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# Machine-learning a virus assembly fitness landscape

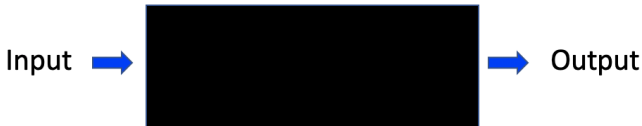
SIAM Algebraic geometry, data science and fundamental physics  
Bern, July 12, 2019

Pierre-Philippe Dechant

work with Y-H He and R Twarock

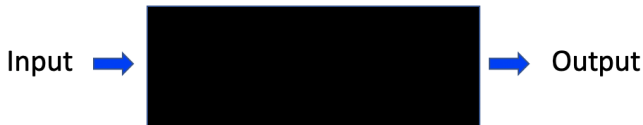
Pro Vice Chancellor's Office, York St John University  
York Cross-disciplinary Centre for Systems Analysis, University of York  
Department of Mathematics, University of York

# Rationale



- **Input vector:** Genotype/Phenotype of length 12 (packaging signal strengths in 3 bands)
- **Output vector:** Assembly efficiency (out of 2000 possible capsids)
- **Black box:** Molecular dynamics simulations (computationally very costly)

# Rationale



- **Input vector:** Genotype/Phenotype of length 12 (packaging signal strengths in 3 bands)
- **Output vector:** Assembly efficiency (out of 2000 possible capsids)
- **Black box:** Machine learning via a neural network

# Rationale

	Genome	Fitness
0	111111111111	200
1	111111111112	1393
2	111111111113	1869
3	111111111121	1597
4	111111111122	1896
5	111111111123	1960
6	111111111131	1875
7	111111111132	1959
8	111111111133	1961
9	111111111211	1639
10	111111111212	1683
11	111111111213	1895
12	111111111221	1848
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15	111111111231	1904
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17	111111111233	1959
18	111111111311	1852
19	111111111312	1858

$3^{12} \sim \frac{1}{2}$  Million data points

1

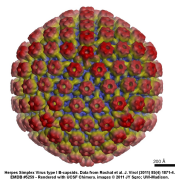
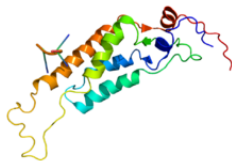
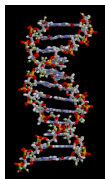
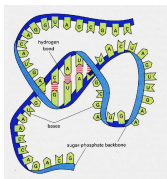
- Virus structure and assembly
- Toy model and evolutionary fitness landscape

2

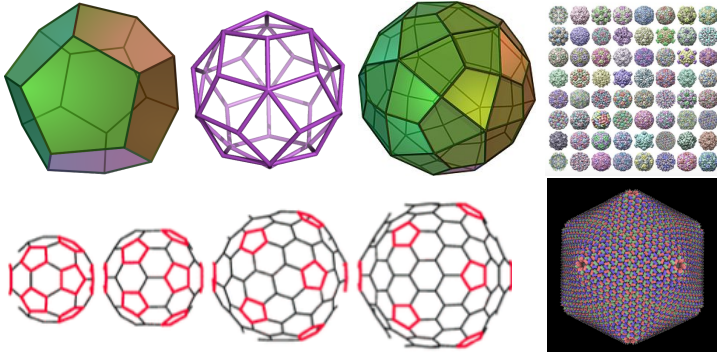
- Neural networks
- Predictions

# What is a Virus?

- Piece of **genetic information** in the form of RNA or DNA
- Protected by a **protein shell: capsid** made of **geometric protein building block**



