Crystallization Data

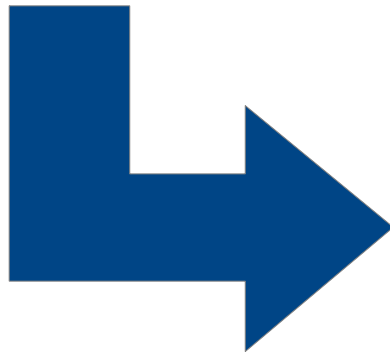


Which sample contains a crystallized protein?  
*(Can we make this decision for 3 million samples?)*

# Real Data, Local Data



HWI lab work



CCR processing



# 1. Laboratory Work: HWI



- A protein is placed in 1536 wells on an experimental plate.
- A different chemical cocktail is added to each well.
- Photos of each well are taken at different timepoints.

*Which proteins crystallized in which cocktails, at which timepoints?*

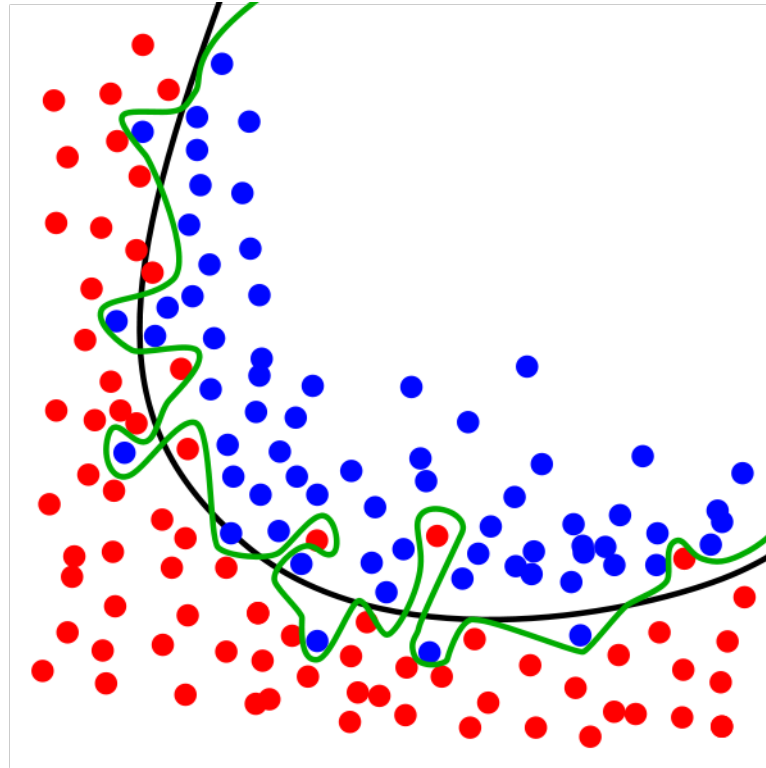
## 2. Automatic Classifier: CCR



An automatic classifier helps identify crystallized samples:

- Compute measures that describe the photo of each sample.
- Classifier assigns probability that each sample contains crystallized protein.

### 3. But...



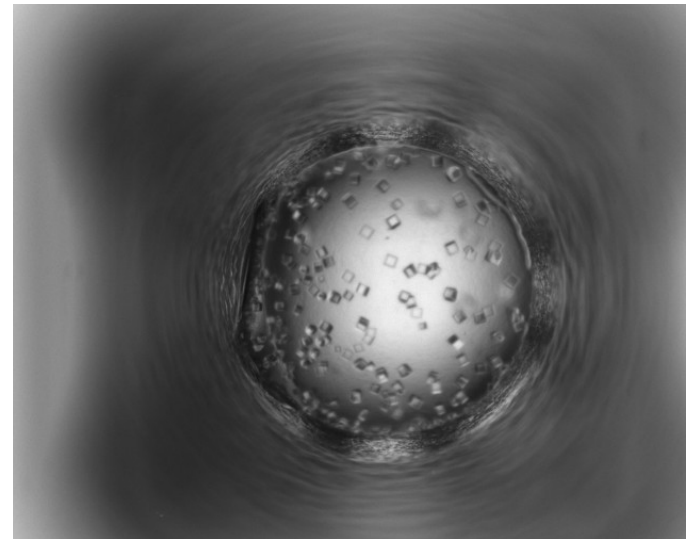
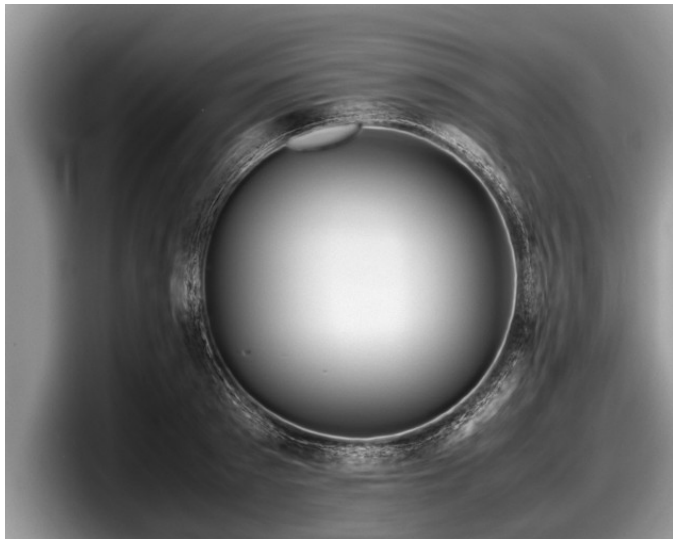
The classifier is only  $\sim 70\%$  accurate, so:

