Al/ML for prediction of biological properties of molecules

Module 0. Introduction to drug discovery

Gemma Turon & Miquel Duran-Frigola Ersilia Open Source Initiative (<u>www.ersilia.io</u>) 18th - 27th of September, 2023



Welcome and introduction to the course



We are a small and young tech nonprofit aimed at reducing inequality in global health.

We equip laboratories in LMICs with artificial intelligence tools for infectious disease research.

Free & open source

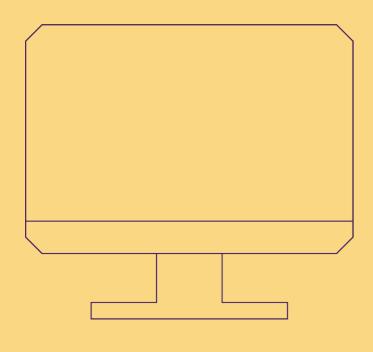
Public code
Open access
No patents

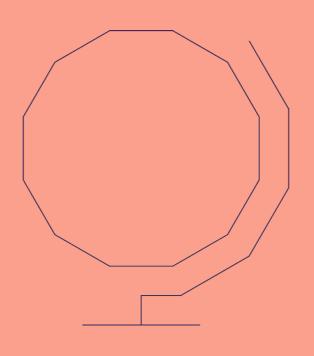
In-country research

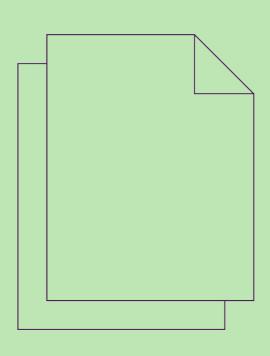
Local scientific leadership

Sustainable collaborations

Capacity building Low-resource tools







Course facilitators

Ersilia



Gemma Turon, PhD Molecular biology & biomedicine gemma@ersilia.io @TuronGemma



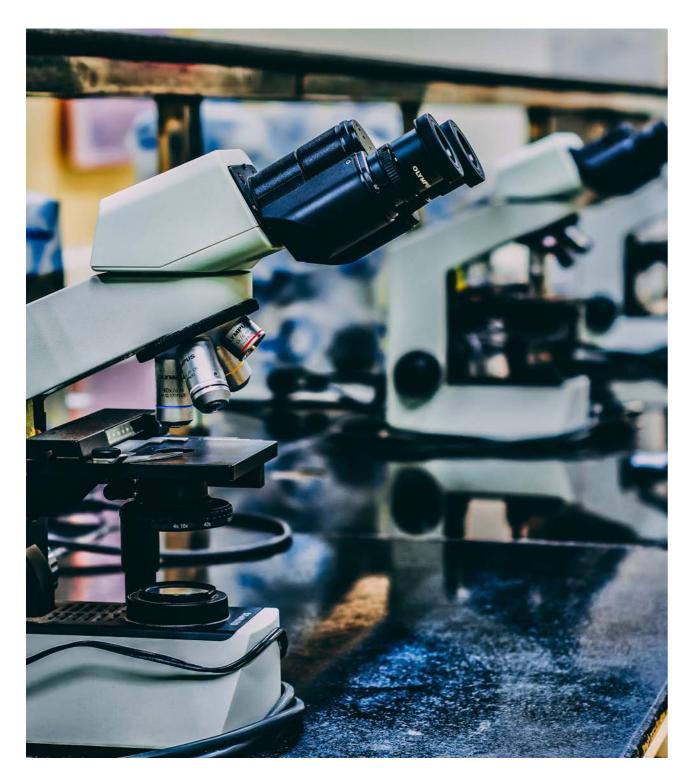
Miquel Duran-Frigola, PhD Computational biology & chemistry miquel@ersilia.io @mduranfrigola