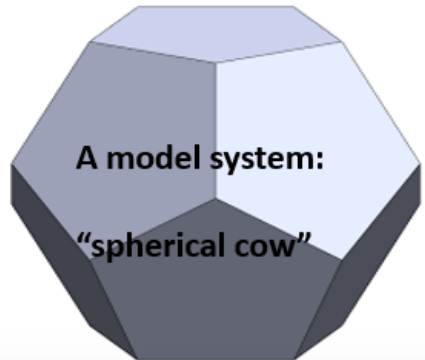
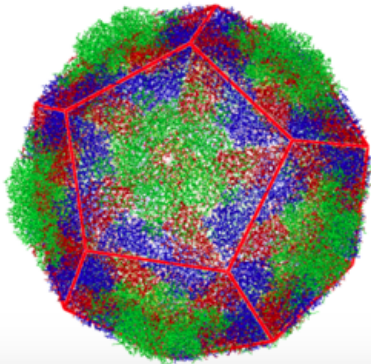
# Most viruses are icosahedral



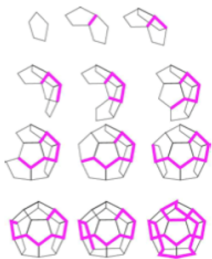
- Highly developed structure theory
- Nucleic acid component thought to be disordered



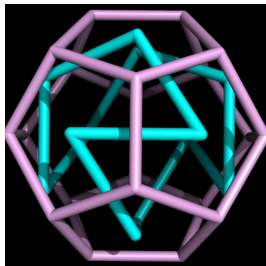
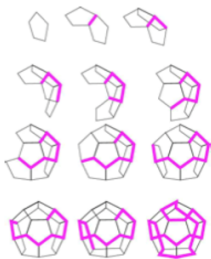
# Simplest model: a dodecahedron



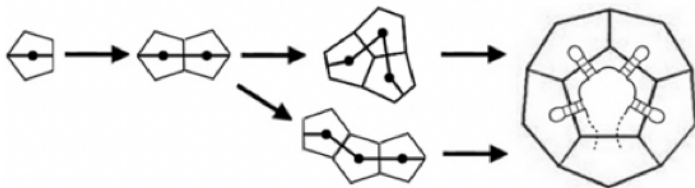
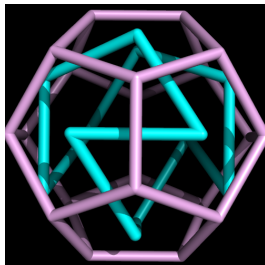
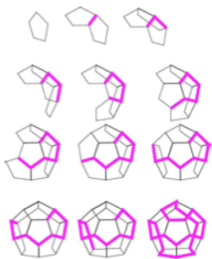
# Assembly and thermodynamics – Hamiltonian paths



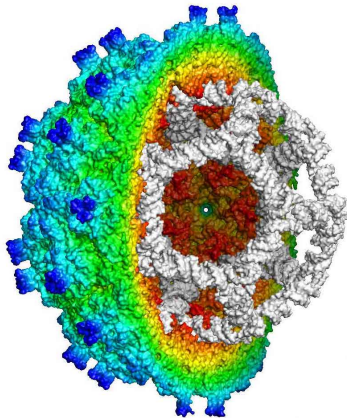
# Assembly and thermodynamics – Hamiltonian paths



# Assembly and thermodynamics – Hamiltonian paths

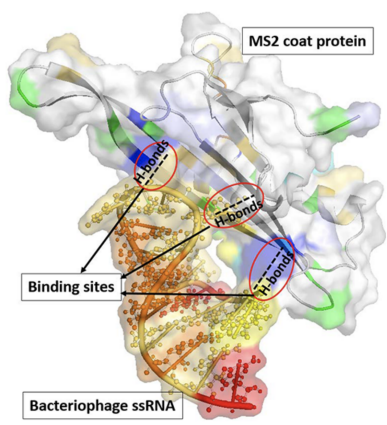
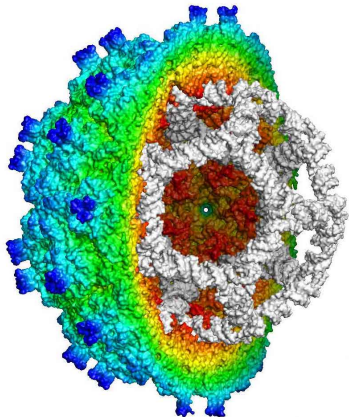


