

"Doing statistics is like doing crosswords except that one cannot know for sure whether one has found the solution."

– John Tukey

The Annals of Statistics 2002, Vol. 30, No. 6, 1535–1575

JOHN W. TUKEY: HIS LIFE AND PROFESSIONAL CONTRIBUTIONS<sup>1</sup>

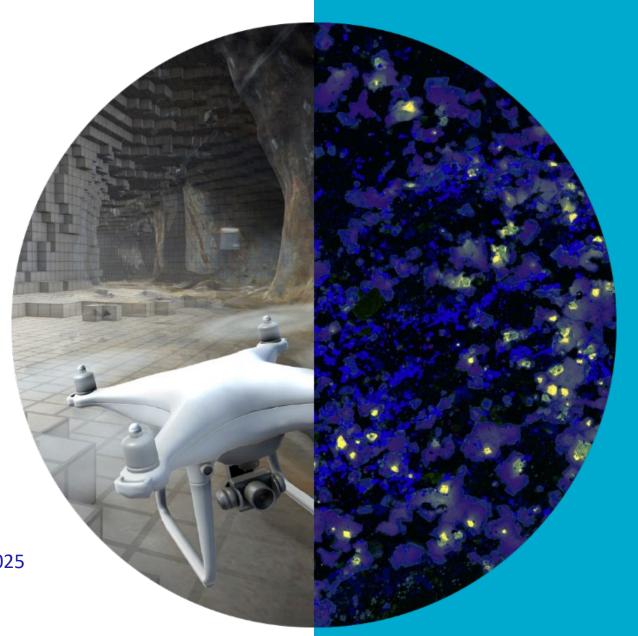
BY DAVID R. BRILLINGER



On Finding
Good
Experiments
(in life science)

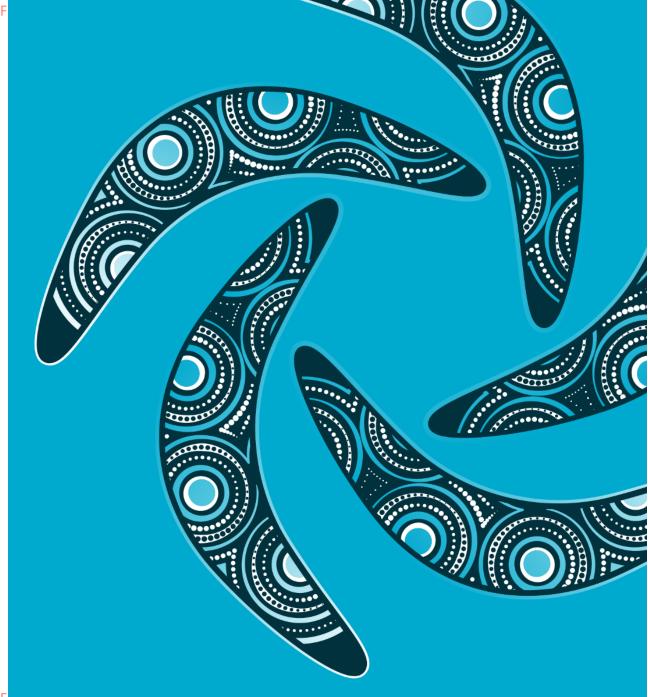
Cheng Soon Ong, Data61 and ANU 25 November 2025

Biometrics in the Bush Capital 2025 International Biometric Society



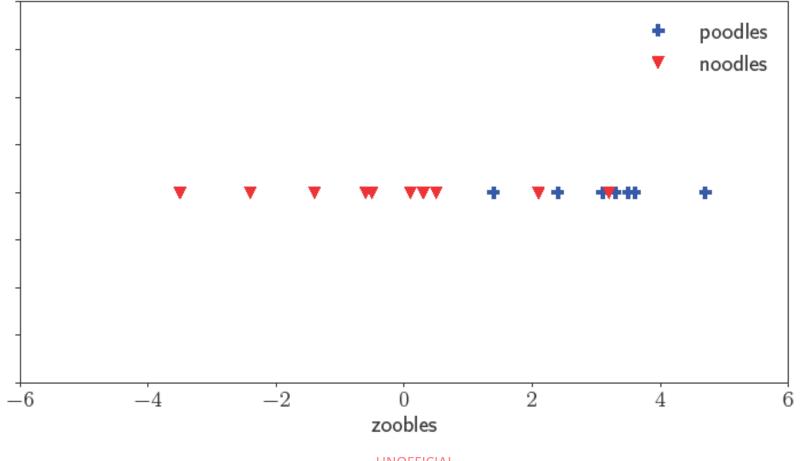


I would like to acknowledge the Ngunnawal people, the traditional custodians whose ancestral lands we're meeting on today, and pay my respect to their Elders past and present.



#### Given some data

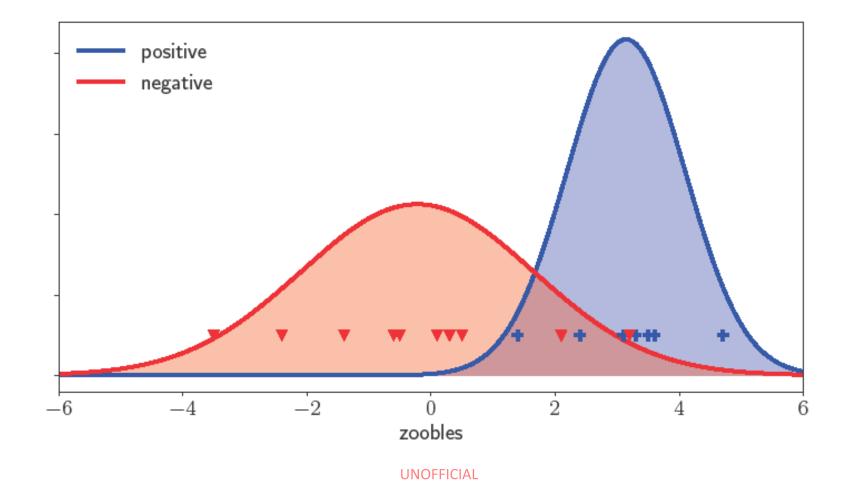
Classify blue plus vs red triangles, based on features





