

# Welcome to: Protein Engineering and Design

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Winter 2022

# Introduction

Name

Pronouns

Lab/year

What are you hoping to learn from this class

How do you evaluate your coding/biochemistry skills

What are you looking forward to the most in 2022

# Class core values

1. Be **respectful** to yourself and others
2. Be **confident** and believe in yourself
3. Always do your **best**
4. Be **cooperative**
5. Be **creative**
6. Have **fun**
7. Be **patient** with yourself while you learn
8. Don't be shy to **ask "stupid" questions**

# About our class

What to bring?

- Yourself

- Your attention and curiosity

- Your laptops

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## What to bring?

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## What do I need to know?

- What is a protein

- Protein secondary structure

- What is an amino acid

- General of protein folding

# About our class

Pre-class assessments (So you think you know X)

- Quiz to check your knowledge on the topic

- Short videos/readings that will bring you up to speed

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## Post-class assignments

- Short quizzes

- Assay questions

- Readings (for journal club)

- Running a guided code

- ...

# Activities

Pre and post class assignments

In class activities

- Asking questions, submitting in-class work, presence

- Either through canvas or google colab (gmail account)

- 1 session allowed absence (excluding first session, ask me if you need more)



# Activities

- Pre and post class assignments

- In class activities

- Journal presentation

  - Moderators – give backup information, take care of organization, ask questions

  - Everyone else – present figures

# Activities

Pre and post class assignments

In class activities

Journal presentation

Proposal write-up

- 1-page describing your aims and ideas (410)

- 1-page describing your aims and ideas + 1-2 page method description (510)

# Activities

Pre and post class assignments

In class activities

Journal presentation

Proposal write-up

Mock study section

Grant review and feedback

# Panels/Guests

Expert lectures on protein structure prediction

Dr. Afua Nyarko (OSU)

Dr. Richard Cooley (OSU)

Dr. Elizabeth Kellog (Cornell)

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## Industry panel

Arzeda, Novo Nordisk, Bayers, Ginkgo Bioworks

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## Startup CEO

Dr. Daniel Adriano Silva

(previous CEO of Neoleukin, now CEO at Monodbio)

# Feedback

## Assignments and activities

Detailed feedback provided by instructor/TAs

Answering questions during hands-on sessions

Help navigate the paper for moderating group

Office hours: Tuesdays 9-10 AM

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- Mid-term and final feedback

- Personal feedback (email, anonymous feedback)

- 2 + 1 feedback every two weeks



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Slack ?

# Questions?

Week 1, Lecture 1

# Protein engineering: The why, what and how

# Learning Objectives

1. Describe goals of protein engineering and its applications
2. Identify proper method for different applications of protein engineering methods
3. Critically evaluate the application of protein engineering in different scenarios

# Protein Engineering

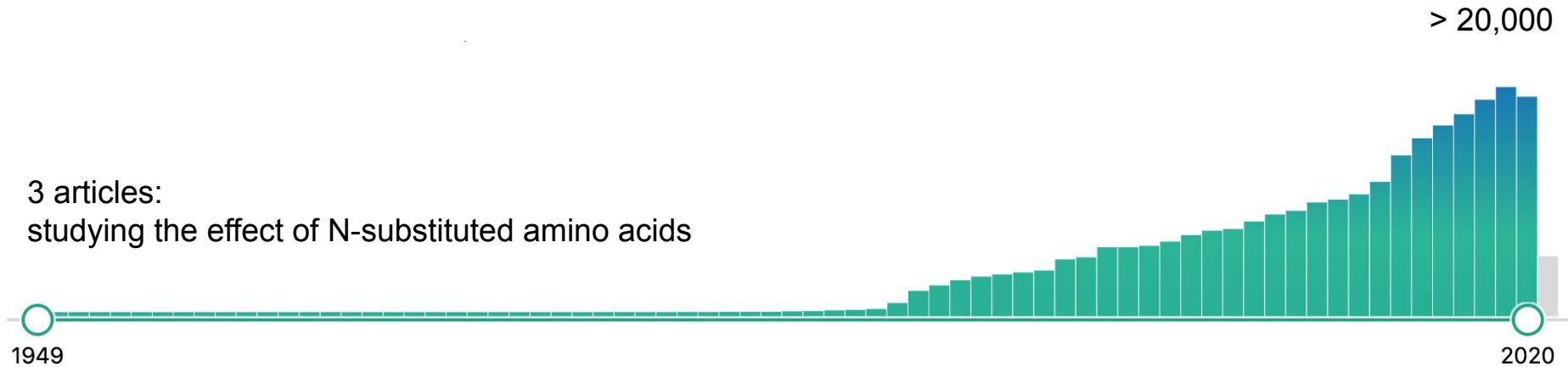
What is protein engineering?