Objectives of t

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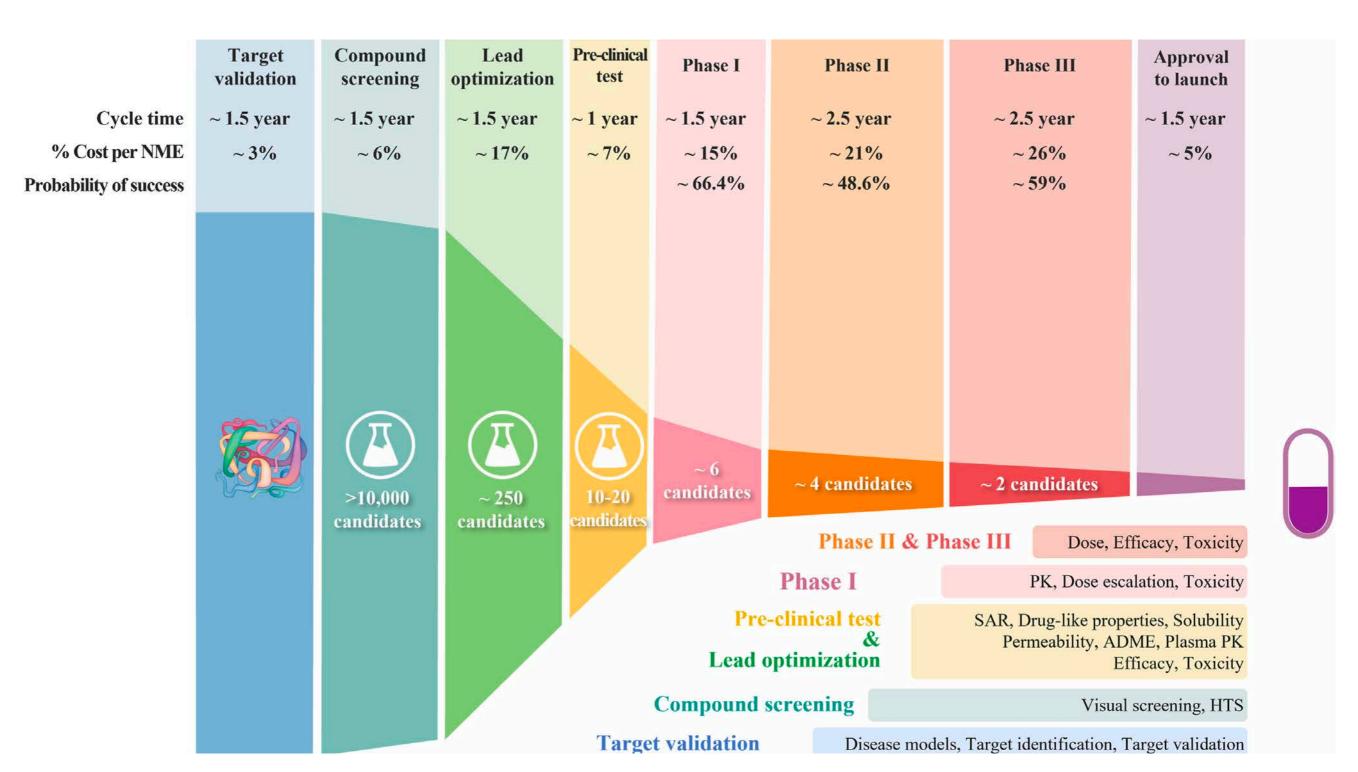
Objectives of the course



- Understanding the uses and limitations of Al for drug discovery
- Learning how to apply Al to your ongoing research
- Getting the basic coding skills for data science
- Collecting tools and resources for further work

The drug discovery pipeline and the promise of Al

Drug discovery pipeline



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Al in the drug discovery pipeline

pipeline

Compound Lead optimization

Pre-clinical test

Clinical tests

Market launch

-omics data analysis

Target validation

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Target druggability

Bioactivity prediction

Chemical space analysis

ADMET property prediction

Physicochemical optimisation

De novo drug design

Clinical trial design

Patient selection

Virtual cohorts

Patient monitoring

Al in the drug discovery pipeline

Compound Target validation Lead optimization screening -omics data analysis Target druggability Bioactivity prediction Chemical space analysis **ADMET** property prediction Physicochemical optimisation De novo drug design Clinical trial design Patient selection Virtual cohorts