#### Fit a model to data

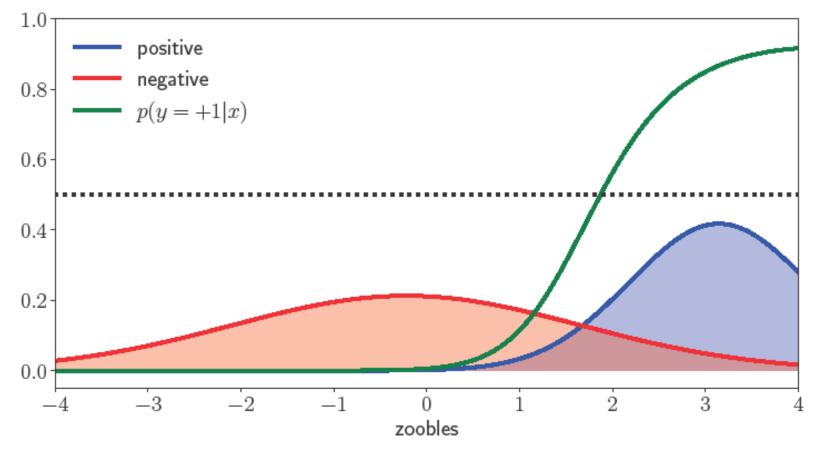
Estimate a Gaussian for each class conditional





#### Build a classifier

Compute the posterior probability of blue plus





## What is machine learning?

- Mostly about prediction
  - Examples/covariates/features
  - Labels/annotations/target variables

$$x_1, \ldots, x_n \sim \mathcal{X}$$
  
 $y_1, \ldots, y_n \sim \mathcal{Y}$ 

Predictor

$$f_{\theta}(x): \mathcal{X} \to \mathcal{Y}$$

• Estimate the best predictor = training =  $\min_{\theta} \ell(f_{\theta})$  (given loss)





#### Finding good experiments



What is an **experiment**?



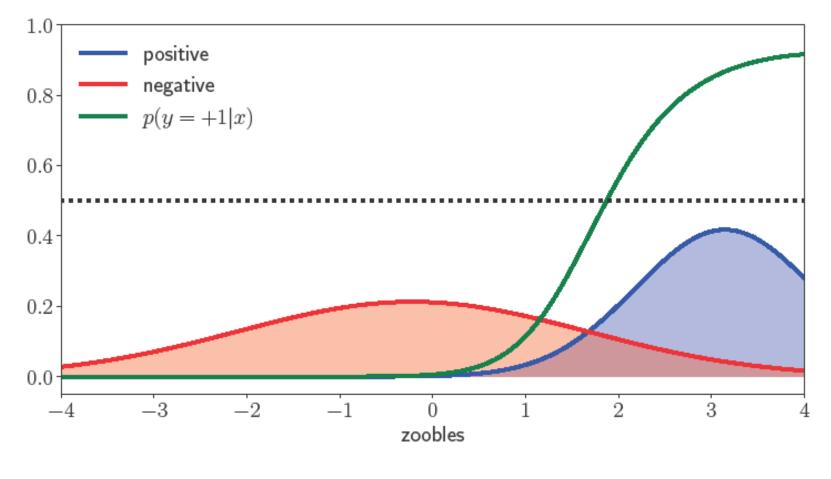
How do we find good experiments?



What do we mean by "good"?

### Recall what is a predictor

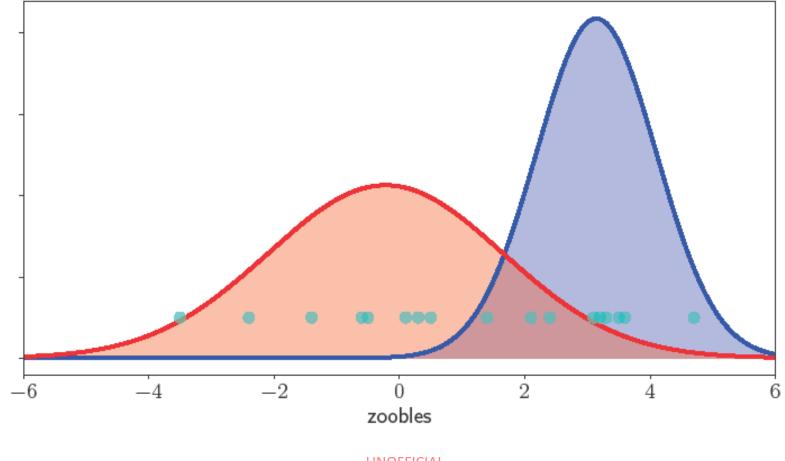
Compute the posterior probability of blue plus





#### **Active Learning**

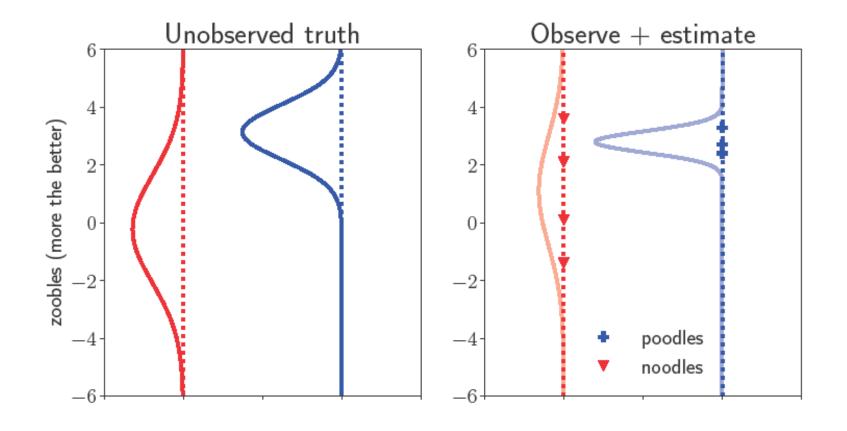
Want to build a predictor without paying for a lot of labels





