#### **Integrating Mathematics and Machine Learning for Drug Design**

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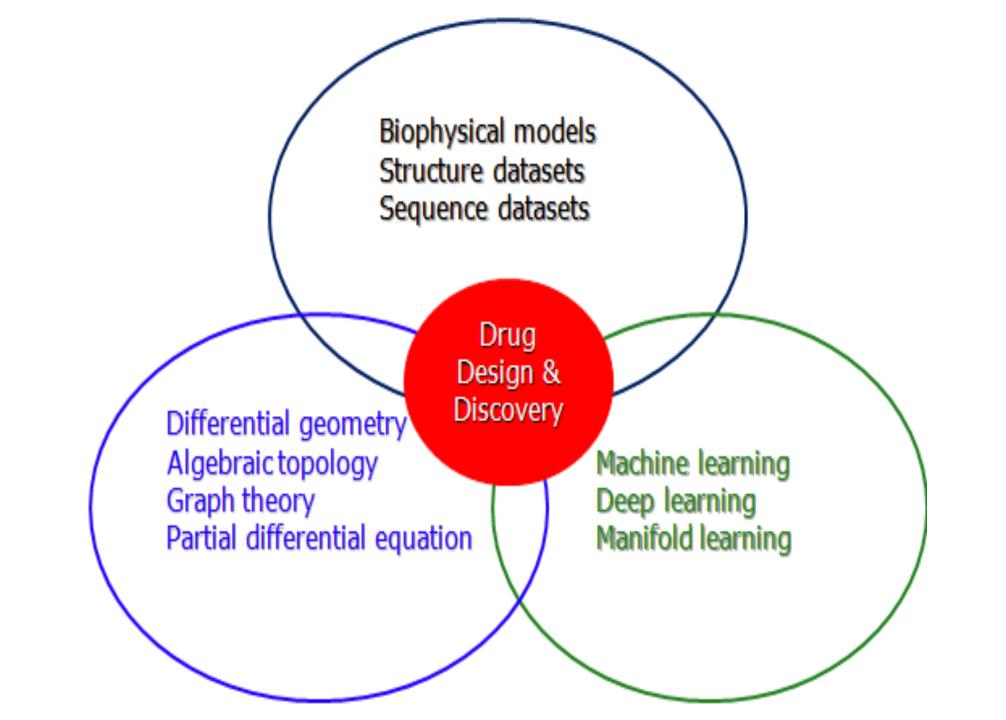
**NSF, NIH, MSU and BMS** 



