Health & Care Cluster
of Large Scale Pilots

RADICAL HEALTH FESTIVAL Helsinki
12 June 2023

AI in hospitals: are we ready for it?”
Challenges and opportunities of AI deployment in hospitals

tumorscope

HOSMARTAI
AI for the smart hospital of the future

http://tumorscope.be

TumorScope

Digital Health Research Platform

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Prognosis of cancer patients and their response to treatment combining multi-omics data

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HOSMARTAI
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WHY?

- *Focus on Glioma – Rare disease*
- *Heterogenous, treatment subjective*
- *Personalised treatment*
- *Collection of data*

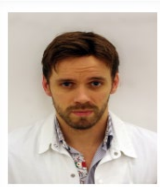
WHAT?

- *Digital health research platform*
- *To enable multimodal data and advanced AI-driven analytics*
- *Automated genetic and image data interpretation*

TEAM: VUB and UZB Hospital


Wim Vranken
Supervisor
Bio-informatics


Jef Vandemeulebroucke
Supervisor
Medical image analysis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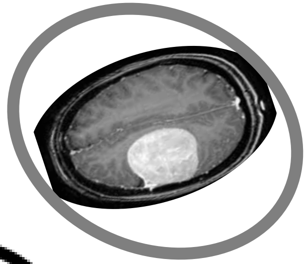
Tasks performed at UZB and VUB



Data Collection

Genetic data,
Image data
UZB hospital

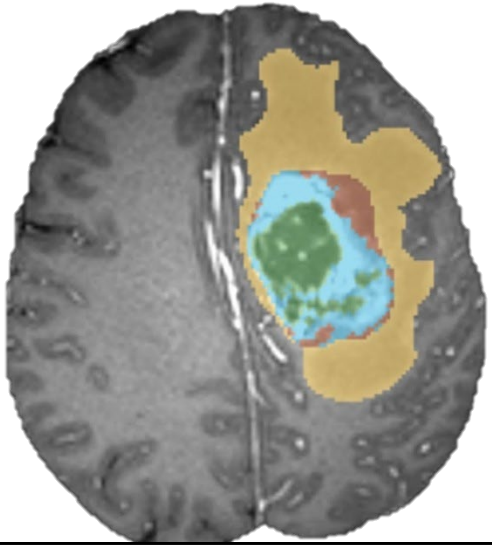
Data integration

Digital Health Platform in collaboration with ICT UZB

AI Analysis

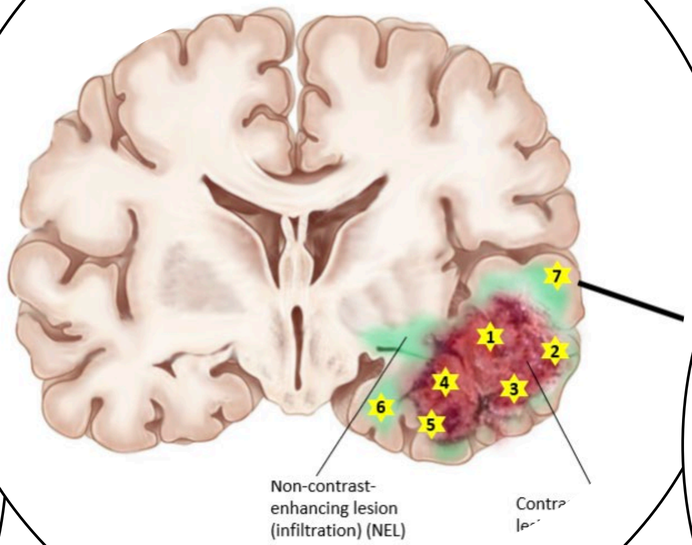
Tumor Image segmentation
Mutation analysis
Radiomics

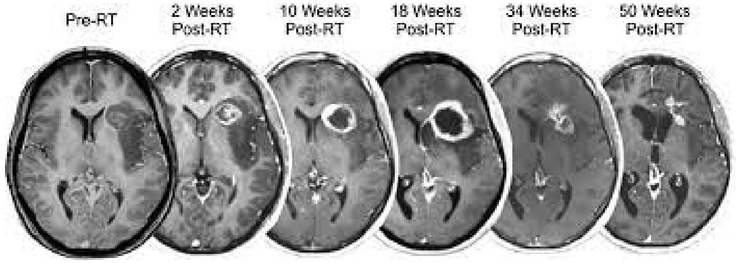
Tumor image analysis



Basic tumor regions and tumor infiltration

Intratumoral heterogeneity





Therapy-related changes

Tumor image segmentation Tool: Dataset details

Trained, validated and tested using the Brain Tumor segmentation (BraTS) Challenge dataset of the 2020 challenge

- 369 subjects
- each with T1, contrast-enhanced T1, T2 and FLAIR MR Image
- expert annotated ground truth for necrosis, enhanced tumor, and edema region.