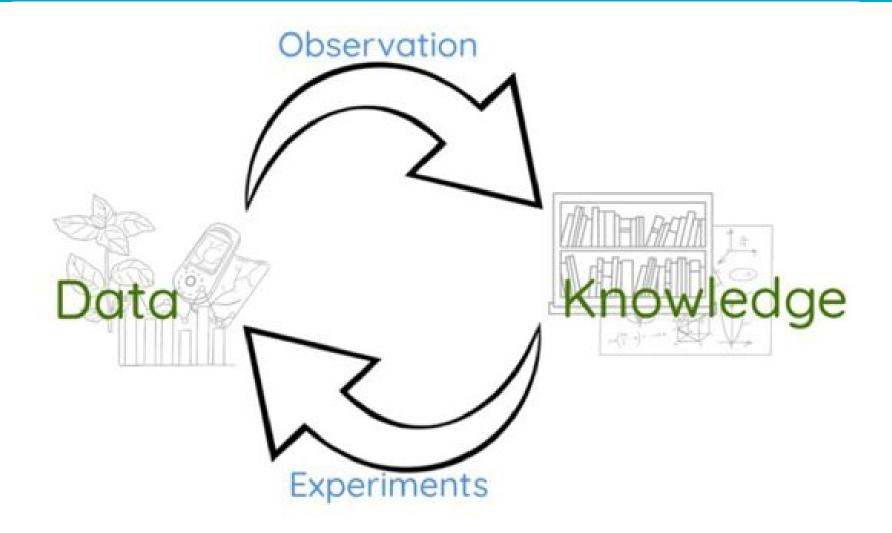
## Bandits / Bayesian optimisation

Want to maximise the outcome of different choices





#### The scientific method





## Using a predictor to adaptively choose data

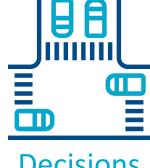
Given a predictor

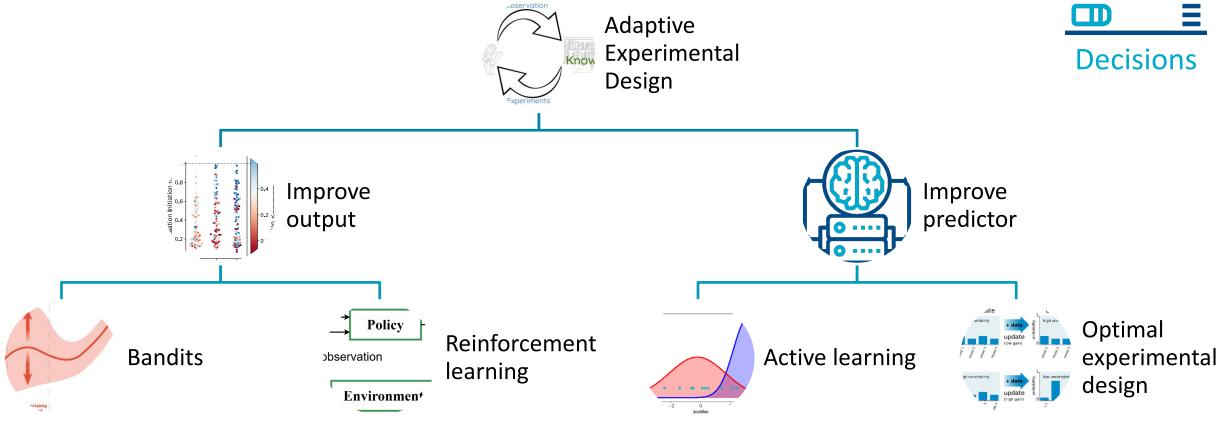
$$f_{\theta}(x): \mathcal{X} \to \mathcal{Y}$$

- We could collect data (perform an experiment) to:
  - Bandits Improve the output of the predictor, that is better  $f(\boldsymbol{x})$
  - Active Learning Improve the predictor/model itself, that is better heta



### Decision making





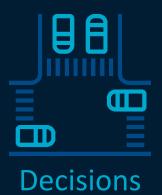
- https://researchoutreach.org/articles/adaptive-experiments-machine-learning-help-scientific-discovery/
- Chades, Blau, Ong, Machine Learning for Biological Design, Chap 19, Synthetic Biology (2<sup>nd</sup> ed), 2024

  UNOFFICIAL





### Three messages





What is an experiment?



How do we find good experiments?

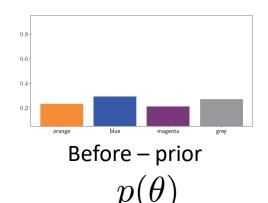


What do we mean by "good"?

## Information gain – ecological modelling

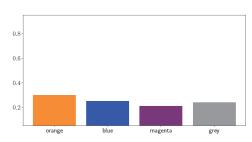
 Find experiments to improve the model's parameters