## 3D distribution: RNA-CP contacts



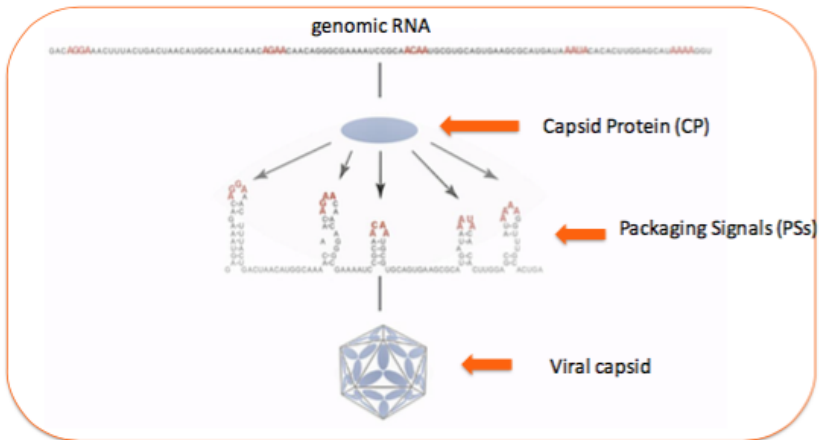
There are **specific interactions** between **RNA** and coat protein (**CP**)  
given by icosahedral **symmetry** axes

## 3D distribution: RNA-CP contacts

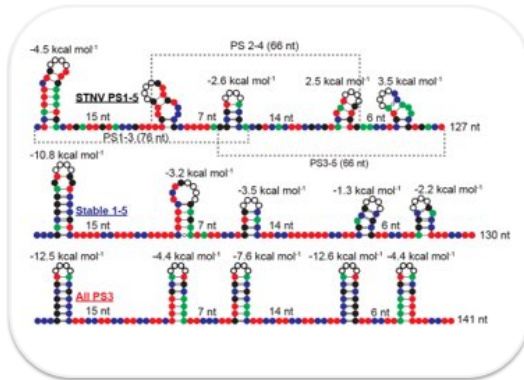


There are **specific interactions** between **RNA** and coat protein (**CP**) given by icosahedral **symmetry** axes

# Packaging signal-mediated assembly



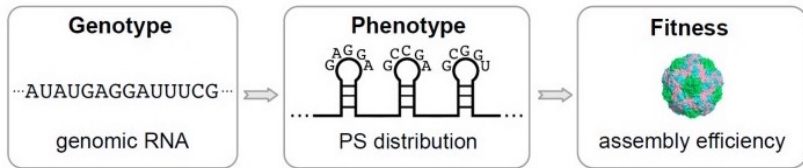
# Engineering Packaging Signals to make VLPs



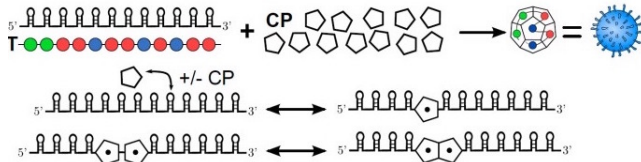
Virus-like particles with **improved** PS sequences assemble **twice** as **efficiently**. Potential applications to **vaccines** or **drug delivery**.