*Human expert classifies each sample. This is the final word.*

# 39936 Experimental Records

We have a photograph of each experiment:

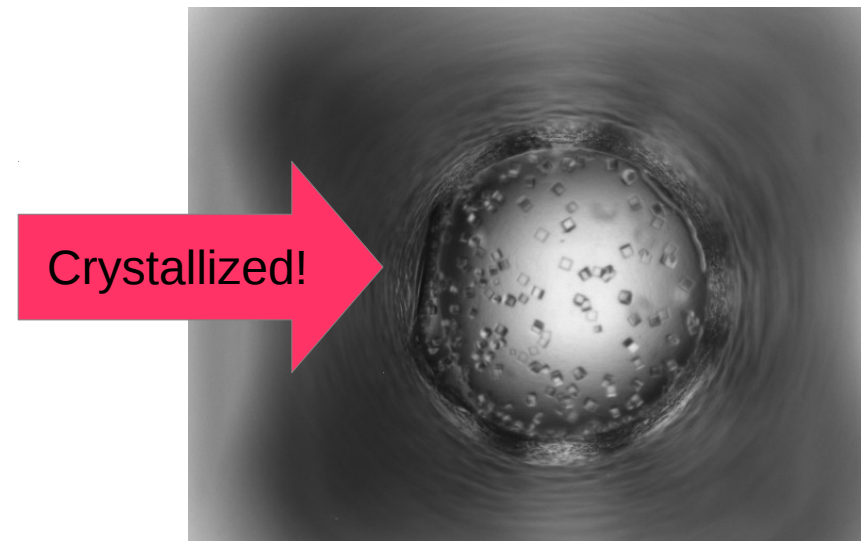
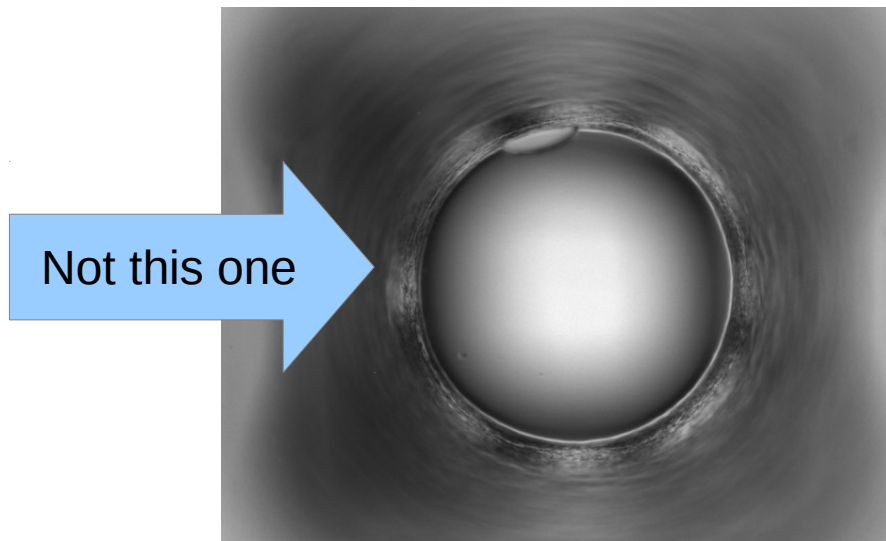
- 13 proteins
- In 1536 chemical cocktails
- At 2 different time points