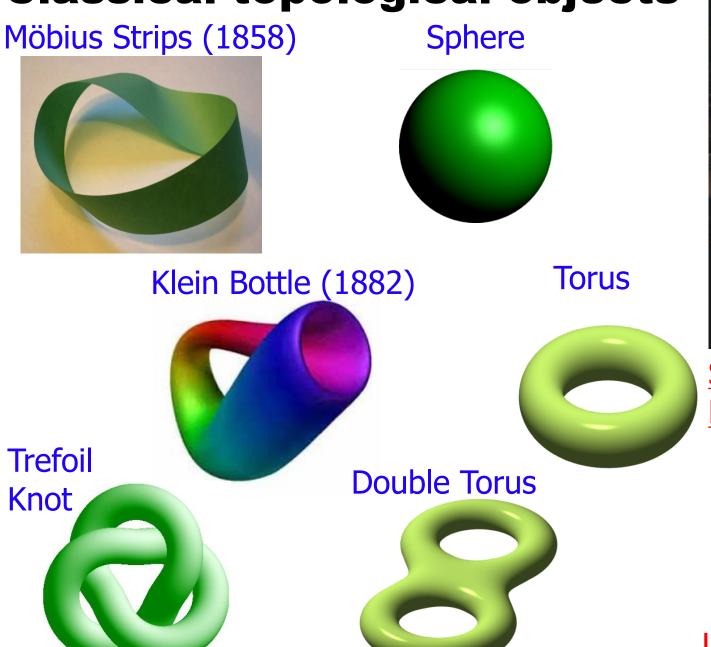


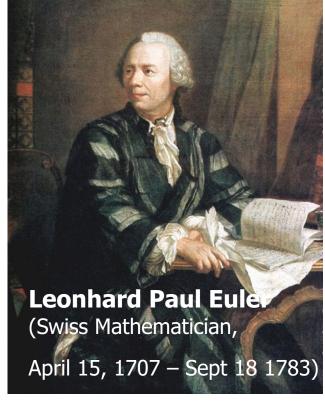


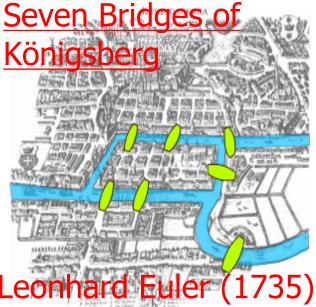




# Classical topological objects







# **Topological invariants: Betti numbers**

 $\beta_0$  is the number of connected components.

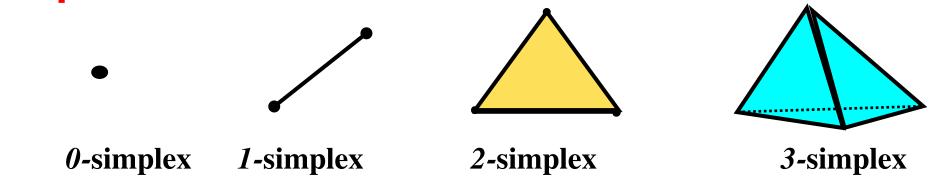
 $\beta_1$  is the number of tunnels or circles.

 $\beta_2$  is the number of cavities or voids.

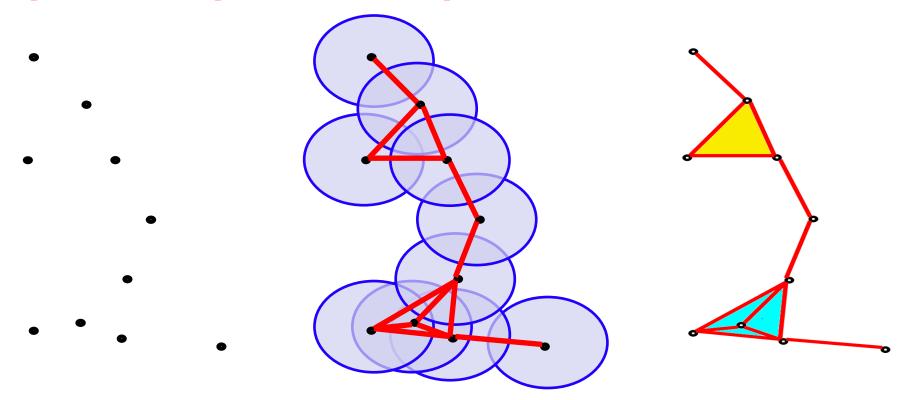
Point	Circle	Sphere	Torus
$\beta_0 = 1$	$\beta_0 = 1$	$\beta_0 = 1$	$\beta_0 = 1$
$\beta_0 = 1$ $\beta_1 = 0$	$\beta_1 = 1$	$\beta_1 = 0$	$\beta_0 = 1$ $\beta_1 = 2$
$\beta_2 = 0$	$\beta_2 = 0$	$\beta_2 = 1$	$\beta_2 = 1$

## Vietoris-Rips complexes of planar point sets

## **Simplexes:**



#### Simplicial complexes of ten points:



## **Topological modeling - Persistent homology**

#### Simplexes:







*0-*simplex *1-*simplex

2-simplex

3-simplex

**k-chain:**  $\sum c_i \sigma_i^k$ 

Chain group:  $C_{\iota}(K,Z_{\gamma})$ 

#### **Boundary operator:**

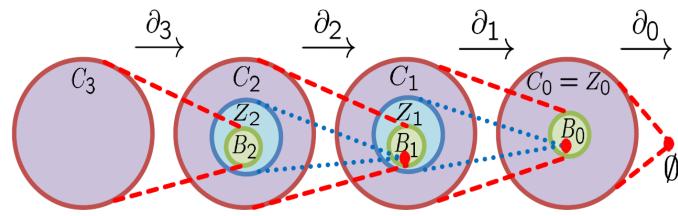
$$\partial_k \sigma^k = \sum_{i=0}^k (-1)^i \{ v_0, v_1, ..., \hat{v}_i, ..., v_k \}$$