Imagine parameters have only 4 states



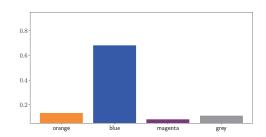


Take a sample  ${f D}$ 



Uninformative experiment

$$p(\theta|\mathbf{D})$$



Informative experiment

$$\mathbb{E}_{\mathbf{D} \sim \mathcal{X}, \mathcal{Y}}$$

Don't know which data we're going to get

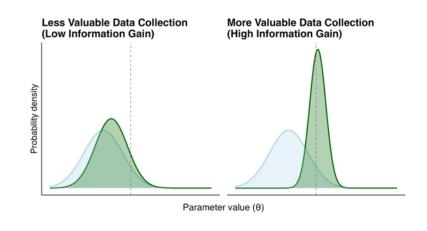
$$D[p(\theta|\mathbf{D})]$$

Difference between posterior and prior



### Species distribution model

- African lovegrass
- Beta-Bernoulli presence model



Prior - Posterior



Owen Forbes

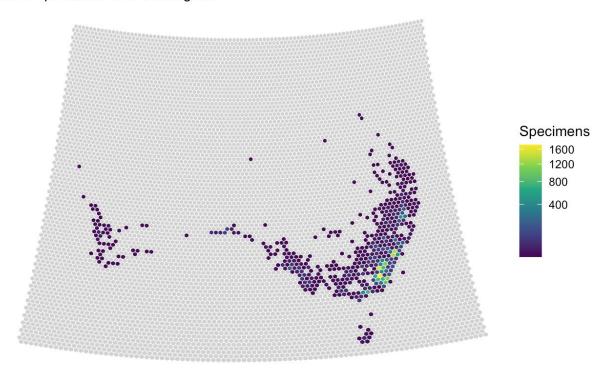


Pete Thrall



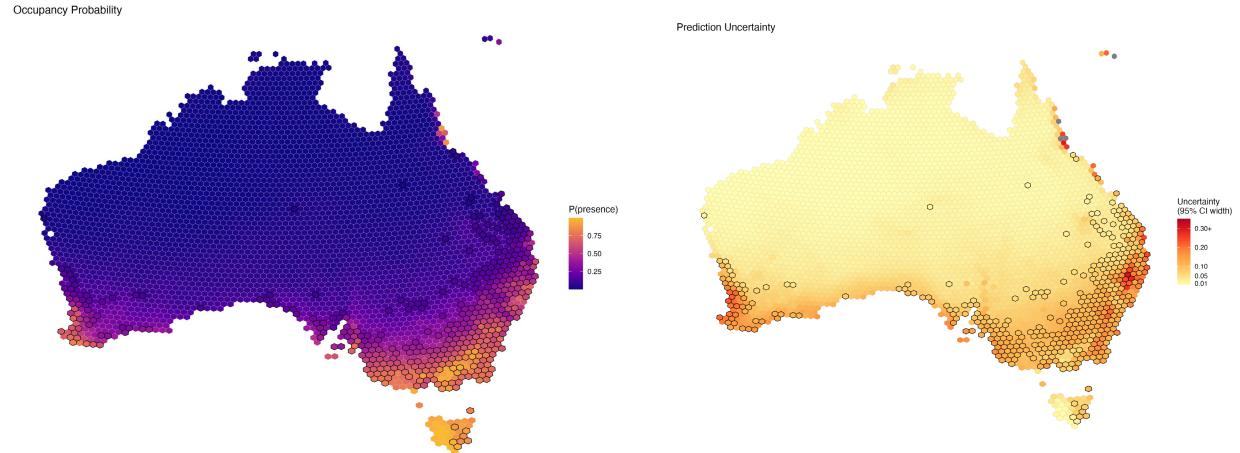
**Andrew Young** 

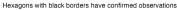
Eragrostis curvula (African Lovegrass) Distribution - 50km Hexagons 23249 specimens in 474 hexagons





# Prediction and uncertainty

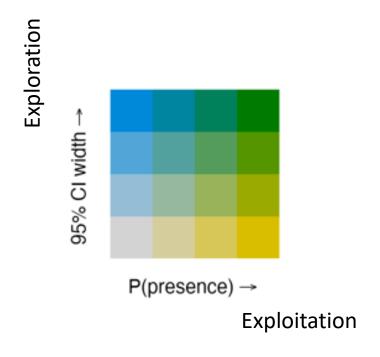




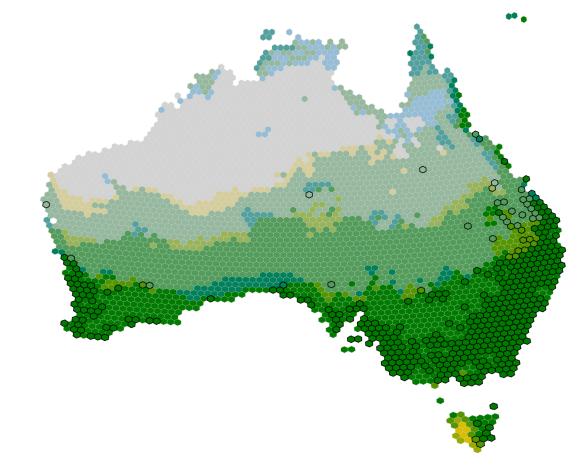


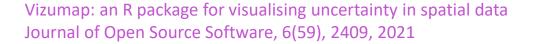
### Prediction and uncertainty

Unify into one plot



Combined: Estimate + Uncertainty



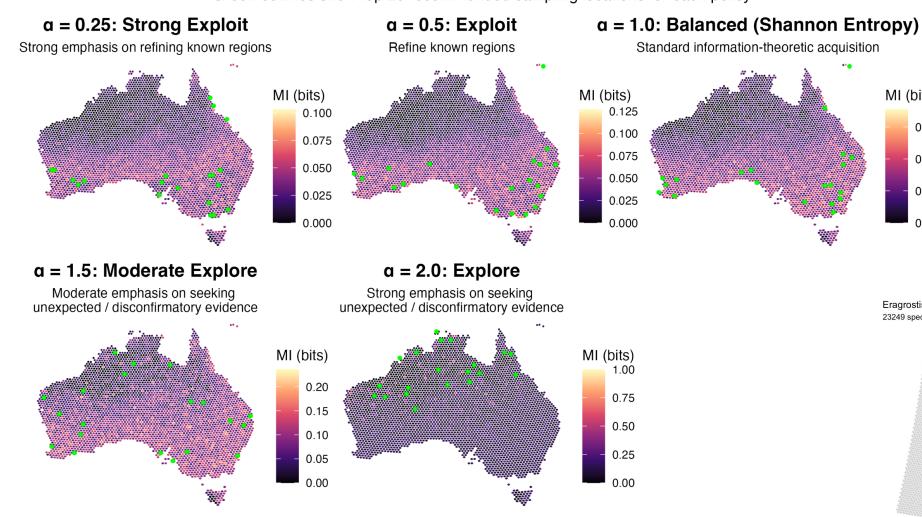




## Exploration - exploitation

Fig 2: Acquisition Function Recommendations by Alpha for Renyi Entropy Search

Green outlines show top 20 recommended sampling locations for each policy



Eragrostis curvula (African Lovegrass) Distribution - 50km Hexagons 23249 specimens in 474 hexagons

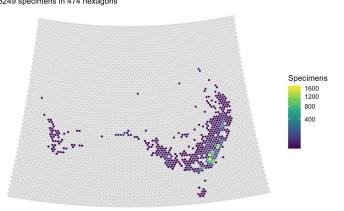
MI (bits)

0.15

0.10

0.05

0.00





#### Higher gene expression

- Ribosomal binding site
- Given 6 letters of a genome, predict gene expression
- Sequence kernel
- Use Bayesian optimisation (GP-BUCB, kriging believer)
- 4 experimental cycles
- 35% stronger than engineered sequence



Mengyan Zhang, Oxford





Huw Hayman Zumpe, Nourish



ACS Synthetic Biology Volume 11, Issue 7

July 15, 2022 Pages 2221-2526

#### ARTICI

Machine Learning Guided Batched Design of a Bacterial Ribosome Binding Site

#### View article page

Mengyan Zhang, Maciej Bartosz Holowko, Huw Hayman Zumpe and Cheng Soon Ong

77 CITE

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## CSIRO's BioFoundry

• Engineering biology:

is the set of methods for designing, building, and testing engineered biological systems



Hafna Ahmed



Chie Ishitate



Candice Jones MPI Marburg



Adrian Marsh



**Robert Speight** 





### What's the objective?

Design Ribosome Binding Site (RBS) sequences



Optimize the protein expression level.