# Genotype – Phenotype – Fitness map

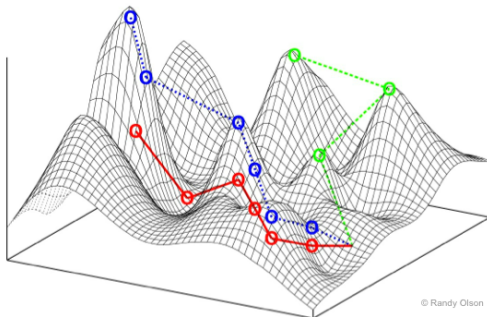


# Simplest model: the dodecahedron



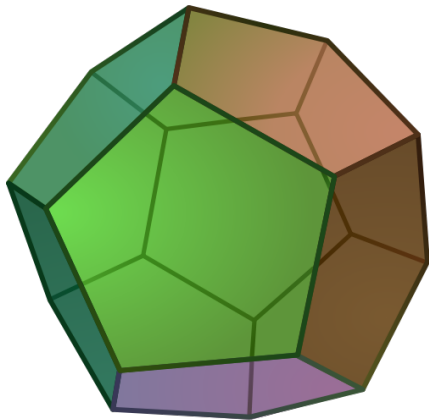
- 12 PSs in 3 bands (strong/intermediate/weak, 12/8/4, 3/2/1, green/blue/red)
- Molecular dynamics **simulation**: stochastically select one possible reaction at a time
- Enough **resources** for 2000 virus capsids

# Fitness Landscape



Generally **messy** (many contributions) and difficult to quantify.  
Here capture the **assembly** contribution for the phenotype space of  $3^{12}$  points with (stochastic) assembly **efficiency** ( $< 2000$ ).

# Fundamental Physics



# Genotype–fitness map

	Genome	Fitness
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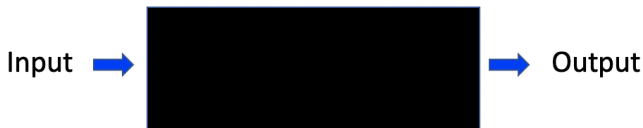
1

- Virus structure and assembly
- Toy model and evolutionary fitness landscape

2

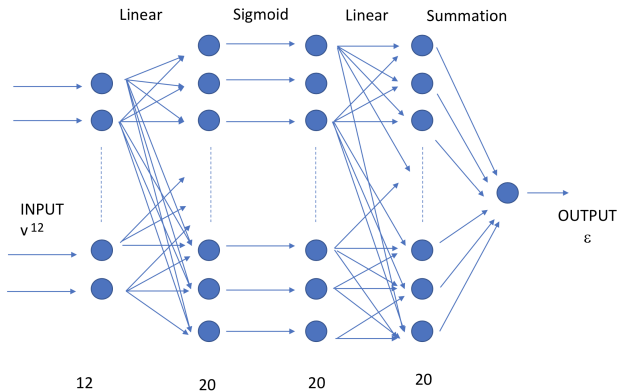
- Neural networks
- Predictions

# Rationale



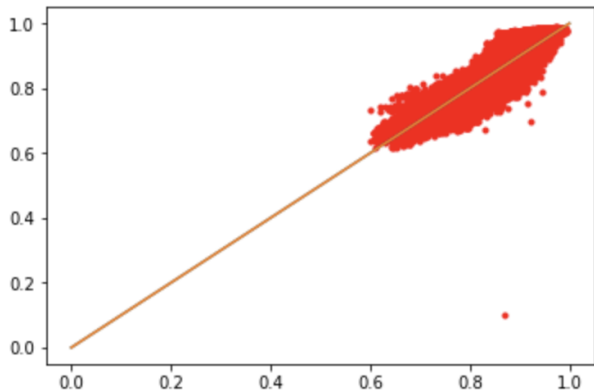
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# Machine Learning with a Neural Network



