



# Machine Learning & High-Content Screening for Drug Development/ Repurposing

Sašo Džeroski

Jozef Stefan Institute, Ljubljana, Slovenia

Team: Dragi Kocev,  
Panče Panov, Tomaž

Stepišnik, Martin Breskvar

**Interreg**  
ITALIA-SLOVENIJA

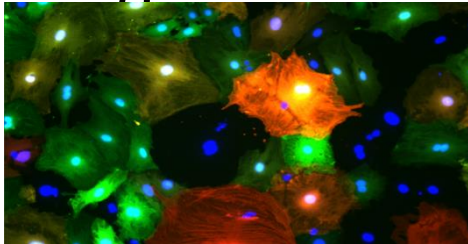


**TRAIN**

Progetto standard co-finanziato dal Fondo europeo di sviluppo regionale  
Standardni projekt sofinancira Evropski sklad za regionalni razvoj

# High-content screening

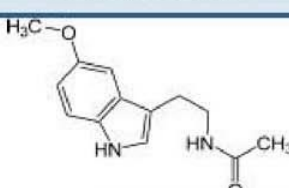
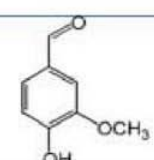
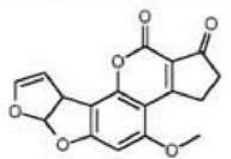
- Compound screens
- Genomic screens (miRNA screens)
- Images taken under the microscope



- Use machine learning to learn models for virtual compound screening, identify novel candidates

# Learning from Compound Screens

## Learning structure-activity Relationships

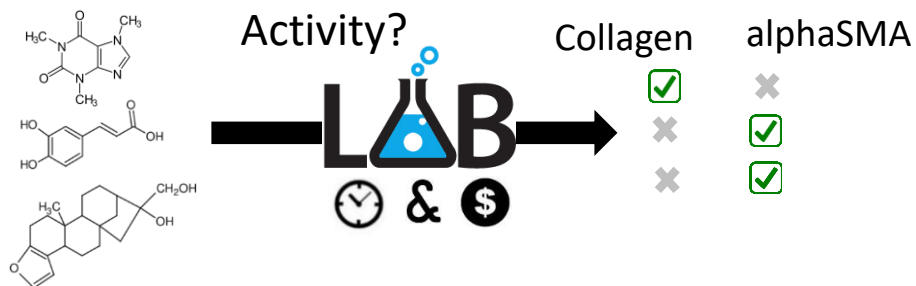
	input datatype specification	output datatype specification
	input: molecule datatype	output: real datatype
	compound	activity
data example		0.25
		0.28
		0.37