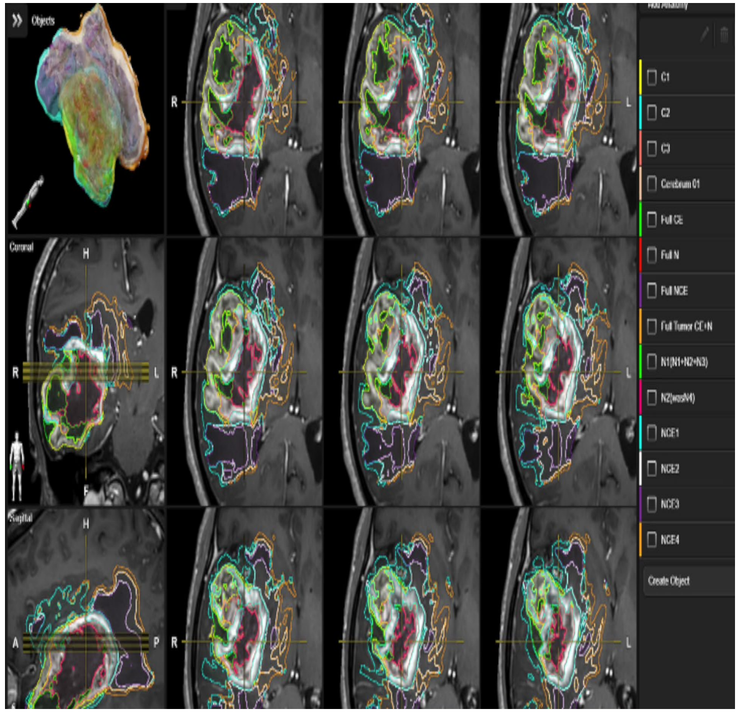
Training set	269 subjects 73%
Validation set	70 subjects 19%
Test set	30 subjects 8%

Challenge dataset

- Retrospective data being collected at the hospital
- ~100 patients with recurrent glioblastoma(FET-PET data)

Restricted UZB dataset

Accurate automatic segmentation of basic tumor sub-regions



AI on Genetic Tumor data

Driver/ Passenger mutation analysis tool

Driver mutations provide an advantage for tumor growth

Passenger mutations are the byproduct of tumor growth

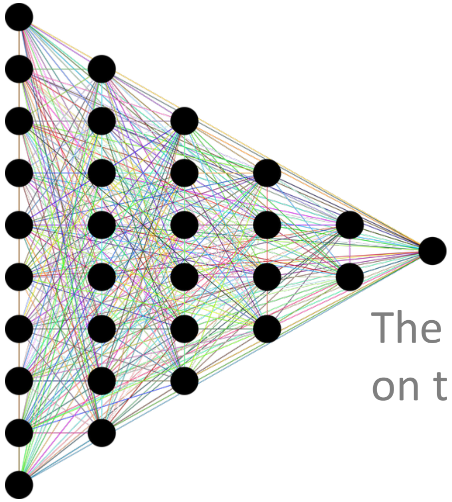
Personalised medicine

Personalised mutant discovery

Molecular understanding

Personalised treatment

Development of driver/passenger mutation prediction tool

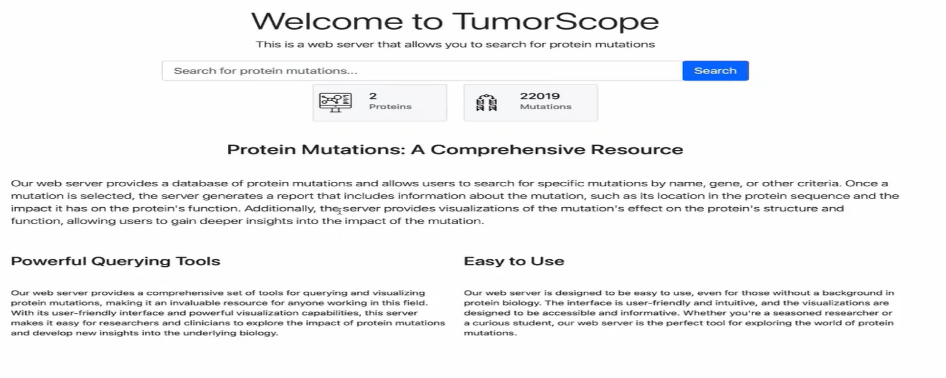


The mutation predictor tool is based on the deep learning framework

The Pre-Trained models were trained on 3 different databases

Different datasets are integrated to make the data unbiased.