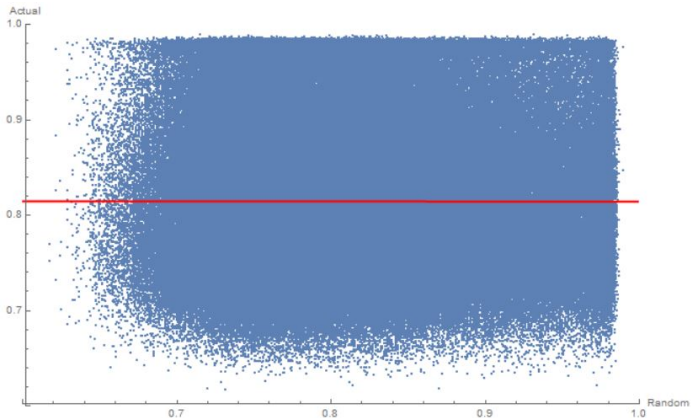


# Predictions



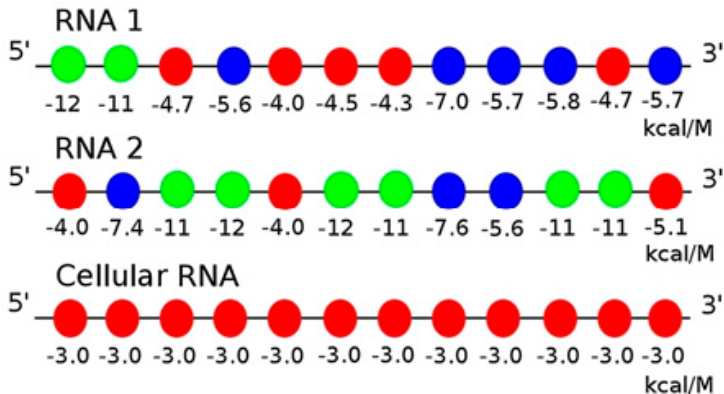
predicted vs actual value of assembly efficiency

# Predictions



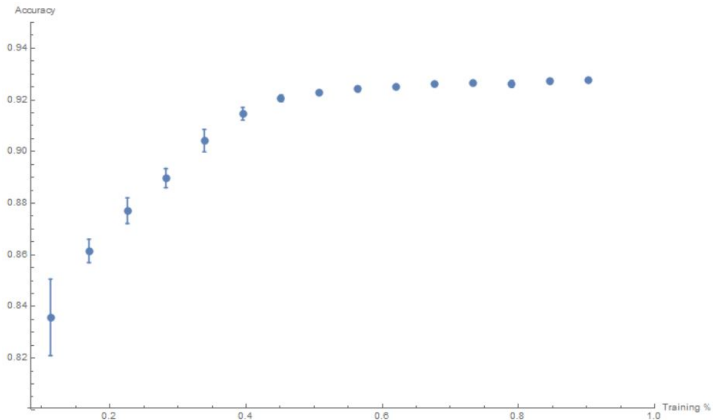
vs **random** assignments of assembly efficiency

# Not just random, intrinsic features?

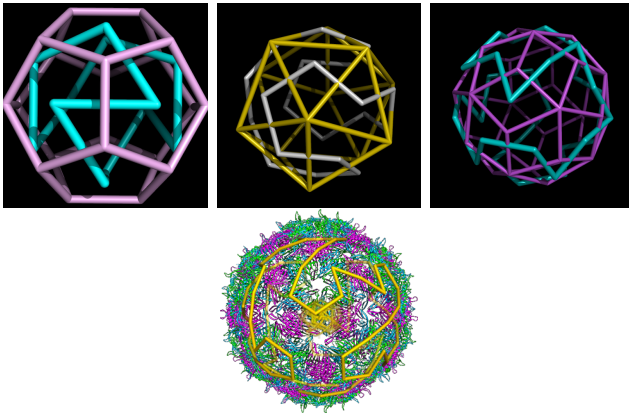


Definite **starting point** with strong binding, then weaker binding in an **error-correcting** bit, driven to completion by **thermodynamics**

# Learning Curve



# Conclusions



Do more **realistic** models in future – geometry, binding **gradation**.  
**Partially** explore the landscape and predict the rest (procedurally)?

Thank you!

Machine-learning a virus assembly fitness landscape

P-P Dechant, Y-H He, arXiv preprint arXiv:1901.05051, 2019