# Learning from compound screens

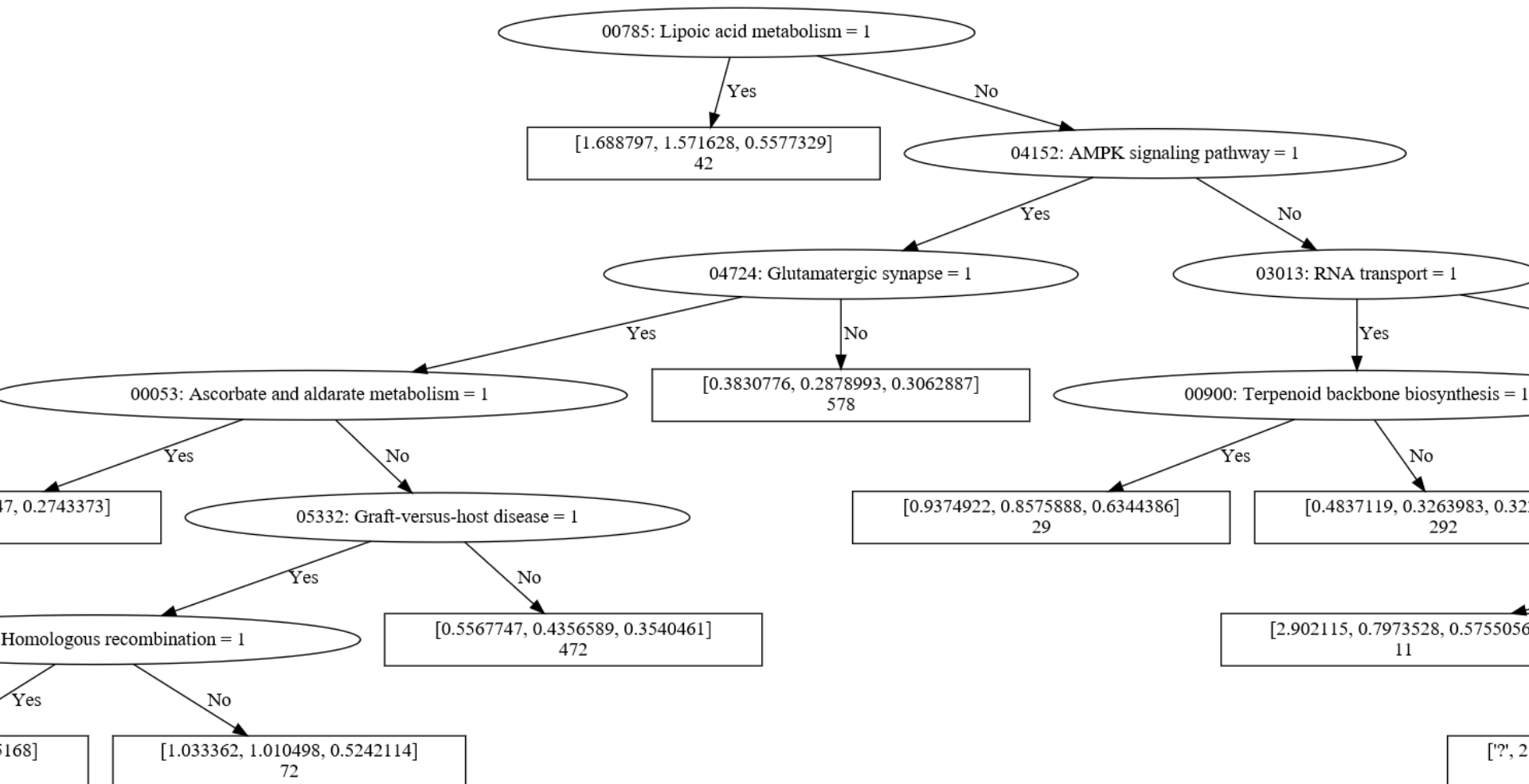
Compound screen data

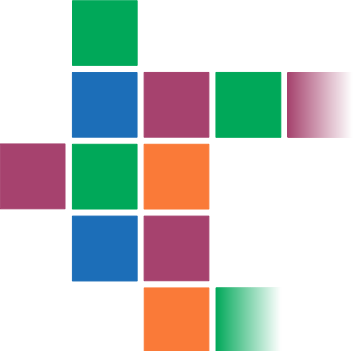
	Descriptive space				Target space	
Example 1	1	TRUE	0.49	0.69	0.68	3.91
Example 2	2	FALSE	0.08	0.07	0.56	7.59
Example 3	1	FALSE	0.08	0.07	0.10	7.57
Example 4	2	TRUE	0.49	0.69	0.08	8.86
...	...				...	...





# The ML technology: Multi-target regression trees





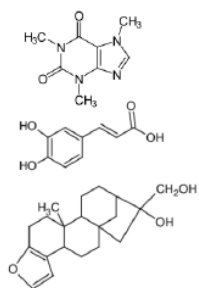
# Virtual screening

Labeled data

	Descriptive space				Target space	
Example 1	1	TRUE	0.49	0.69	0.68	3.91
Example 2	2	FALSE	0.08	0.07	0.56	7.59
Example 3	1	FALSE	0.08	0.07	0.10	7.57
Example 4	2	TRUE	0.49	0.69	0.08	8.86
...	...				...	...