Pre-clinical test

Clinical tests

Market launch

Patient monitoring

- Reduce number of compounds synthesised
- Reduce number of animals used
- Avoid failure at most expensive stages
- Decrease overall costs and reduce time to launch

Al in the drug discovery pipeline

Compound Target validation screening -omics data analysis Target druggability Bioactivity prediction Chemical space analysis **ADMET** property prediction Physicochemical optimisation De novo drug design Clinical trial design Patient selection Virtual cohorts

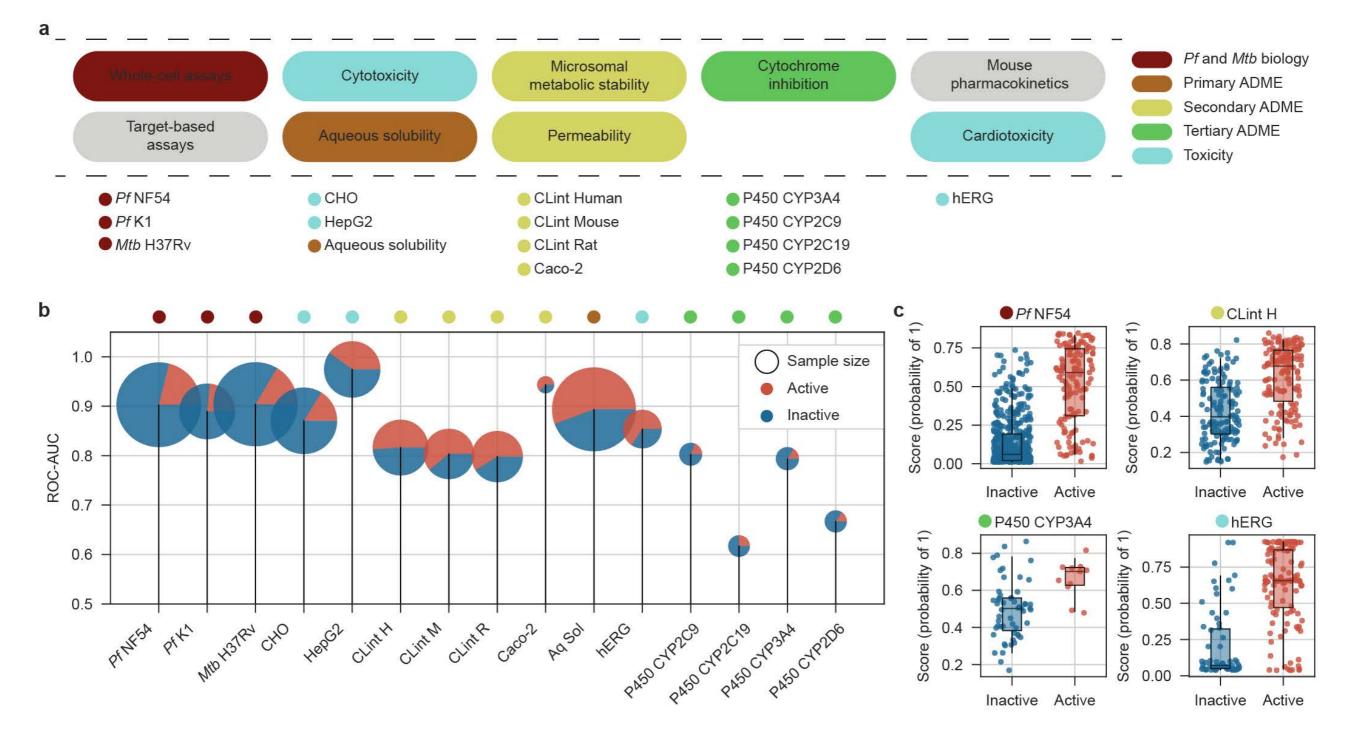
Lead optimization Pre-clinical test Clinical tests