# Protein Engineering

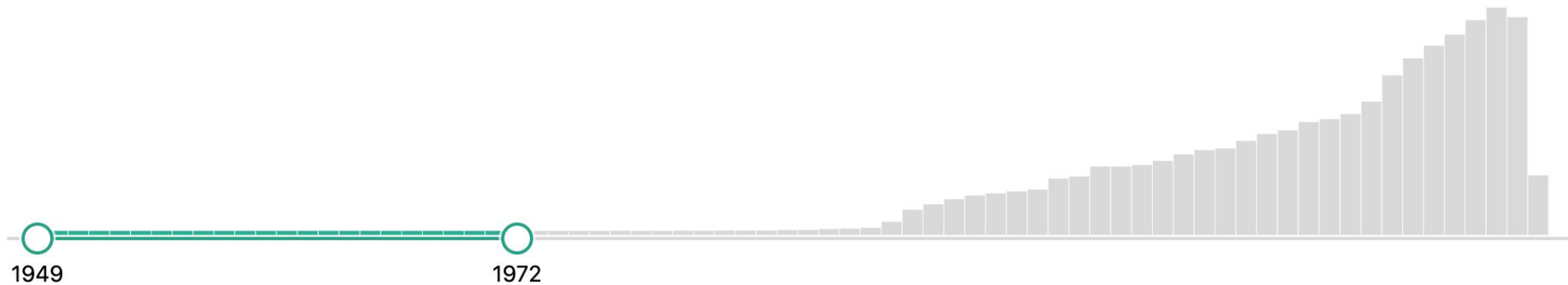
What is protein engineering?

Why do we need to engineer proteins?