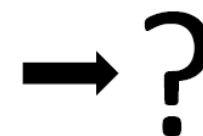
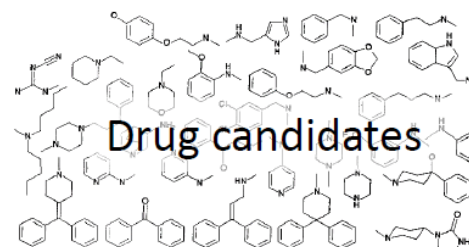
Unlabeled data

Example N+1	1	TRUE	0.86	0.35	?	?
Example N+2	2	FALSE	0.09	0.05	?	?
Example N+3	4	FALSE	0.07	0.01	?	?
Example N+4	2	TRUE	0.91	0.78	?	?
Example N+5	2	TRUE	0.42	0.69	?	?
...	...				...	...



Learn

VIRTUAL SCREENING  
MODEL

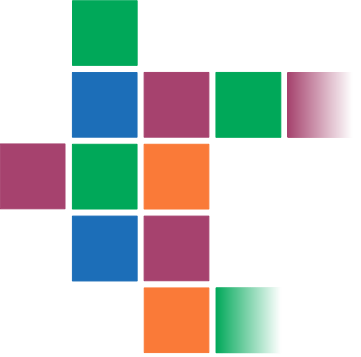


Predict



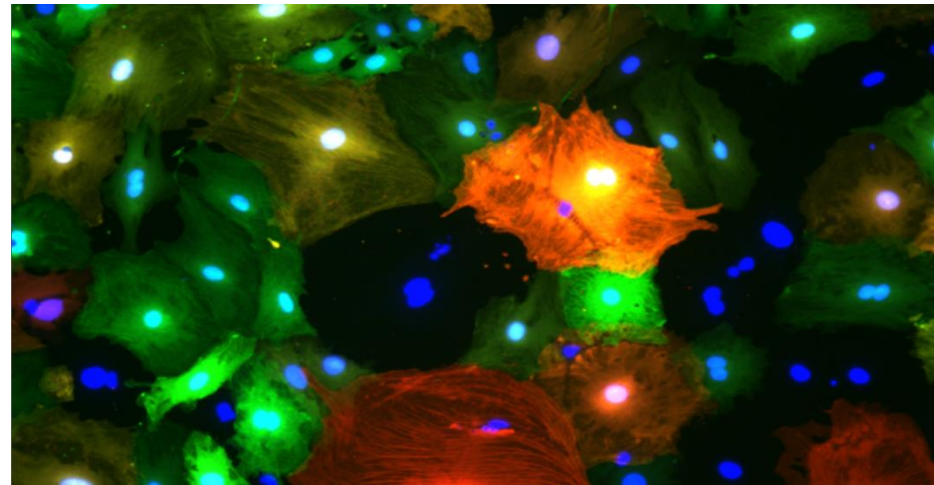
# Analyzing data from High-contents Screens

- Compounds described by fingerprints
- Generated by open-source chemoinformatics SW library RDkit
- The FCFP2 fingerprints were used (1024 features)
- Also considered profiles of targeted proteins
- These are the attributes
  
- Assays photographed under the microscope
- Features extracted from images
- These are then the targets



# Reducing fibrosis in myocardial infarction

- High content screen using a library of 640 FDA approved drugs (ENZO)
- Identify drugs to reduce fibrosis in myocardial infarction
- Screen used murine cardiac fibroblasts which differentiate into myofibroblasts in culture, expressing increased alpha SMA-RFP and collagen-alpha1-EGFP
- Targets: Intensity of
  - alphaSMA
  - Collagen
- Attributes
  - Fingerprints





# Testing the predictions

- Some domain-specific knowledge / constraints applied: Predicted compounds filtered for FDA approved drugs that are not corticosteroids
- SMILE strings used in Chemmine to identify substances with structural similarity to non commercial compounds with high predicted values
- Three related compounds identified which are described in literature to have an anti-fibrotic effect
- Four related compounds identified which were not previously described to have an anti-fibrotic effect
- Tested in the wet-lab and one works really well 😊

# Experiences within the project

- Analyzed several different screens
  - Compound screens
  - miRNA screens
- Found we can use models learned from miRNA screens to perform virtual compound screening
- Excellent collaboration with ICGEB
- Attractive virtual reality representation