Market launch

Patient monitoring

- Reduce number of compounds synthesised
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An example of a virtual screening cascade



Basic Al concepts for molecular modelling

Supervised

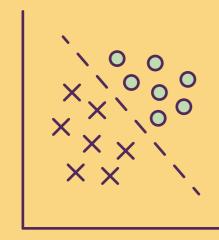
Labeled data Classification Regression

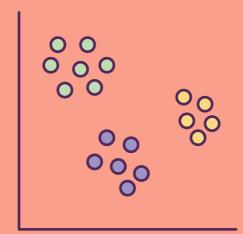
Unsupervised

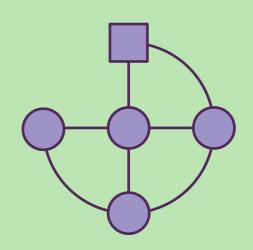
Unlabelled data
Clustering
2D projection
Similarity search

Reinforcement

Interaction with environment & agent Generative models



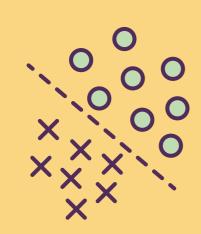




Supervised machine learning

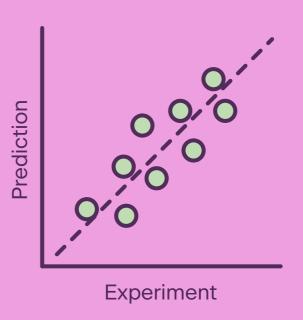
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Classification



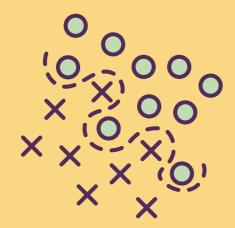
Prediction task: Active = 1 Inactive = 0