$$Z_{k} = \operatorname{Ker} \partial_{k}$$

$$B_{k} = \operatorname{Im} \partial_{k+1}$$

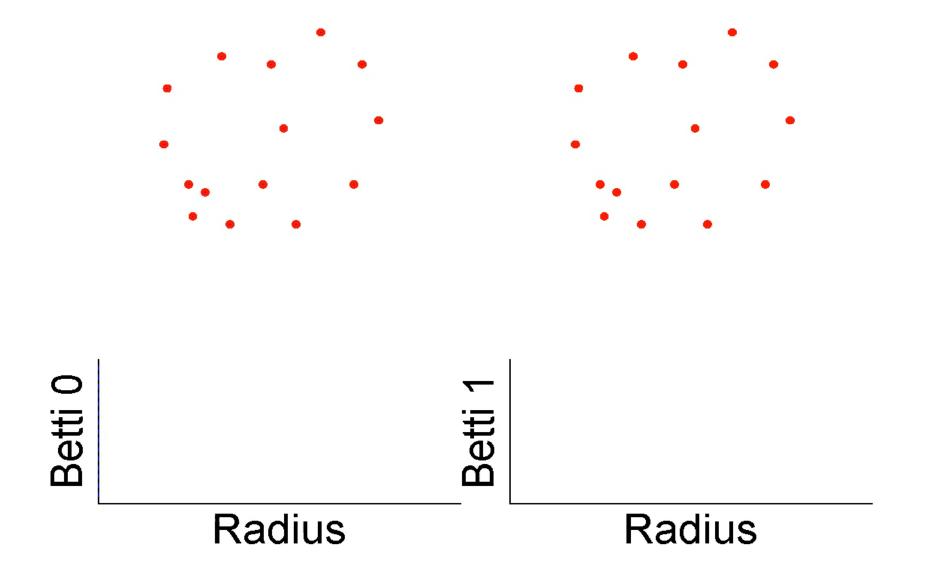
$$H_{k} = \frac{Z_{k}}{B_{k}}$$

$$\beta_{k} = \operatorname{Rank} (H_{k})$$

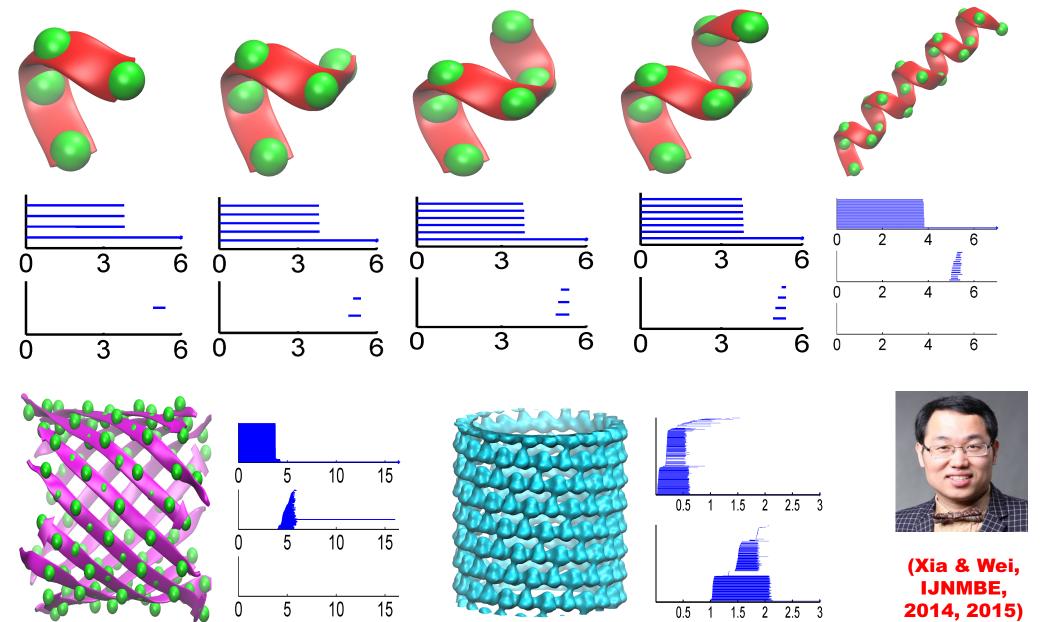


Frosini and Nandi (1999), Robins (1999), Edelsbrunner, Letscher and Zomorodian (2002), Edelsbrunner and Harer, (2007) Kaczynski, Mischaikow and Mrozek (2004), Zomorodian and Carlsson (2005), Ghrist (2008),