# Engineering proteins is an old concept

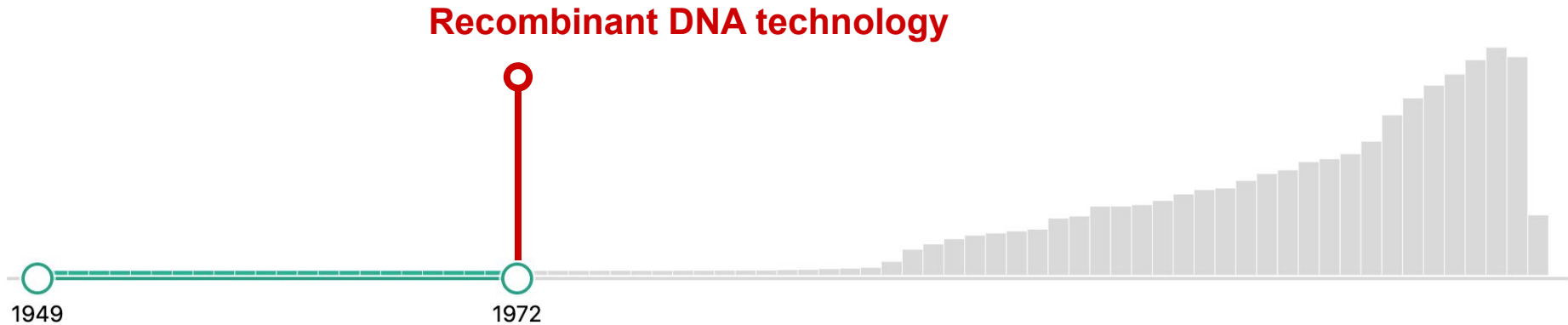


# Early engineering attempts was focused on understanding the role of natural variants

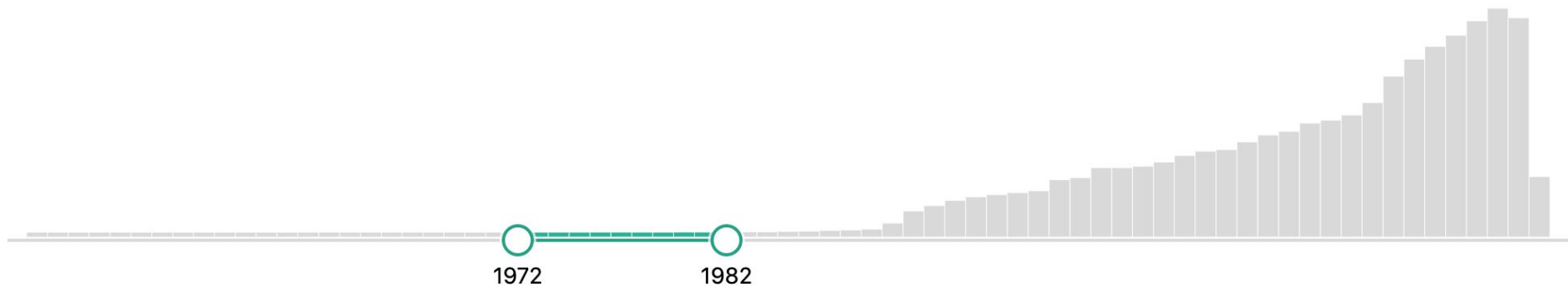




# Rise of recombinant DNA technology was a hallmark in protein engineering



# Recombinant protein expression allowed researchers to express proteins in high yields

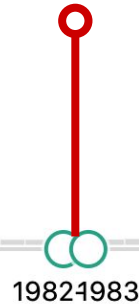


# The idea of designing new proteins emerged with the ability to express proteins

## Whither protein structures?

*from S. D. Dover*

THE pipe-dream of designing and producing a protein to carry out a specific task has been brought nearer reality by the advent of recombinant DNA which offers the possibility of isolating, mutating and cloning particular genes. The resulting change in amino acid sequence specified could produce the intended structural change in the protein. But this will only be possible with an adequate theory of the effect of sequence changes on structure, based firmly on experimental structural information. Without this



# The idea of designing new proteins emerged with the ability to express proteins

## ARTICLES

### Protein engineering

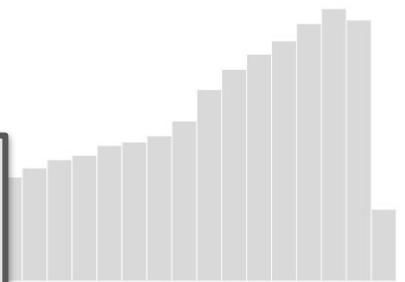
KM Ulmer

+ See all authors and affiliations

*Science* 11 Feb 1983:  
Vol. 219, Issue 4585, pp. 666-671  
DOI: 10.1126/science.6572017

#### Abstract

The prospects for protein engineering, including the roles of x-ray crystallography, chemical synthesis of DNA, and computer modelling of protein structure and folding, are discussed. It is now possible to attempt to modify many different properties of proteins by combining information on crystal structure and protein chemistry with artificial gene synthesis. Such techniques offer the potential for altering protein structure and function in ways not possible by any other method.



# The idea of designing new proteins emerged with the ability to express proteins

## Enzyme engineering

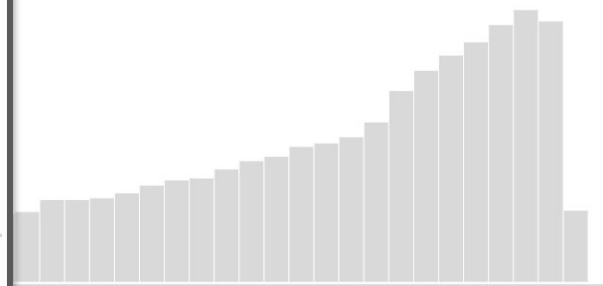
[William H. Rastetter](#) 

*Applied Biochemistry and Biotechnology* **8**, 423–436(1983) | [Cite this article](#)

175 Accesses | 8 Citations | [Metrics](#)

### Abstract

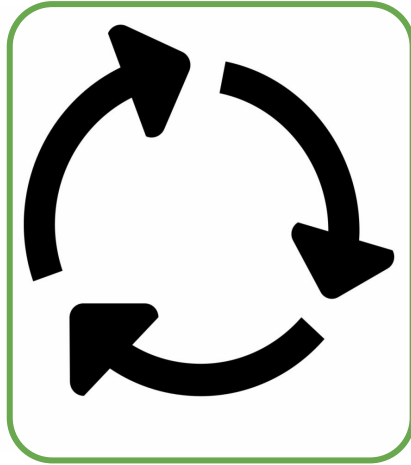
Enzyme research and development efforts have been shaped by the tools and concepts available for enzyme production and utilization. A new phase of enzymology characterized by the production of modified protein catalysts has begun, made possible by recombinant DNA technology.