Regression



Prediction task: IC50 value

Overfitting



Confidence

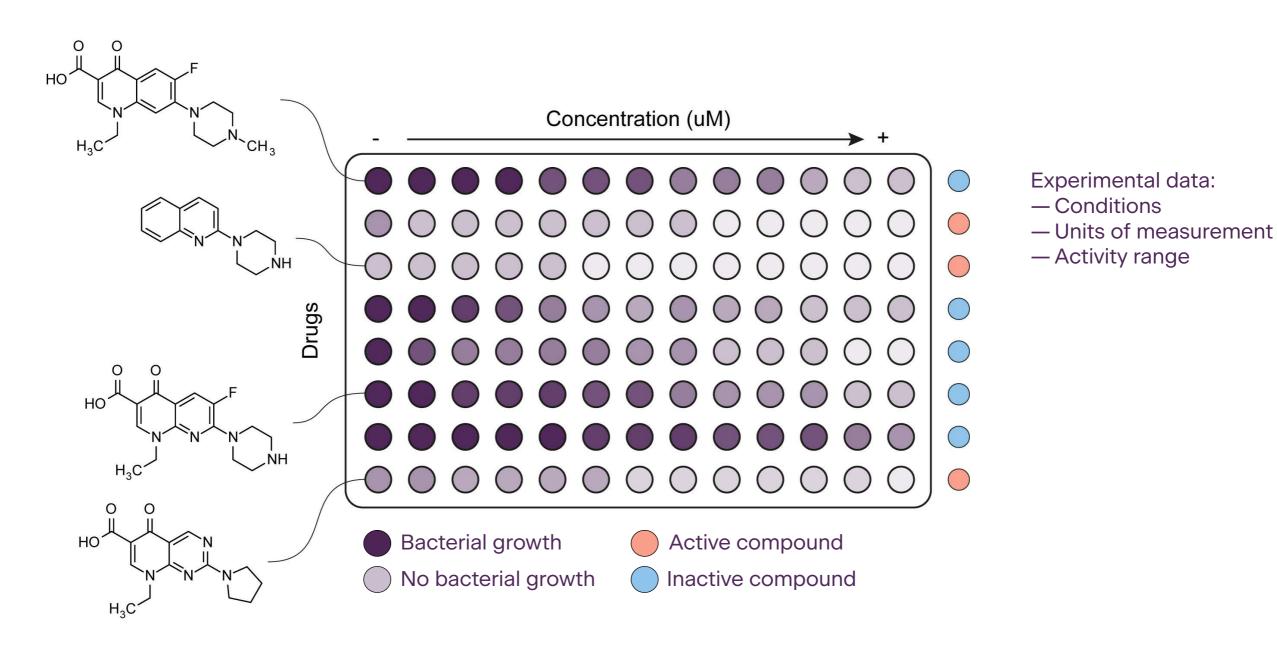
Imbalance

Interpretability

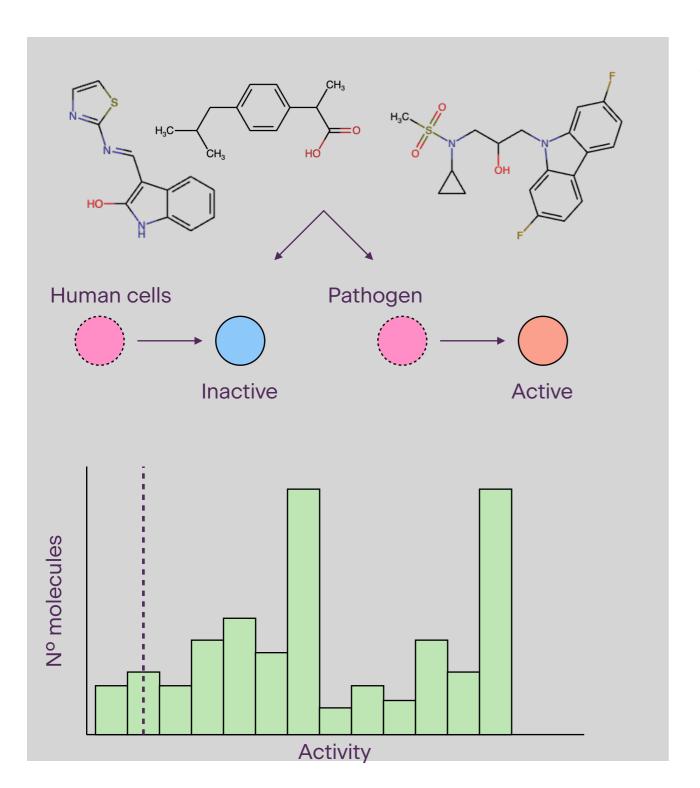
Basic components of an Al/IVIL model for bioactivity prediction