# Filtration, Vietoris-Rips complexes, and persistent barcodes (Xia, Wei, 2014)

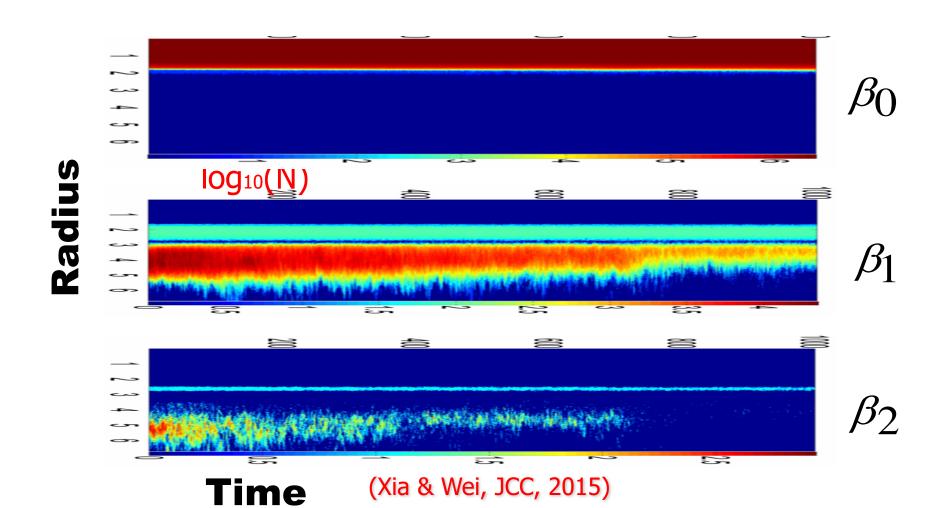


# Topological fingerprints of an alpha helix



# 2D persistence in protein 1UBQ unfolding

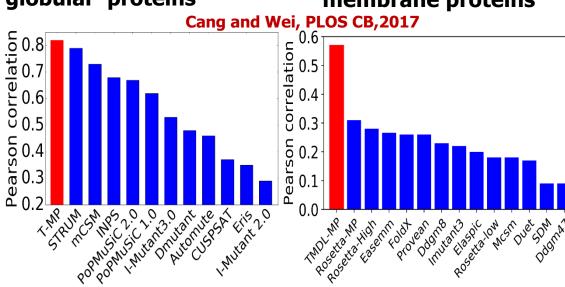


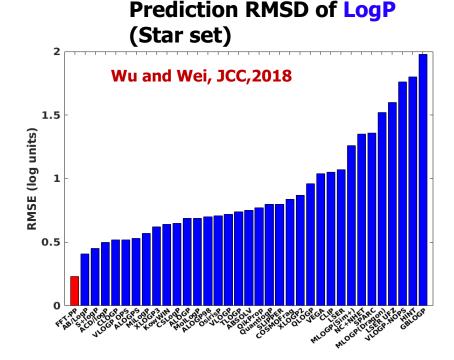


#### **Topological learning based predictions**

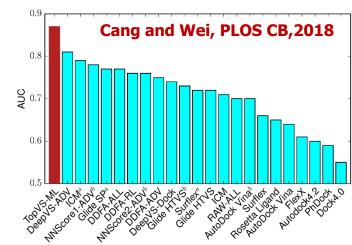
Prediction correlations for 2648 mutations on globular proteins