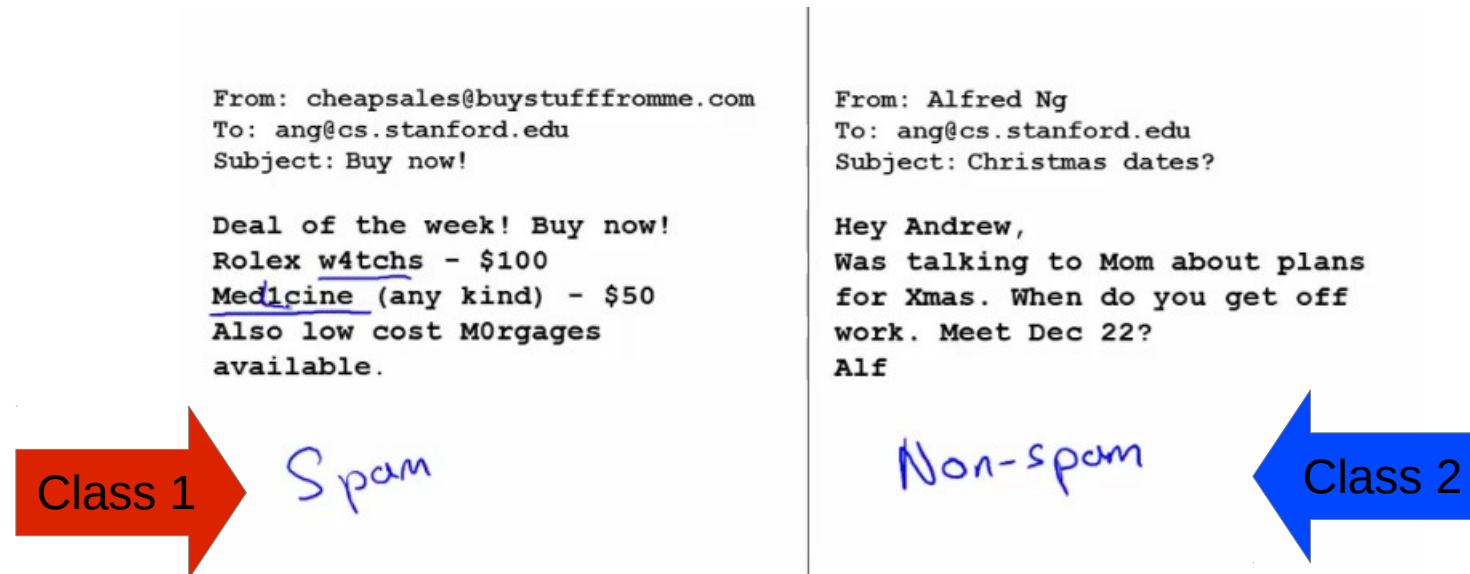
# 39936 Experimental Records

We have information about each one:

- Classifier score (value between 0 and 1)
- Human assignment (*truth*): crystal/non-crystal
- Some other stuff...



# Automated Classifiers

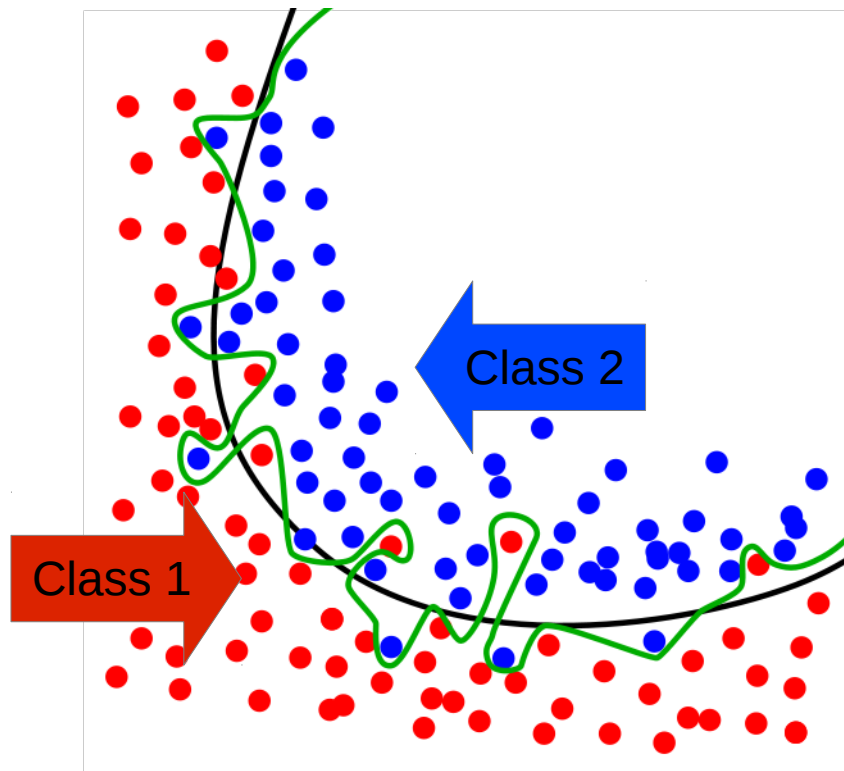


This classifier has assigned data points into two classes, 1 and 2.



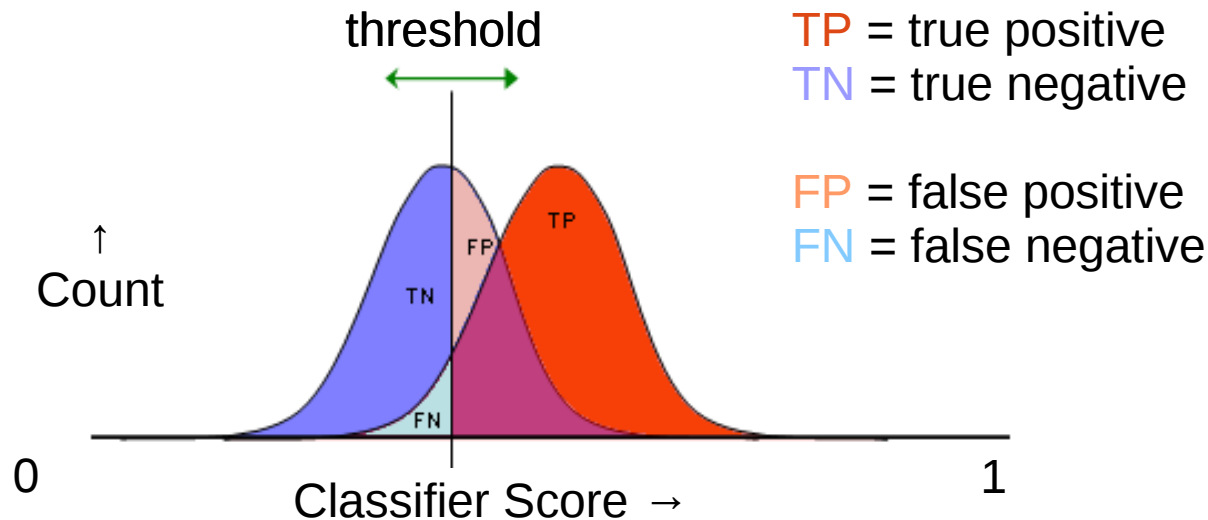
# Automated Classifiers

How does this work?