Development of driver/passenger mutation prediction tool



Welcome to TumorScope

This is a web server that allows you to search for protein mutations

Protein Mutations: A Comprehensive Resource

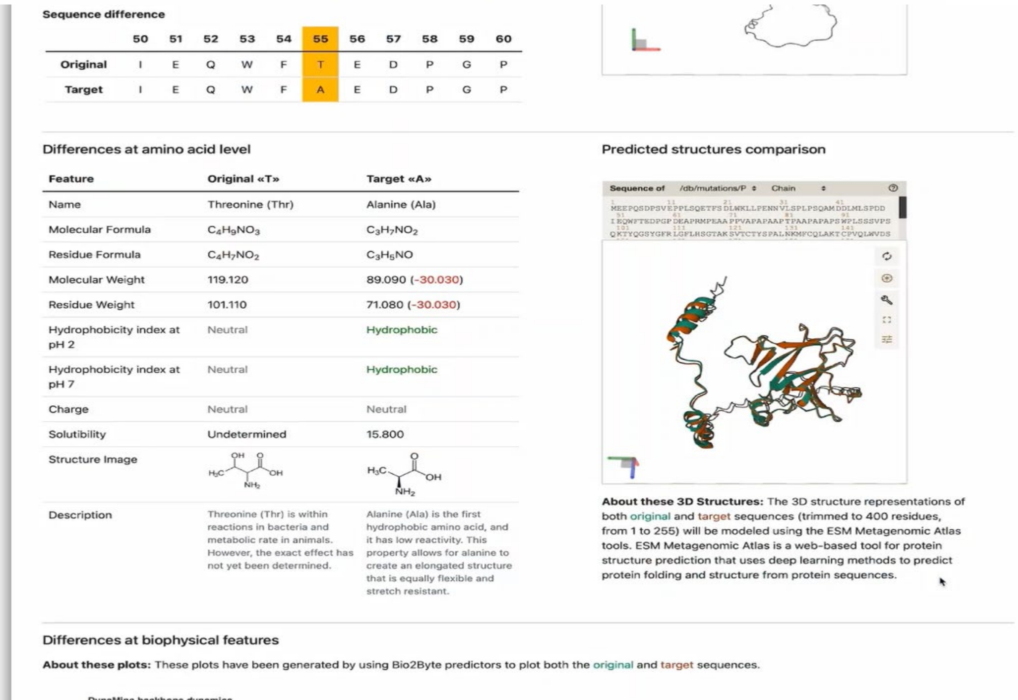
Our web server provides a database of protein mutations and allows users to search for specific mutations by name, gene, or other criteria. Once a mutation is selected, the server generates a report that includes information about the mutation, such as its location in the protein sequence and the impact it has on the protein's function. Additionally, the server provides visualizations of the mutation's effect on the protein's structure and function, allowing users to gain deeper insights into the impact of the mutation.

Powerful Querying Tools

Our web server provides a comprehensive set of tools for querying and visualizing protein mutations, making it an invaluable resource for anyone working in this field. With its user-friendly interface and powerful visualization capabilities, this server makes it easy for researchers and clinicians to explore the impact of protein mutations and develop new insights into the underlying biology.

Easy to Use

Our web server is designed to be easy to use, even for those without a background in protein biology. The interface is user-friendly and intuitive, and the visualizations are designed to be accessible and informative. Whether you're a seasoned researcher or a curious student, our web server is the perfect tool for exploring the world of protein mutations.



Sequence difference

	50	51	52	53	54	55	56	57	58	59	60
Original	I	E	Q	W	F	T	E	D	P	G	P
Target	I	E	Q	W	F	A	E	D	P	G	P

Differences at amino acid level

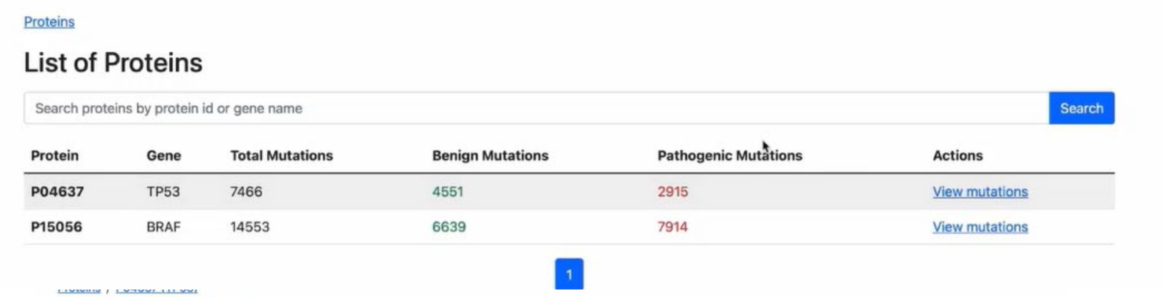
Feature	Original «T»	Target «A»
Name	Threonine (Thr)	Alanine (Ala)
Molecular Formula	$C_4H_9NO_3$	$C_3H_7NO_2$
Residue Formula	$C_4H_7NO_2$	C_3H_5NO
Molecular Weight	119.120	89.090 (-30.030)
Residue Weight	101.110	71.080 (-30.030)
Hydrophobicity index at pH 2	Neutral	Hydrophobic
Hydrophobicity index at pH 7	Neutral	Hydrophobic
Charge	Neutral	Neutral
Solutibility	Undetermined	15.800
Structure Image		
Description	Threonine (Thr) is within reactions in bacteria and metabolic rate in animals. However, the exact effect has not yet been determined.	Alanine (Ala) is the first hydrophobic amino acid, and it has low reactivity. This property allows for alanine to create an elongated structure that is equally flexible and stretch resistant.