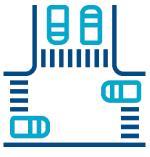
RBS sequence	Normalized* Protein Expression Level
TTTAAGA <mark>GTTATA</mark> TATACAT	1.58
TTTAAGA <mark>ATATGC</mark> TATACAT	1.42
TTTAAGACTCGGATATACAT	0.14
TTTAAGAGTTTTTTATACAT	2.88

Core part (design space):  $4^6$  = 4096 possibilities in total

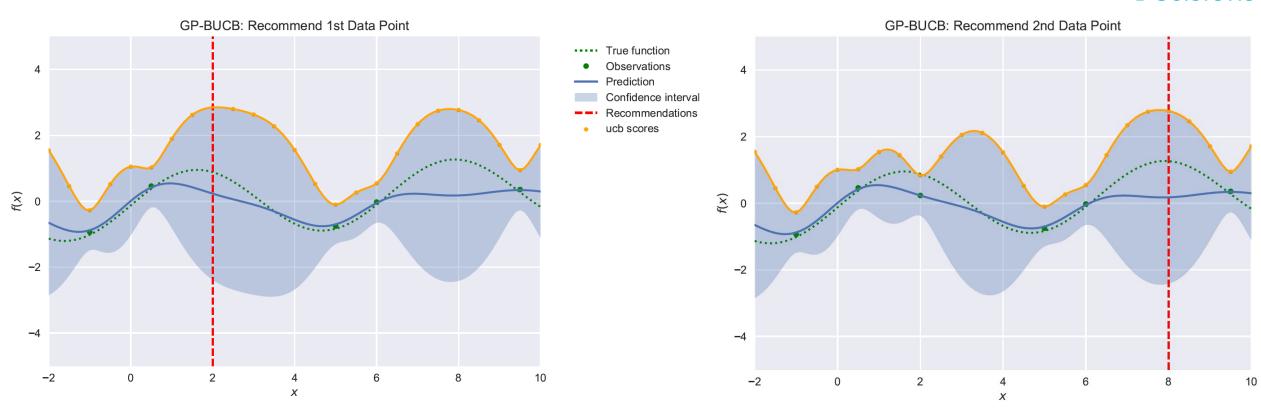


## Upper confidence bound

#### A particular bandit algorithm

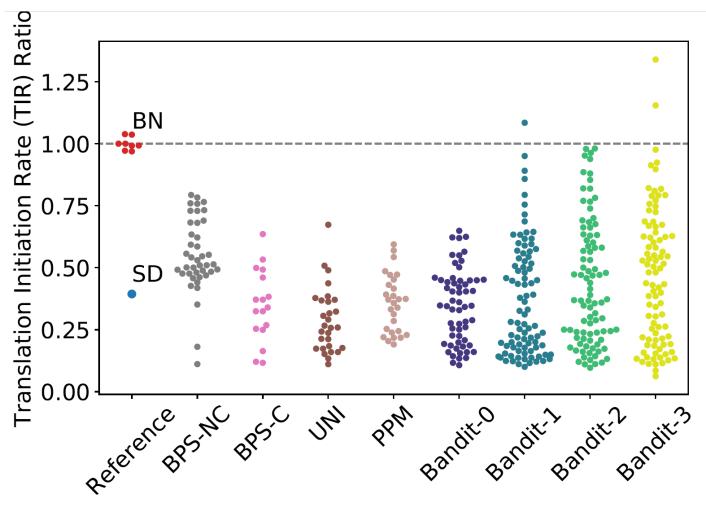


**Decisions** 





## ML recommends good designs



# **TTTAAGANNNNNNTATACAT**ATG -20 **Feature** -1

- Hard to search by evolving sequences
- 4 experimental cycles
- 35% stronger than engineered sequence

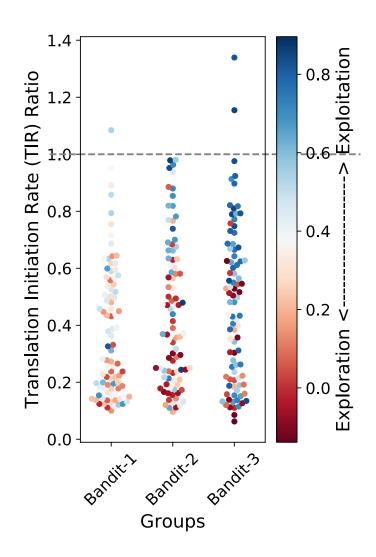
Zhang, Holowko, Hayman Zumpe, and Ong, Machine learning guided design for ribosome binding site. ACS Synthetic Biology, 2022