- Classifier is run multiple times on each data point
- The results are converted to a probability that a crystal was seen

# Classifier Performance



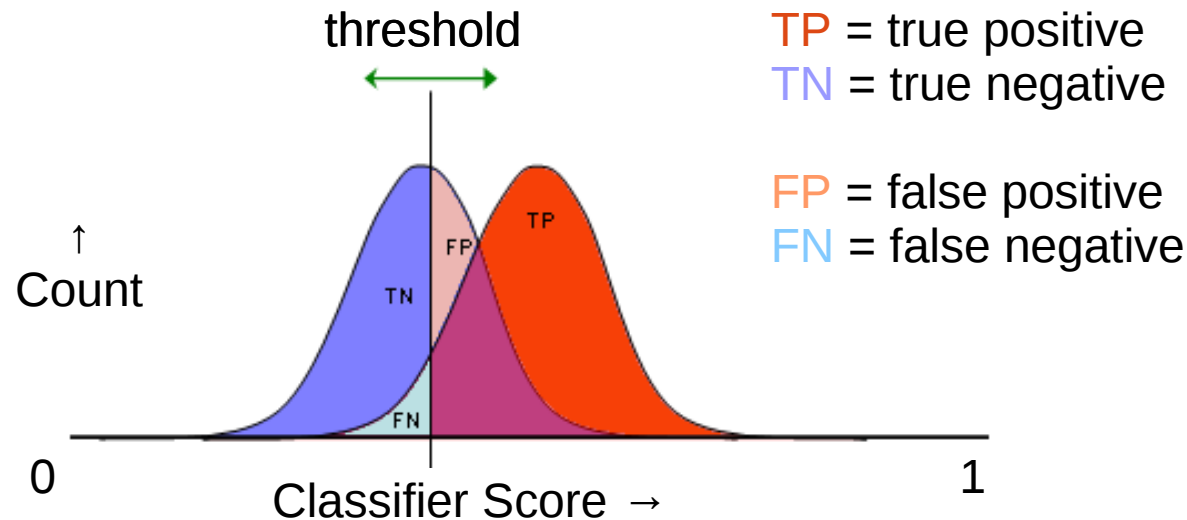
Our classifier assigns scores that lie between 0 and 1.

We can overplot two kernel density plots:

- One of human-classified crystal examples
- One of human-classified non-crystal examples

...both with classifier score on the x axis

# Classifier Performance

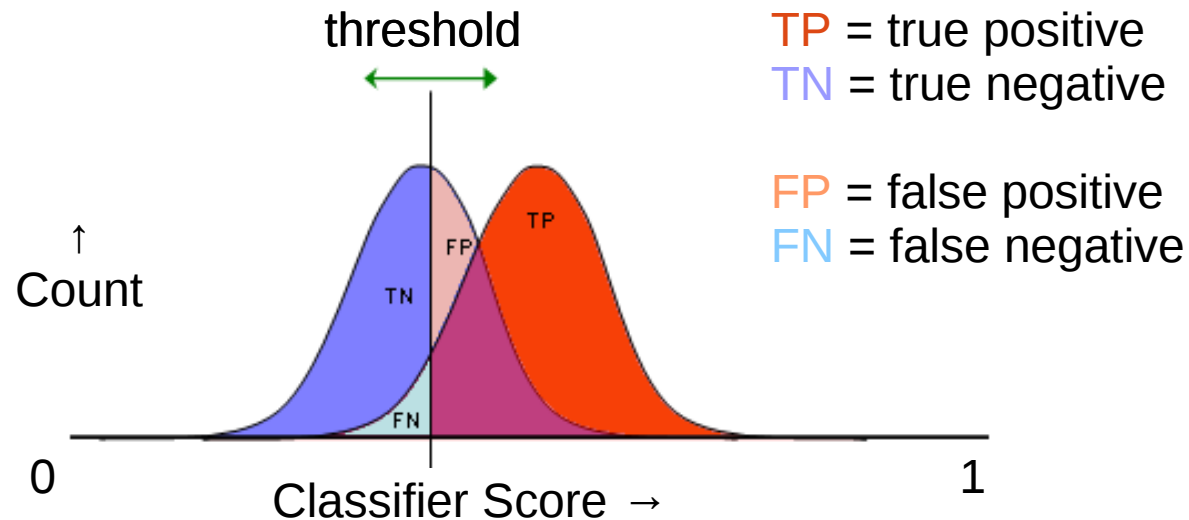


Pick a threshold (cut point) for classifier scores:

- above it, consider all examples to be positive (crystal)
- below it, consider all examples to be negative (not crystal).

No matter where we cut, we get some classifications wrong!