# Four methods of protein engineering



Rational Design



Directed Evolution



De Novo Design



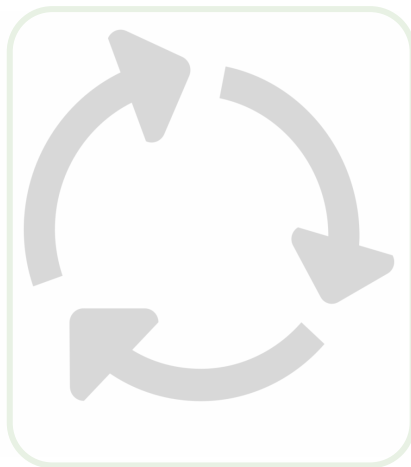
Machine Learning

# Rational Design

uses prior knowledge, often structure guided to engineer proteins



Rational Design



Directed Evolution



De Novo Design



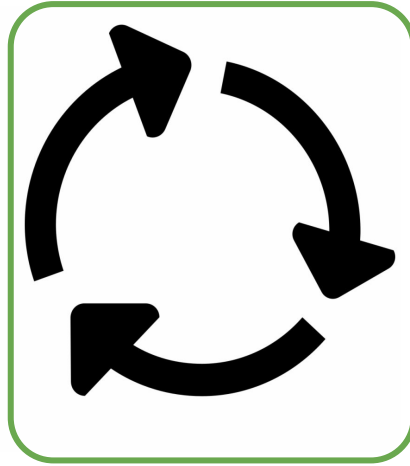
Machine Learning

# Directed Evolution

uses a process of mutation and selection, inspired by evolution.