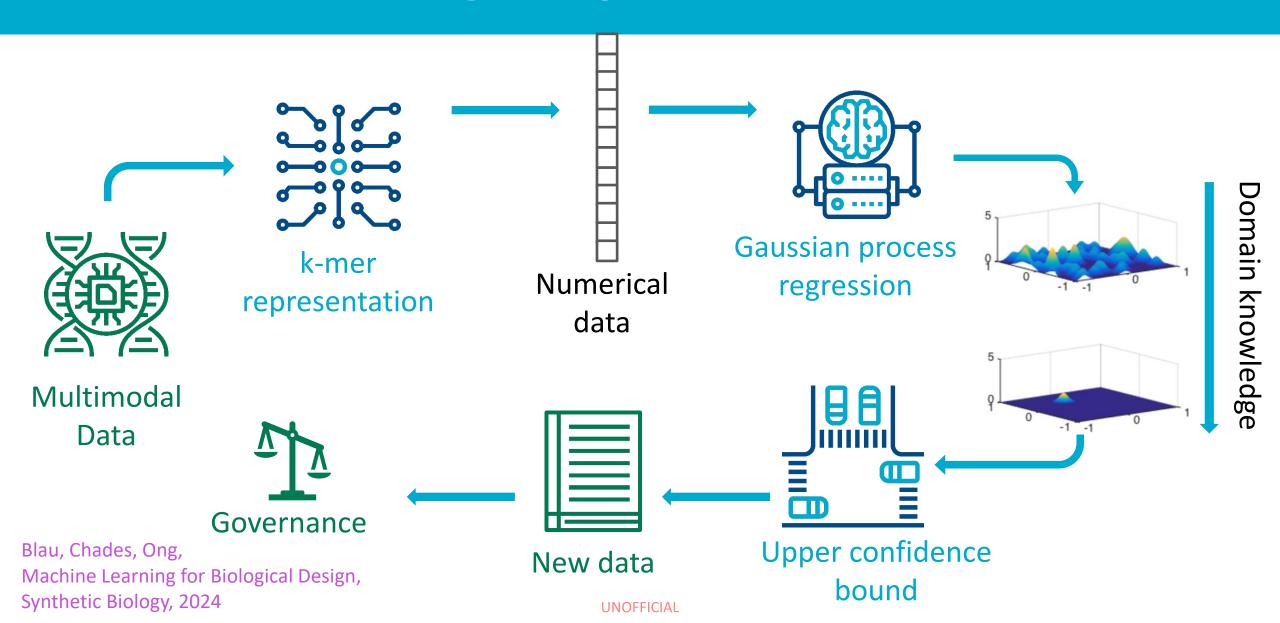
## **Exploration-Exploitation Trade-off**

- Exploration: unknown (untested) RBS design space with potentially high label
- Exploitation: querying areas that are predicted to give relatively high labels.

Which genome should we grow?



## Machine learning for genomics





#### Work in progress: find plastic degrading enzymes

**Enzyme** – a short protein sequence, acts as a catalyst for a chemical reaction. Represented as a string of amino acid letters but has a 3D form.

Aim: we want to be able to find useful enzymes that can digest plastic

Challenge – search space is **VAST** 

Atoms in universe: 1080

Seconds since Big Bang: 10<sup>17</sup>

#### ppEST: Aryl esterase

MGTLLVVGDSISAAFGLDSRQGWVALLEKRLSEEGFEHSVVNASISGDTSAGGAARLSALLAEHKPELVIIELGGNDGL RGQPPAQLQQNLASMVEQSQQAGAKVLLLGMKLPPNYGVRYTTAFAQVFTDLAEQKQVSLVPFFLEGVGGVPGM MQADGIHPAEAAQEILLDNVWPTLKPML



#### 20<sup>200</sup> possible (substitution) variants!



Asiri Wijesinghe



Allen Zhu



Lu Zhang

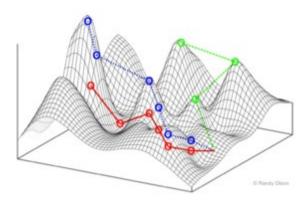


Asher Bender

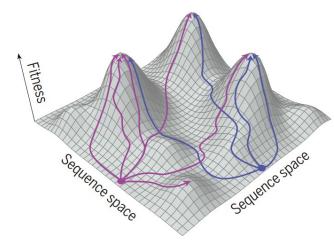


#### Fitness landscape

- A metaphor in evolutionary biology
- Each of the horizontal axes represents some notion of sequence variation
- The vertical axis captures some property of interest (so-called fitness)
- Open question how to represent



Wikipedia: Sewall Wright



Papkou et al., Science 382, 901 (2023)

Low

High

#### Our idea: Islands of fitness

- Desiderata: want to find only "fit" sequences
- Intuition: Many sequences are not viable, and we cannot measure their fitness



Aerial View of Seventy Islands, Micronesia, Palau

by Reinhard Dirscherl

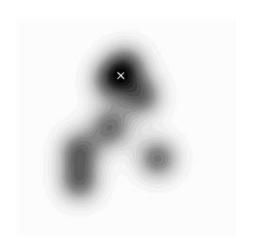
#### **Active Generation**

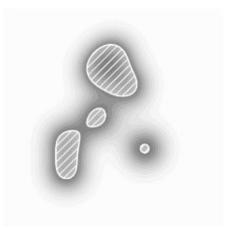
• Goal: We want to generate from a (conditional) probability density  $p(x \mid y > \tau)$ 

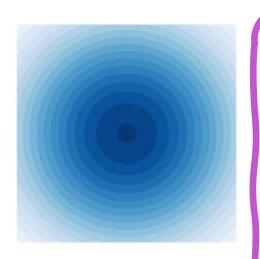
Where x is the space of sequences and y is the fitness value  $\tau$  is a parameter that identifies "fit" sequences

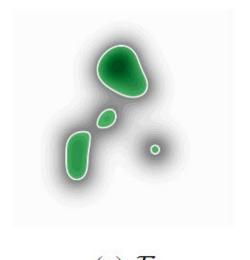


#### Variational Search Distributions









(a)  $\operatorname{argmax}_{\mathbf{x}} y(\mathbf{x})$ 

 $\mathbf{x}, y(\mathbf{x})$  (b)  $\mathcal{S}$ 

(c)  $p(\mathbf{x})$ 

(d)  $p(\mathbf{x}|y > \tau)$ 

2(11/9 / 1)

(e)  $\mathcal{F}$ 

Find the fittest

Set of viable sequences

Prior

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Posterior

Ground truth







Steinberg, Oliveira, Ong, Bonilla, Variational Search Distributions, ICLR 2025 https://arxiv.org/abs/2409.06142

Dan Steinberg

Rafael Oliveira

IIIII



## Solving active generation

- Frame online black box optimization
   as sequential learning of conditional generation
- In each round of the sequence, there are two steps