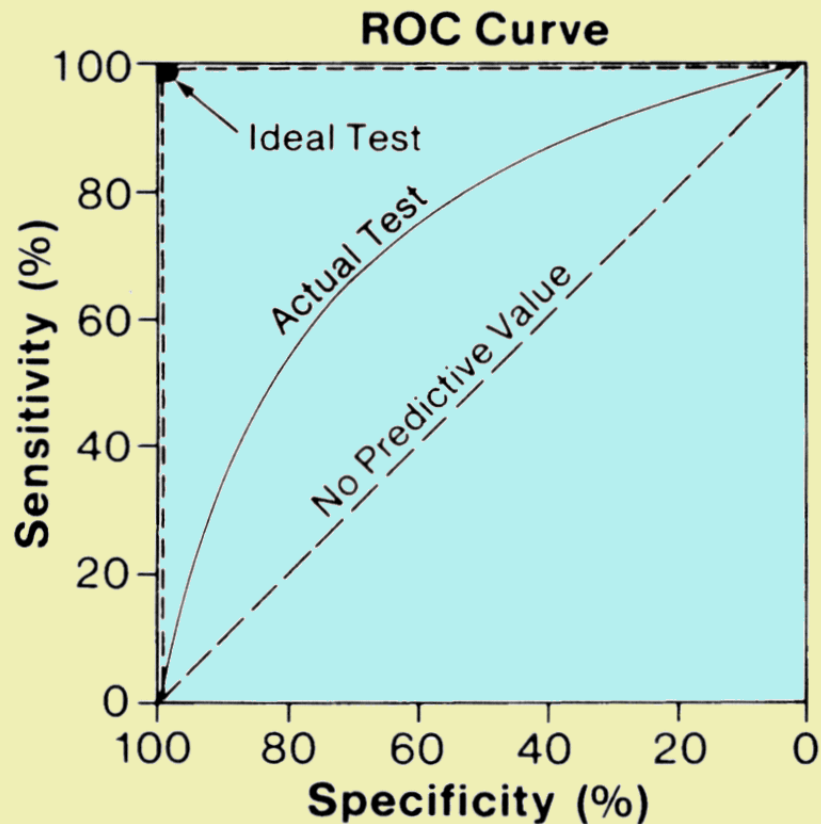
# Classifier Performance



After we pick a threshold, we can see four types of outcomes:

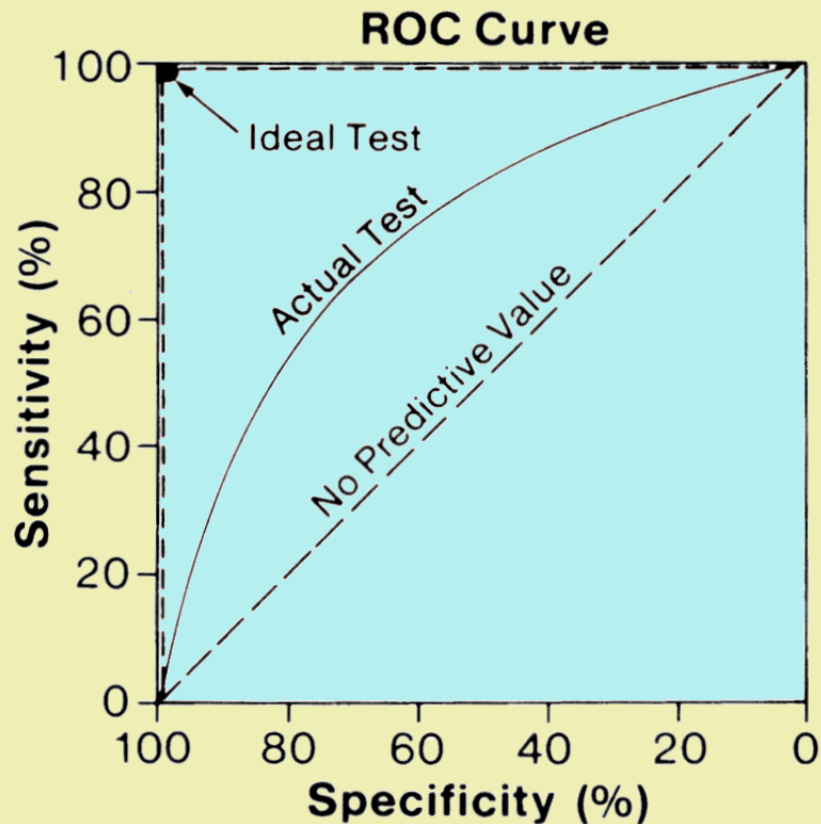
- True and False Positive (crystal)
- True and False Negative (not crystal).

# ROC Plots and Classifiers



- Evaluate the performance of a binary classifier
- Vary the threshold or cut point, vary the sensitivity/specificity ratio

# Sensitivity vs. Specificity



- Specificity (true negative rate): the ability to classify non-crystals as non-crystals.
- Sensitivity (true positive rate): the ability to classify crystals as crystals



# Meet Your HWI Dataset

The data frames:

- experiment: 39936 rows
- sample: 13 proteins
- drop: 3930 rows (1536 chemical cocktails)
- expUrl: 39936 rows (one per experiment)



$$\begin{array}{ccccccc} 13 & \times & 1536 & \times & 2 & = & 39936 \\ \text{proteins} & & \text{cocktails} & & \text{timepoints} & & \text{experiments} \end{array}$$

# Experiment Data: 39936 Rows

experiment data frame describes the crystallization experiments:

- **read\_no**: 39936 values, identifies experiment
- **sample\_id, plate\_no**: 13 values, identifies protein
- **week\_no**: 2 timepoints
- **cocktail\_no**: 1536 unique values
- **human\_crystal**: crystal or not?
- **class3\_crystal**: probability of crystal

$$\begin{array}{ccccccc} 13 & \times & 1536 & \times & 2 & = & 39936 \\ \text{proteins} & & \text{cocktails} & & \text{timepoints} & & \text{experiments} \end{array}$$

# Sample Data: 13 Different Proteins

sample data frame describes the proteins:

- Identify each protein:
  - sample\_id, p\_number, targetdb\_status, name
- experimental\_molecular\_weight
- concentration of the protein
- seq: sequence of amino acids in protein
- seq\_len: number of amino acids
- targetdb\_ref: PDB (Protein Data Bank, [www.rcsb.org](http://www.rcsb.org))
- targetdb\_status: unique protein code on PDB