Predicted structures comparison

About these 3D Structures: The 3D structure representations of both original and target sequences (trimmed to 400 residues, from 1 to 255) will be modeled using the ESM Metagenomic Atlas tools. ESM Metagenomic Atlas is a web-based tool for protein structure prediction that uses deep learning methods to predict protein folding and structure from protein sequences.

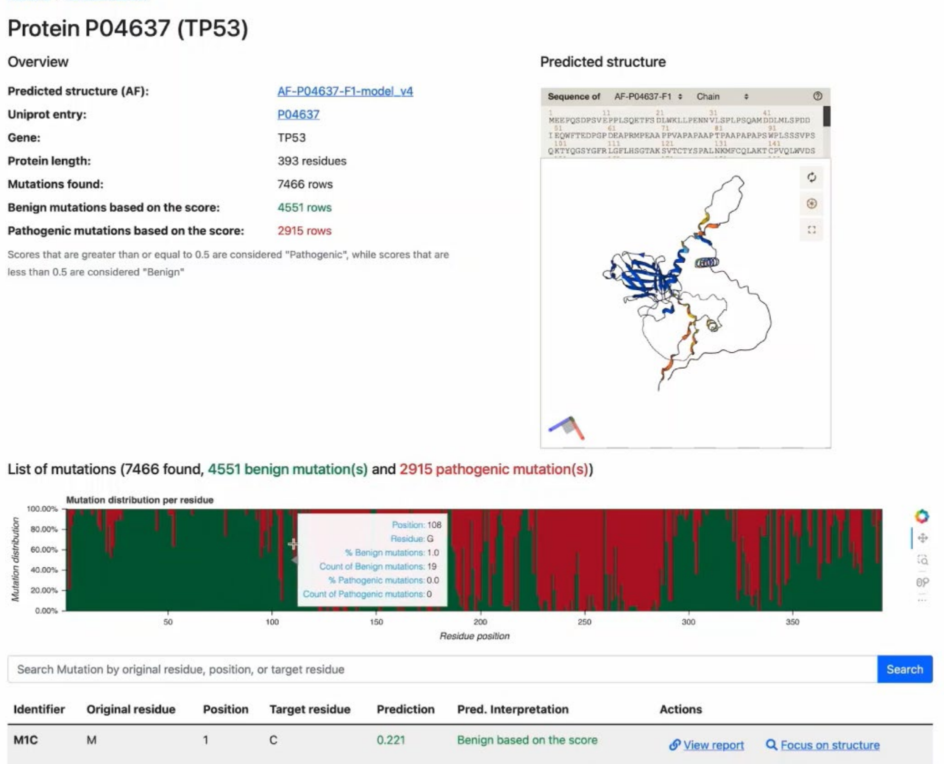
Differences at biophysical features

About these plots: These plots have been generated by using Bio2Byte predictors to plot both the original and target sequences.



List of Proteins

Protein	Gene	Total Mutations	Benign Mutations	Pathogenic Mutations	Actions
P04637	TP53	7466	4551	2915	View mutations
P15056	BRAF	14553	6639	7914	View mutations



Protein P04637 (TP53)

Overview

Predicted structure (AF): AF-P04637-F1-model_v4
Uniprot entry: P04637
Gene: TP53
Protein length: 393 residues
Mutations found: 7466 rows
Benign mutations based on the score: 4551 rows
Pathogenic mutations based on the score: 2915 rows

Scores that are greater than or equal to 0.5 are considered "Pathogenic", while scores that are less than 0.5 are considered "Benign"

Predicted structure

List of mutations (7466 found, 4551 benign mutation(s) and 2915 pathogenic mutation(s))

Identifier	Original residue	Position	Target residue	Prediction	Pred. Interpretation	Actions
M1C	M	1	C	0.221	Benign based on the score	View report Focus on structure

Digital Health Platform (DHP)

Collaboration with ICT UZB

Extract relevant data from different departments

Train stakeholders to understand the security/standardization procedures

Demo of AI-based tools

Glioma data analysis research platform

To connect image and genetic data interpretation pipelines

TUMOrSCOPE

Acknowledgements

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Wim Vranken
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Thank you for your Attention!

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