Rational Design



Directed Evolution



De Novo Design



Machine Learning

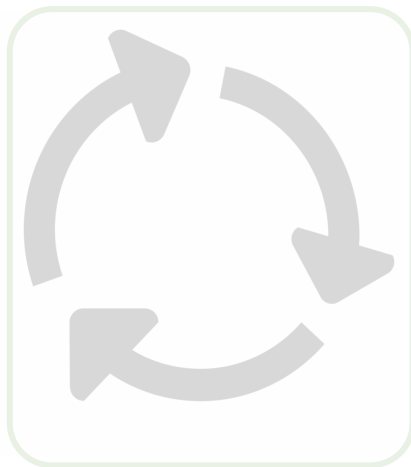


# de Novo Design

creates new proteins often by physics-based and heuristic methods



Rational Design



Directed Evolution



De Novo Design



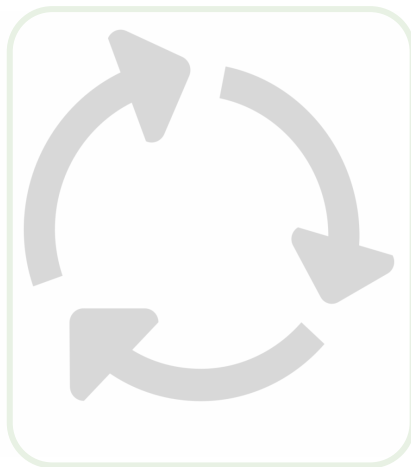
Machine Learning

# Machine Learning

learns from large databases for prediction, classification, generation



Rational Design



Directed Evolution

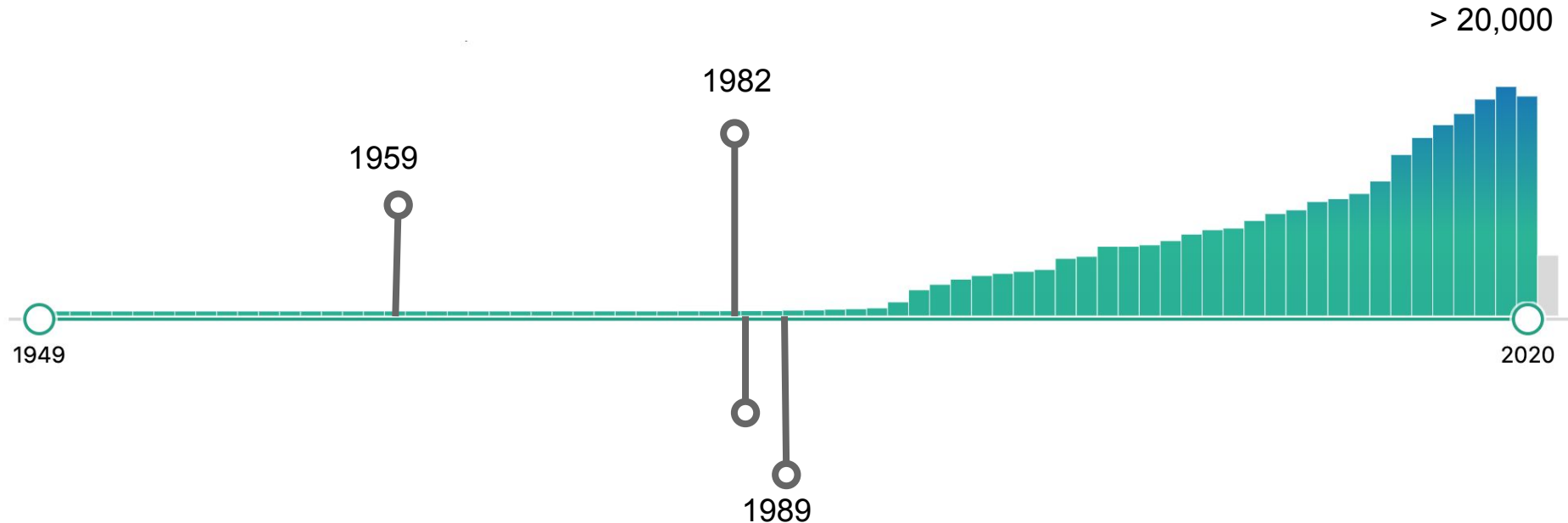


De Novo Design

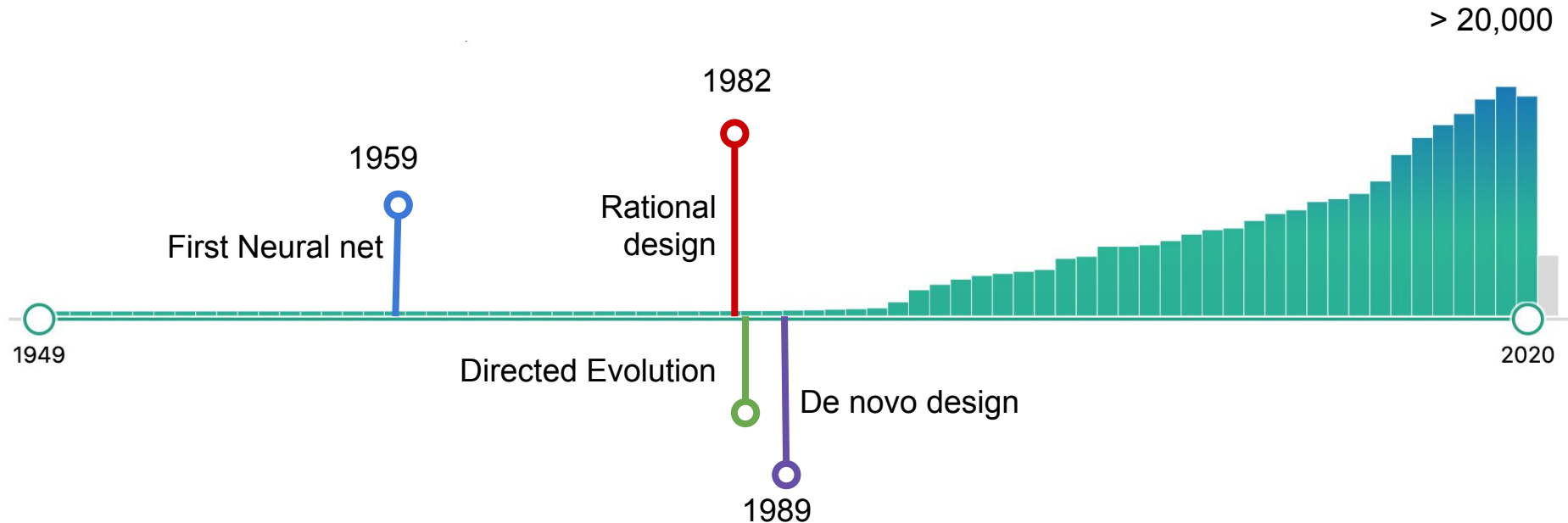


Machine Learning

# Four methods of protein engineering



# Four methods of protein engineering



# Each method has its own advantages and disadvantages

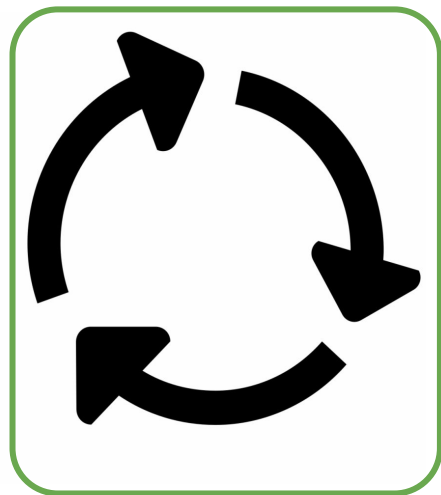


uses prior knowledge, often structure guided to engineer proteins

Advantage	Disadvantage
We're building off of what works → higher chance of success	Limited to what we know
Simpler if you have a good guess	Limited by what exists in nature
Requires fewer resources	You need to know the structure



# Each method has its own advantages and disadvantages

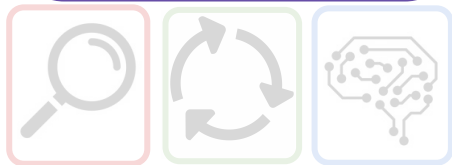


uses a process of mutation and selection,  
inspired by evolution

Advantage	Disadvantage
High throughput and can test many things at once	Sequence space is very large and not everything can be sampled
Don't need prior knowledge	Is not interpretable (we don't know why things worked)
Can screen multiple features at once	We're not sure if we're getting the best result
Random mutations = casting a wider net to make sure things work	You need to have a selection/screening method and you have to have some minimal activity