# Drop Data: 3930 Rows

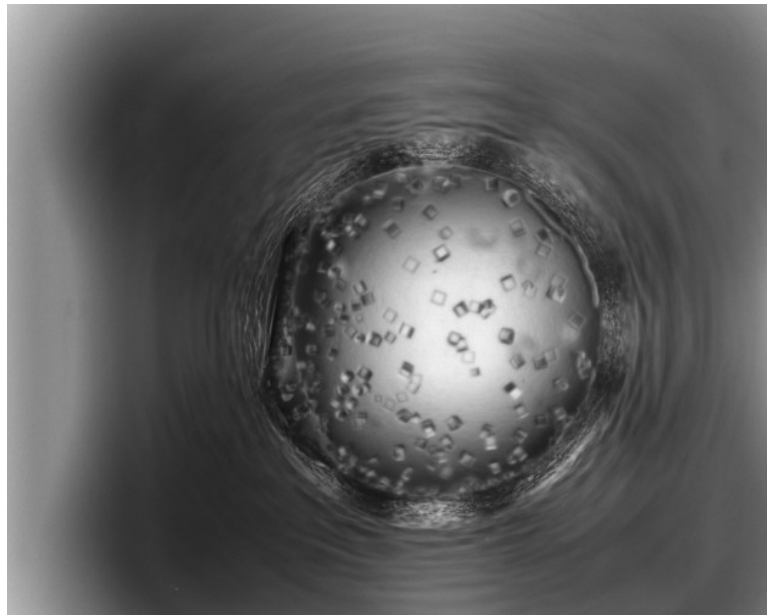
drop data frame describes the components of the chemical cocktails:

- Identify each chemical cocktail (1536 in total):
  - cocktail\_no + solution\_component\_no
- concentration of the solution component
- name of the solution component
- ph: pH of the solution component

# expUrl Data: 39936 Rows

expUrl data frame contents:

- read\_no: identifies experiment
- image\_url: URL of the experiment image





# RStudio: Project Data

HWI data are text files with csv format.

- Formatted to load straight into an R data frame
- Columns are labeled by name

*csv == comma separated values*





# RStudio and csv: Two ways to load data

## 1. RStudio Workspace:

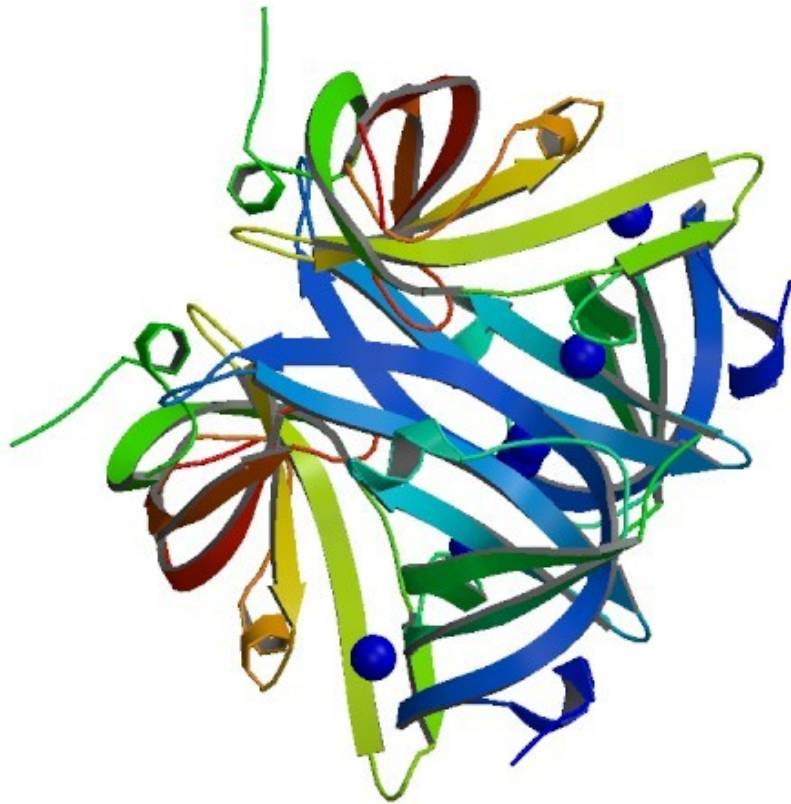
- Select Import Dataset: From Text File
- Select a .csv file to Open
- Use Heading=Yes

## 2. Or, from the command line:

- Set the Working Directory
- Load command:

```
> drop=read.csv("drop.csv")
```

# Exploring Proteins



Protein Data Bank ID: 3dm3

- BLAST algorithm
  - Protein sequence comparison
  - R package: bio3d
  - NCBI BLAST web interface
- Protein Data Bank