Go to menti.org and introduce this code: 8771 8241

Understanding our training dataset

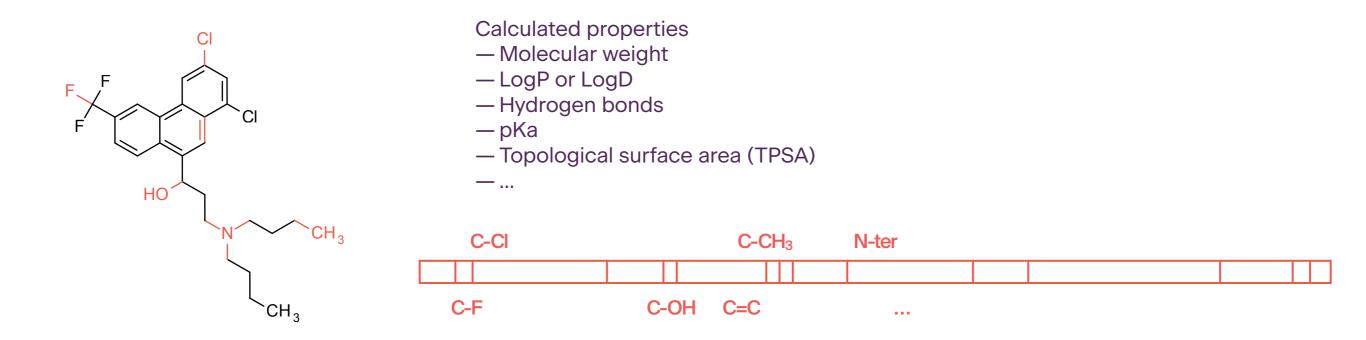


Understanding our training set



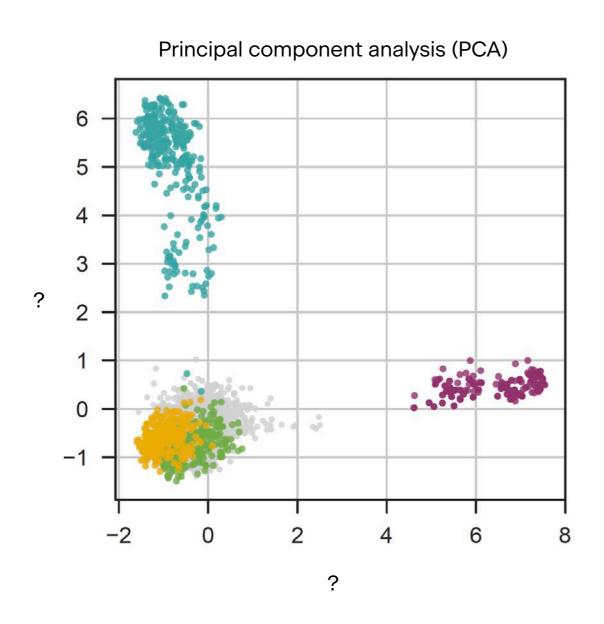
- A few considerations:
- Do we want active or inactive molecules?
- What are good thresholds of bioactivity?
- Are there experimental limits?

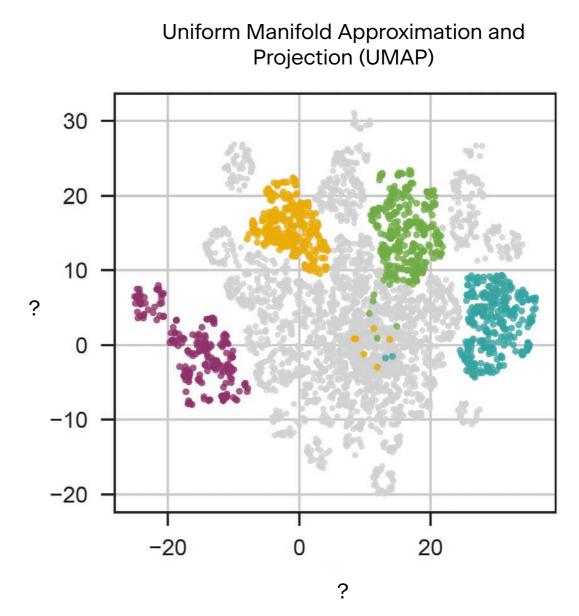
Gathering information about our molecules



Halofantrine belongs to the class of organic compounds known as phenanthrenes and derivatives. These are polycyclic compounds containing a phenanthrene moiety, which is a tricyclic aromatic compound with three non-linearly fused benzene. Halofantrine is a synthetic antimalarial which acts as a blood schizonticide. It is effective against multi drug resistant (including mefloquine resistant) P. falciparum malaria. The mechanism of action of Halofantrine may be similar to that of chloroquine, quinine, and mefloquine; by forming toxic complexes with ferritoporphyrin IX that damage the membrane of the parasite. It appears to inhibit polymerisation of heme molecules (by the parasite enzyme 'heme polymerase'), resulting in the parasite being poisoned by its own waste. Halofantrine has been shown to preferentially block open and inactivated HERG channels leading to some degree of cardiotoxicity. Side effects include coughing noisy, rattling, troubled breathing, loss of appetite, aches and pain in joints, indigestion, and skin itching or rash, et cetera, et cetera.