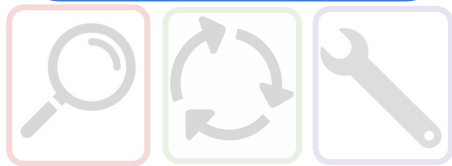
# Each method has its own advantages and disadvantages



creates new proteins often by physics-based and heuristic methods

Advantage	Disadvantage
If it works, it generates really good proteins because it considers all the rules	Low success rate
Novelty = less chance of resistance/defense	novel structures → may cause unknown problems downstream
Can create novel function/structure and is not limited to what we know	While not dependent on prior knowledge, still needs the rules
Great for specificity and full control	

# Each method has its own advantages and disadvantages



learns from large databases for prediction, classification, generation

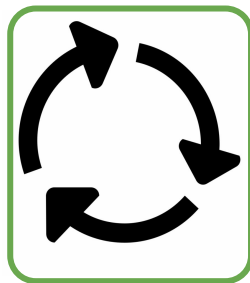
Advantage	Disadvantage
The computational power is getting better	Needs large amount of data
It can uncover new patterns and rules that we can't	Can't be specific/target-based (great for general cases)
Fully reproducible	Can sample new sequences but in the neighborhood of what exist
Can take in multiple considerations into account	



# Match methods to applications



Developing a  
biological logic gate



Generating a protein that  
binds to another protein



Stabilizing an enzyme  
with known structure

Generating a protein  
with a novel fold

Enhancing the activity  
of an enzyme

Generating a fluorescent  
protein smaller than GFP

# For the next lecture:

1. Pre-class assessment for the next lecture  
Needs to be done before the start of class, will be available after this class
2. Post-class assignment – Due next week
3. Make sure you have PyMol installed for the next lecture

Next lecture:  
*It's all about structure!*