# Exploring Proteins: bio3d BLAST

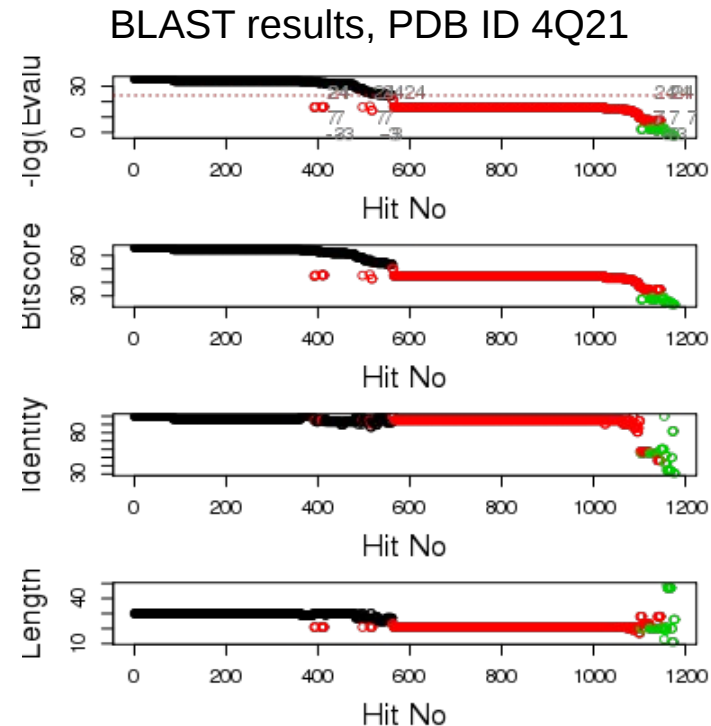
blast.pdb() returns:

- bitscore
- evalue
- mlog.evalue
- pdb.id

bio3d package documentation:  
<http://thegrantlab.org/bio3d/html/index.html>

## plot.blast() returns:

# Summary and plot of BLAST hit statistics



# Exploring Proteins: NCBI BLAST

The screenshot displays the NCBI BLAST web interface. The browser address bar shows the URL: [www.ncbi.nlm.nih.gov/BLAST/Blast.cgi?PAGE=Proteins](http://www.ncbi.nlm.nih.gov/BLAST/Blast.cgi?PAGE=Proteins). The page header includes the BLAST logo and the text "Basic Local Alignment Search Tool". Navigation links for "Home", "Recent Results", "Saved Strategies", and "Help" are present.

The main section is titled "Standard Protein BLAST". Below this, there are tabs for "blastn", "blastp", "blastx", "tblastn", and "tblastx". The "blastp" tab is selected.

The "Enter Query Sequence" section contains a text area with the following sequence:  
EIKDTYNIGELSPGMTATFEGEVISALPIKEFKRADGSIGKLKS  
FIVRDETGSIKRVTLWDNLTDIDVGRGDYVRVRGYIREGYYGG  
LECTANYVEILKKGEKIES

Below the text area are links for "Clear" and "Query subrange", and input fields for "From" and "To".

The "Program Selection" section shows the "Algorithm" dropdown menu. The selected algorithm is "blastp (protein-protein BLAST)". Other options include "PSI-BLAST (Position-Specific Iterated BLAST)", "PHI-BLAST (Pattern Hit Initiated BLAST)", and "DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)".

A large red arrow points to the "BLAST" button. Below the button, there is a checkbox for "Show results in a new window" and a link for "Algorithm parameters".

# Exploring Proteins: rcsb.org

RCSB Protein Data Bank - RCSB PDB - 3DM3 Structure Summary - Mozilla Firefox

Optics ... roc curv... Elite Bi... Sensitiv... Image C... pROC: S... 21 Google ... 2013-06... 2013-06... The Ne... The Ob... W Receive... RCSB...

www.rcsb.org/pdb/explore/explore.do?structureId=3dm3

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RCSB PDB PROTEIN DATA BANK

RCSB PDB-101

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Crystal structure of a domain of a Replication factor A protein, from *Methanocaldococcus jannaschii*. NorthEast Structural Genomics target MjR118E

DOI:10.2210/pdb3dm3/pdb

3DM3 PSI Protein Structure Initiative

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Primary Citation

Crystal structure of a domain of a Replication factor A protein, from *Methanocaldococcus jannaschii*. NorthEast Structural Genomics target MjR118E

Seetharaman, J., Su, M., Maglaqui, M., Janjua, H., Ciccocanti, C., Xiao, R., Nair, R., Everett, J.K., Acton, T.B., Rost, B., Montelione, G.T., Tong, L., Hunt, J.F.

Journal: To be Published

PubMed ID is not available

Molecular Description

Classification: Replication

Structure Weight: 35296.17

Molecule: Replication factor A

Polymer: 1 Type: protein

Chains: A, B, C

Length: 105

Fragment: residues 170-274

Biological Assembly 1

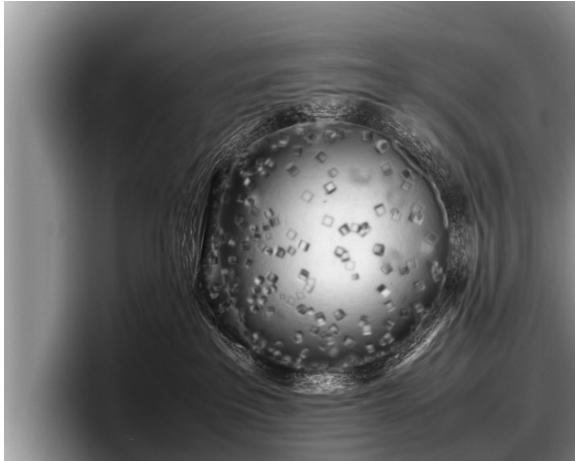
View in 3D More Images...

Biological assembly 1 generated by DISA

Find: 66

Previous Next Highlight all Match case

# Exploring Proteins



Check the data frame expUrl for links to the experimental images.