Fit a binary classifier (CPE),  $z := \mathbf{1}[y > \tau]$  indicates "good"

$$\pi_{\theta}(\mathbf{x}) \approx p(z=1|\mathbf{x})$$



Update the generative model

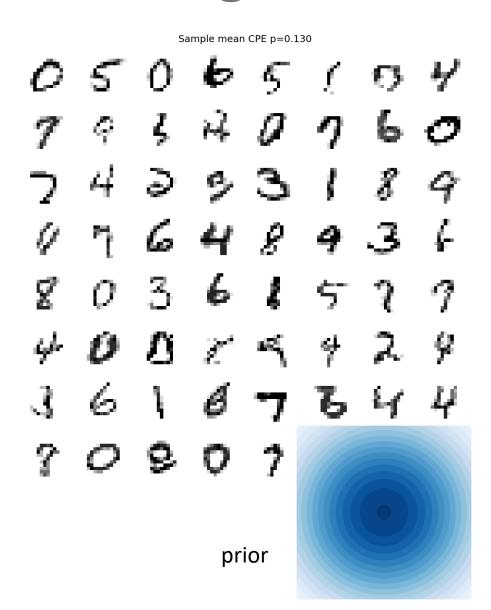
$$\phi_t^* \leftarrow \operatorname*{argmax} \mathcal{L}_{\text{ELBO}}(\phi, \theta_t^*)$$

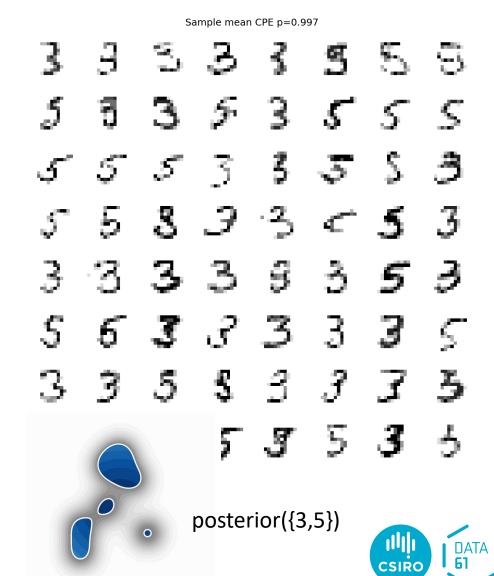
• We choose to maximise the evidence lower bound (variational inference)

$$\mathcal{L}_{\text{ELBO}}(\phi, \theta) = \mathbb{E}_{q_{\phi}(\mathbf{x})}[\log \pi_{\theta}(\mathbf{x})] - \mathbb{D}_{\text{KL}}[q_{\phi}(\mathbf{x}) || p(\mathbf{x} | \mathcal{D}_0)]$$



### Generating unrolled images





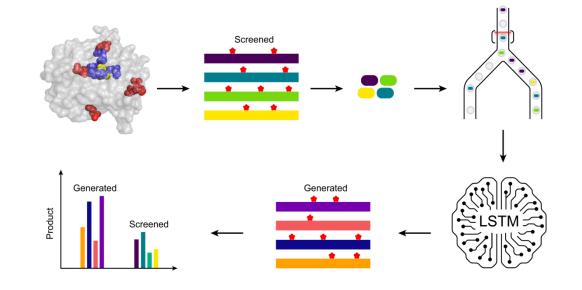
## Early results - peroxygenases

 Peroxygenase is a catalyst that inserts an oxygen atom

Catalyst 
$$H_2O_2$$
  $+$   $(S)-2$   $+$   $3$ 

- Want to engineer specificity into unspecific peroxygenase
- Enzyme library is screened using microfluidic sorting

 Active generation consistently outperformed direct selection from the same screening data



Ultrahigh throughput screening to train generative protein models for engineering specificity into unspecific peroxygenases Nair, Steinberg, et. al.







#### **Active Generation**

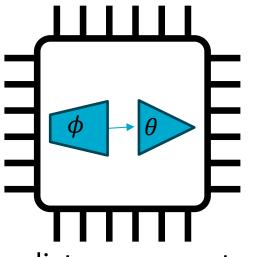
Active generation: find best  $\phi^*$  for generating "good" (or best)  $\mathbf{x}$ 

MKTTTLLFLVGALTQ	1.2
MKTTTLLFLVGTLTQ	3.6
MKTTTLLFLVGALTT	0.3

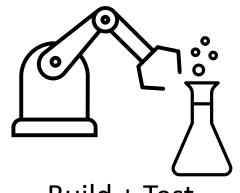
#### Labelled Data

$$\pi_{\theta}(\mathbf{x}) \approx p(z=1|\mathbf{x})$$

$$\phi_t^* \leftarrow \operatorname*{argmax} \mathcal{L}_{\text{ELBO}}(\phi, \theta_t^*)$$



Predictor + generator learning

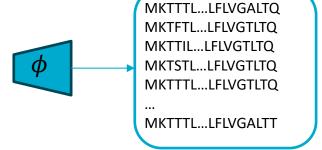


Build + Test

Can "select" from a **vast number** of enzymes (e.g. 20<sup>200</sup>), since they are **generated** 

\*\* we are **not** doing latent space optimisation!

Generate good candidates instead of selecting from a list

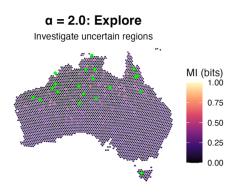


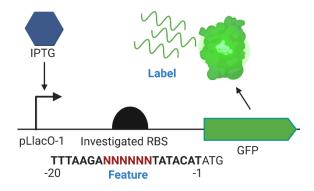
Unlabelled data generation, design is generation



#### Data is measured for a reason

Consider the set of all possible things to measure







- Think of the predictor output as producing features
  - Each calculated feature demonstrates the "importance" of an experiment
  - Can get multiple features by using different predictors
  - Estimate predictive uncertainty to inform decisions
- Adaptively choose the next thing to measure by maximising an objective (machine learning is about defining good objective functions)





## On finding good experiments



What is an experiment?

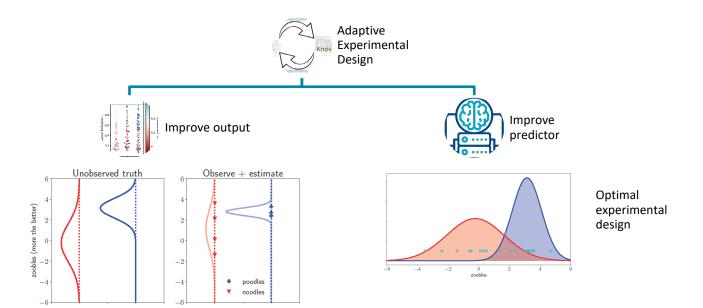


How do we find good experiments?