Prediction correlations for 223 mutations on membrane proteins

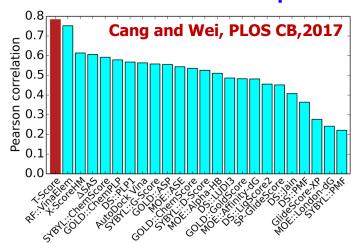




Classification of ligands & decoys
DUD database 128,374 protein-ligand/decoy pairs







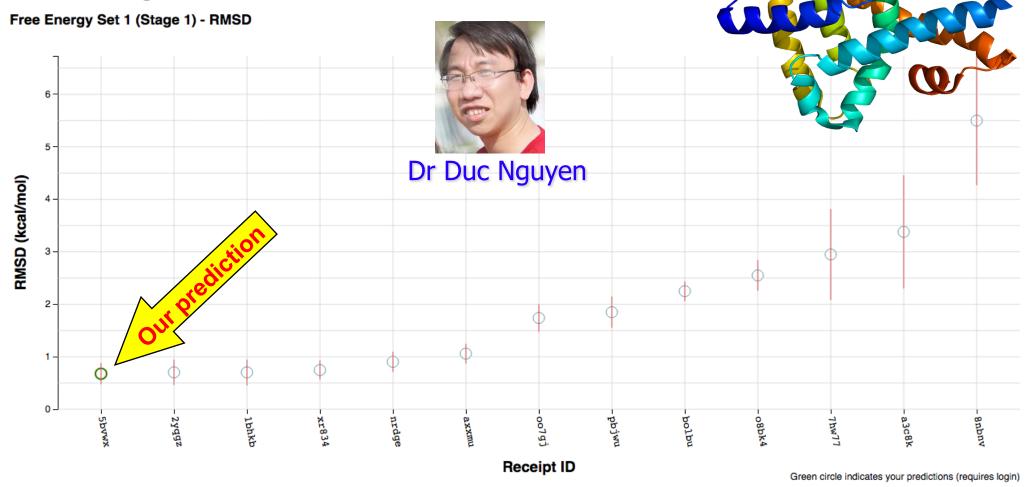
# **Drug Design & Discovery Resource (D3R) Grand Challenge 2**

Given: Farnesoid X receptor (FXR) and 102 ligands

Tasks: Dock 102 ligands to FXR, and compute their

poses, binding free energies and energy ranking

#### **Grand Challenge 2**



## **D3R Grand Challenge 2**

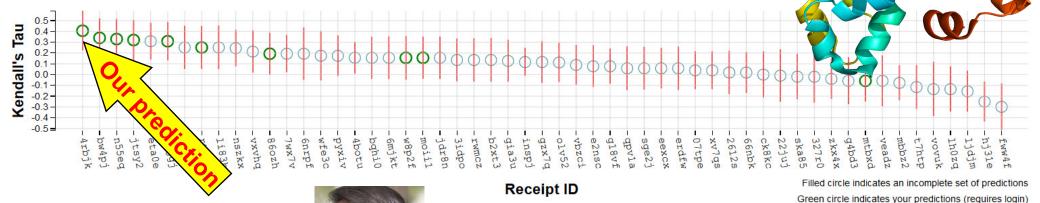
Given: Farnesoid X receptor (FXR) and 102 ligands

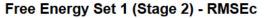
Tasks: Dock 102 ligands to FXR, and compute their