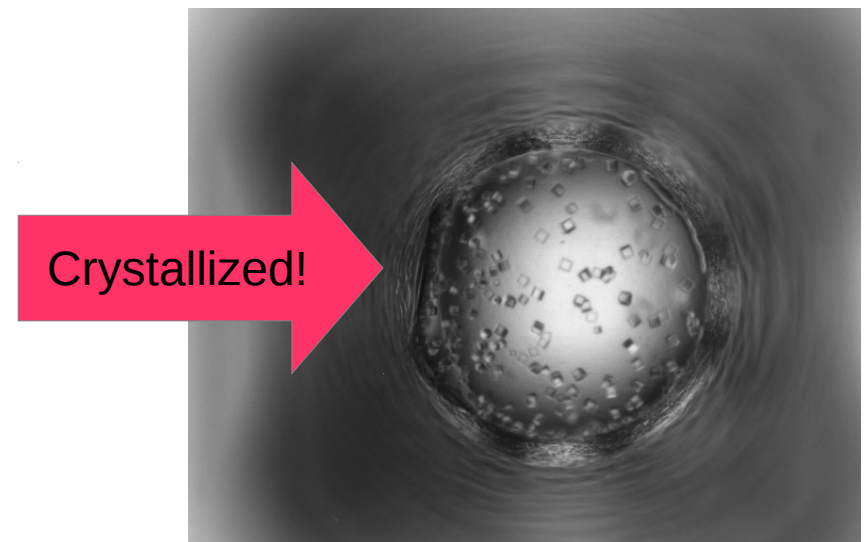
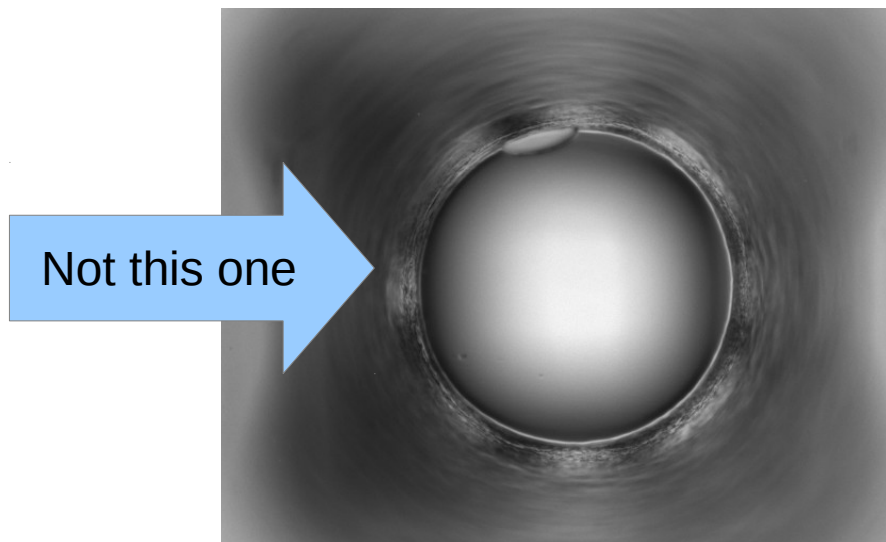
Can you identify the crystallization state?

	read_no	image_url
1	X0000095890696200801181226	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890696200801181226.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890696200801181226.jpg</a>
2	X0000095890384200801181231	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890384200801181231.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890384200801181231.jpg</a>
3	X0000095890001200801181235	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890001200801181235.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890001200801181235.jpg</a>
4	X0000095890488200801181228	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890488200801181228.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890488200801181228.jpg</a>
5	X0000095890504200801181228	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890504200801181228.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890504200801181228.jpg</a>
6	X0000095890926200801181222	<a href="http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890926200801181222.jpg">http://xtuition.ccr.buffalo.edu/image-data/X000009589/X000009589200801181215/X0000095890926200801181222.jpg</a>



# The questions

1. How does the automated *classifier* perform?
2. What trends do we see in *timeseries* data?
3. What trends do we see in crystallization of the proteins across the different *cocktails*?
4. What can we learn about the *proteins*?



# Project: you'll need...

- Data load
  - `read.csv()` R function
- File transfer: WebDAV
  - Copy files to your workstation from [hpc2.org](http://hpc2.org)
  - Useful for creating your presentation slides
- `factorify()` function
  - Apply to a data frame after subsetting; updates factor levels
  - source `generalFactorifyFunction.R`
- Optional: Jmol protein viewer on [hpc2.org](http://hpc2.org)

# 1. Classifier Performance Focus

- Data file: experiment.csv
- Epi R package: ROC()
- R functions:
  - `sapply()`
  - Kernel density estimation: `density()`
  - `data.frame()`
- R graphics:
  - `hist()`, `plot()`
- Provided function `compareDensityPlots()`

## 2. Timeseries Crystallization Focus

- Data files:
  - experiment.csv
  - sample.csv
- R functions:
  - merge(), length(), table(), round()
- R graphics:
  - boxplot(), hist(), pie(), barplot(), legend()

# 3. Cocktail by Protein Focus

- Data files:
  - Experiment.csv
  - Sample.csv
  - Drop.csv
- R functions:
  - table(), unique(), sum(), length(), which(), dim(), merge()
- R graphics: boxplot(), pie(), barplot()

# 4. Protein Exploration Focus

- Data files:
  - expUrl.csv, experiment.csv, sample.csv
- PDB (protein data bank): [www.rcsb.org/pdb](http://www.rcsb.org/pdb)
- NCBI BLAST web interface
- R “bio3d” package: `blast.pdb()`, `plot.blast()`
- R functions:
  - `plot()` – for scatterplots
  - `lm()` – linear model to fit data to a line
  - `abline()` – plot a linear model
  - `cor()` – examine correlations