What do we mean by good?

#### Better measured values or better models



Recall that we can use a machine learning predictor in two ways:

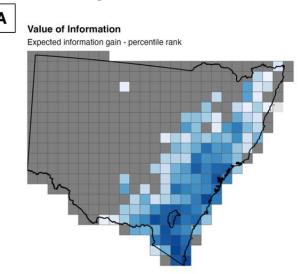
- 1. The parameters of the model
- 2. The output values on a test set

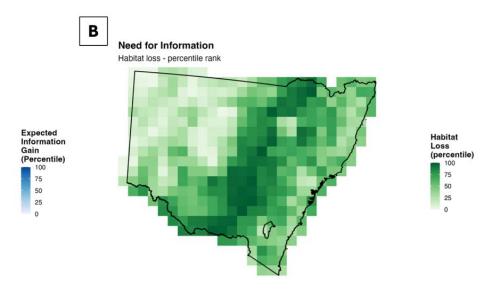


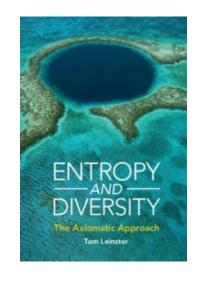


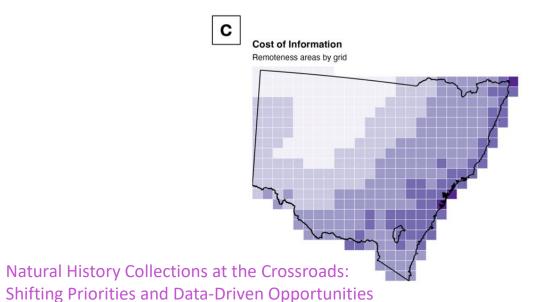
#### Value, need, cost

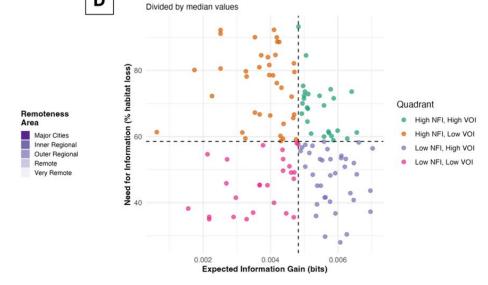
Forbes, Thrall, Young, Ong, Ecology Letters, vol 28, no 8, 2025











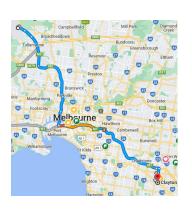
**VOI vs NFI Quadrant Analysis** 

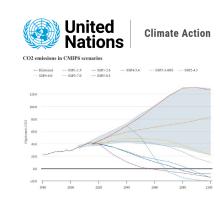


#### ML is **not only** about predictions

#### Predictions vs Decisions vs Actions

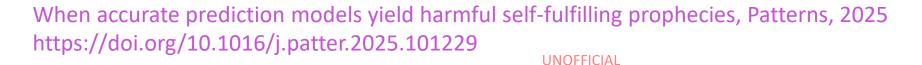


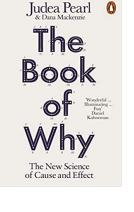




	Weather	Traffic	Climate
<b>Predictions</b>	Will it rain tomorrow?	Jam on M1?	Risk in 2050?
Decisions	Take umbrella?	Train or taxi?	Plan for net zero
Actions	Does not affect weather	Affects traffic!	Want wrong predictions!







#### Pragmatism in International Relations



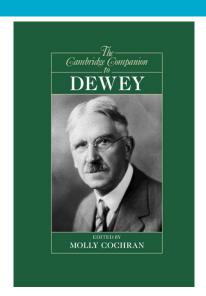
Toni Erskine, ANU

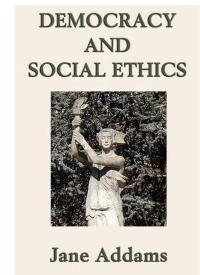


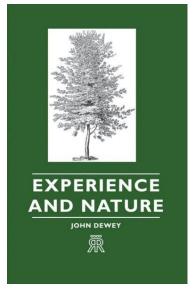
Xueyin Zha, ANU

Need a way to say "good" and "true"

PhD thesis: Normative Truth-Seeking from the Ground Up: Experiential Pathway to Global AI Governance

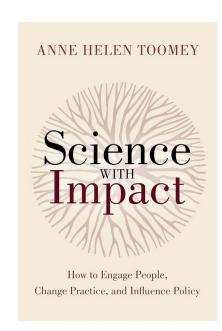






#### We should learn from each other

- Need more than data science
- How to foster cross disciplinary projects?
- π shaped research teams



IEEE TRANSACTIONS ON TECHNOLOGY AND SOCIETY

Four Compelling Reasons to Urgently Integrate AI
Development With Humanities, Social and
Economics Sciences

Iadine Chades<sup>®</sup>, Melanie McGrath<sup>®</sup>, Erin Bohensky, Lucy Carter<sup>®</sup>, Rebecca Coates<sup>®</sup>, Ben Harwood, Md Zahidul Islam, Sevvandi Kandanaarachchi<sup>®</sup>, Cheng Soon Ong<sup>®</sup>, Andrew Reeson<sup>®</sup>, Samantha Stone-Jovicich<sup>®</sup>, Cécile Paris<sup>®</sup>, Mitchell Scovell<sup>®</sup>, Kirsty Wissing<sup>®</sup>, and David M. Douglas<sup>®</sup>

Position: We need responsible, application-driven (RAD) AI research

**Opportunities and Challenges in Designing Genomic Sequences** 

Sarah Hartman <sup>1</sup> Cheng Soon Ong <sup>23</sup> Julia Powles <sup>45</sup> Petra Kuhnert <sup>1</sup>





## On Finding Good Experiments

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What is an experiment?



How do we find good experiments?



What do we mean by good?