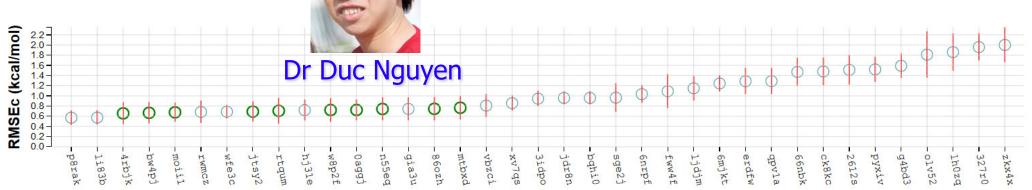
poses, binding free energies and energy ranking

#### **Grand Challenge 2**

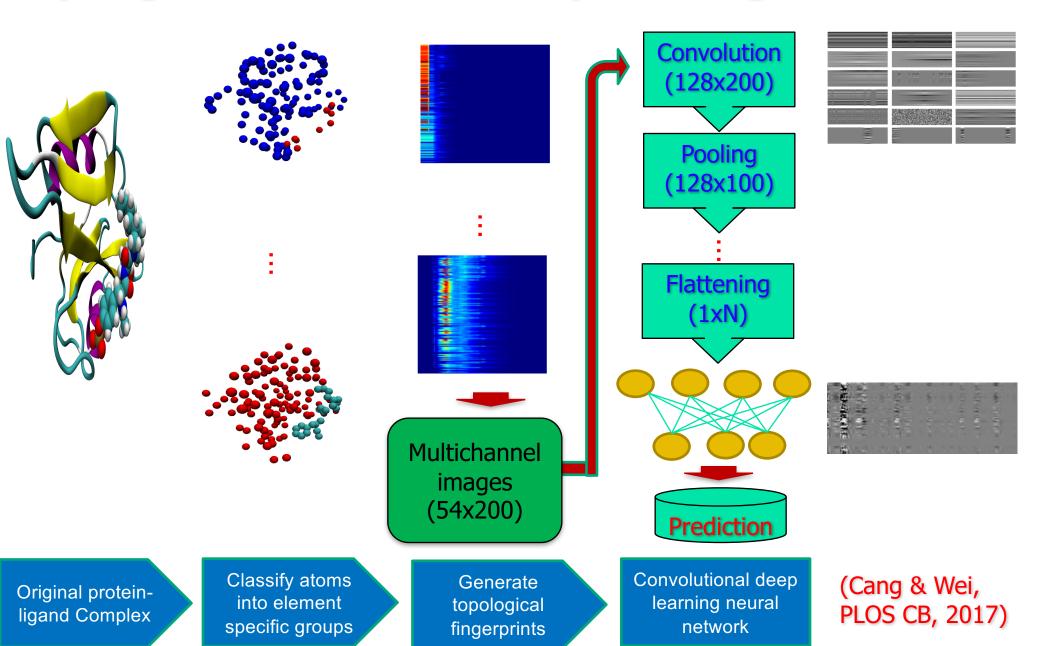
Free Energy Set 1 (Stage 2) - Kendall's Tau







# **Topological convolutional deep Learning architecture**



#### **D3R Grand Challenge 3**

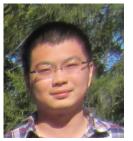
**Preliminary Evaluations, Subject to Revision and Refinement** 

**Cathepsin Stage 1** Pose Predictions (partials)

Scoring (partials)
Free Energy Sets

**Cathepsin Stage 1B** <u>Pose Prediction</u> **Cathepsin Stage 2** <u>Scoring</u> (<u>partials</u>)

Free Energy Sets





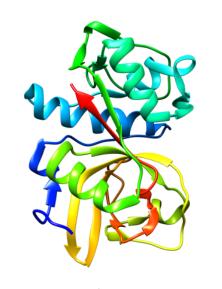


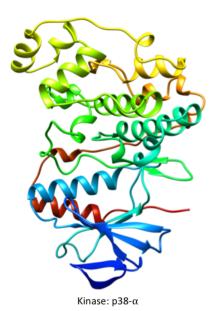
Dr Duc Nguyen

**VEGFR2** Scoring (partials) **JAK SC2** Scoring (partials) **p38-α** Scoring (partials)

TIE2 Scoring (partials)
Free Energy Set 1
Free Energy Set 2

ABL1 Scoring





Cathepsin S