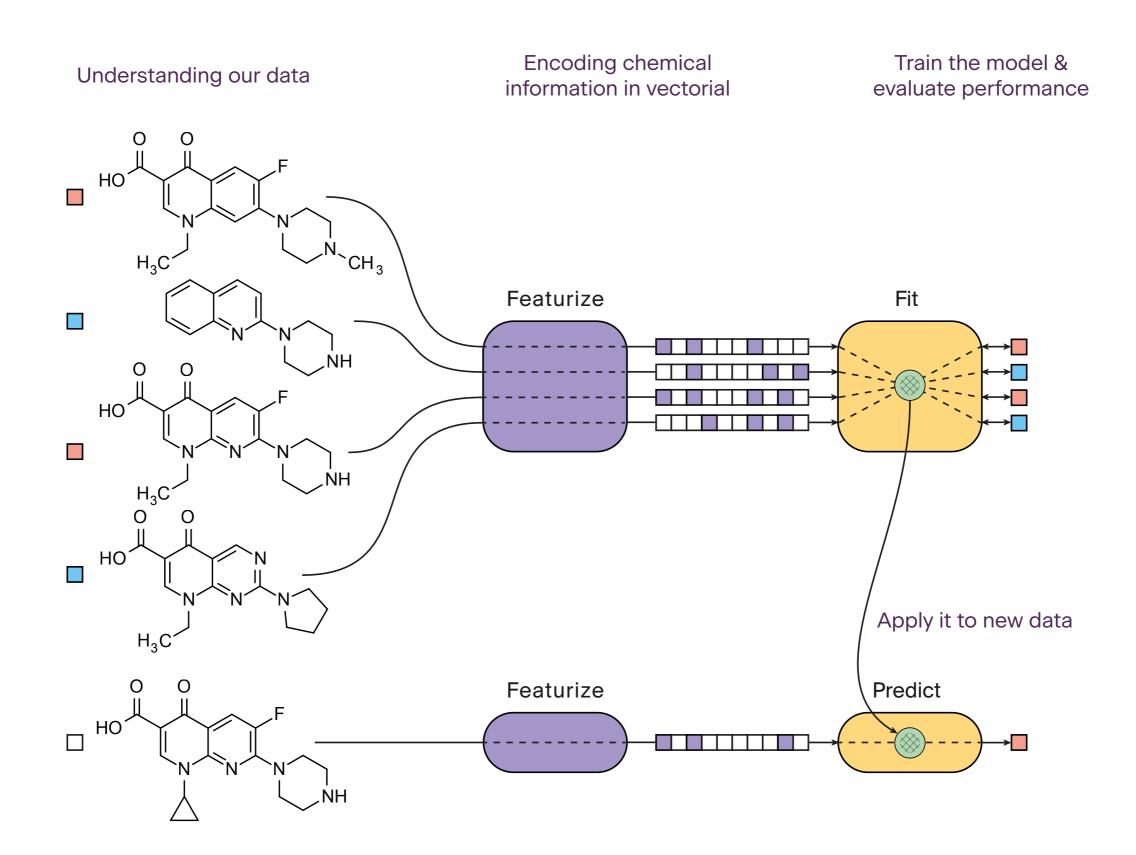
Visualising the chemical space





Building a Al model

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Keywords

- Fingerprint
- Supervised
- Unsupervised
- PCA
- UMAP
- Embeddings
- Overfitting
- Imbalance
- Interpretability/ explainability/ transparency

- Reinforcement
- SMILES
- IC50/EC50
- Confidence
- Outlier
- Applicability domain
- Chemical space
- Cross-validation

Course overview

Course overview

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- Module 1. Using AI models for drug discovery
- Module 2. Setting up our computational environment
- Module 3. The Ersilia Model Hub
- Module 4. Introduction to AI model training and performance evaluation

General schedule

9:00 - 10:00: good morning & setting up

10:00 - 12:30: course part 1

12:30 - 13:30: lunch break

13:30 - 16:00: course part 2

16:00 - 17:00: wrap up & good bye

Get familiar with the these tools!

















