Characterisation on the pathogenic effect of the missense mutations of p53 via machine learning



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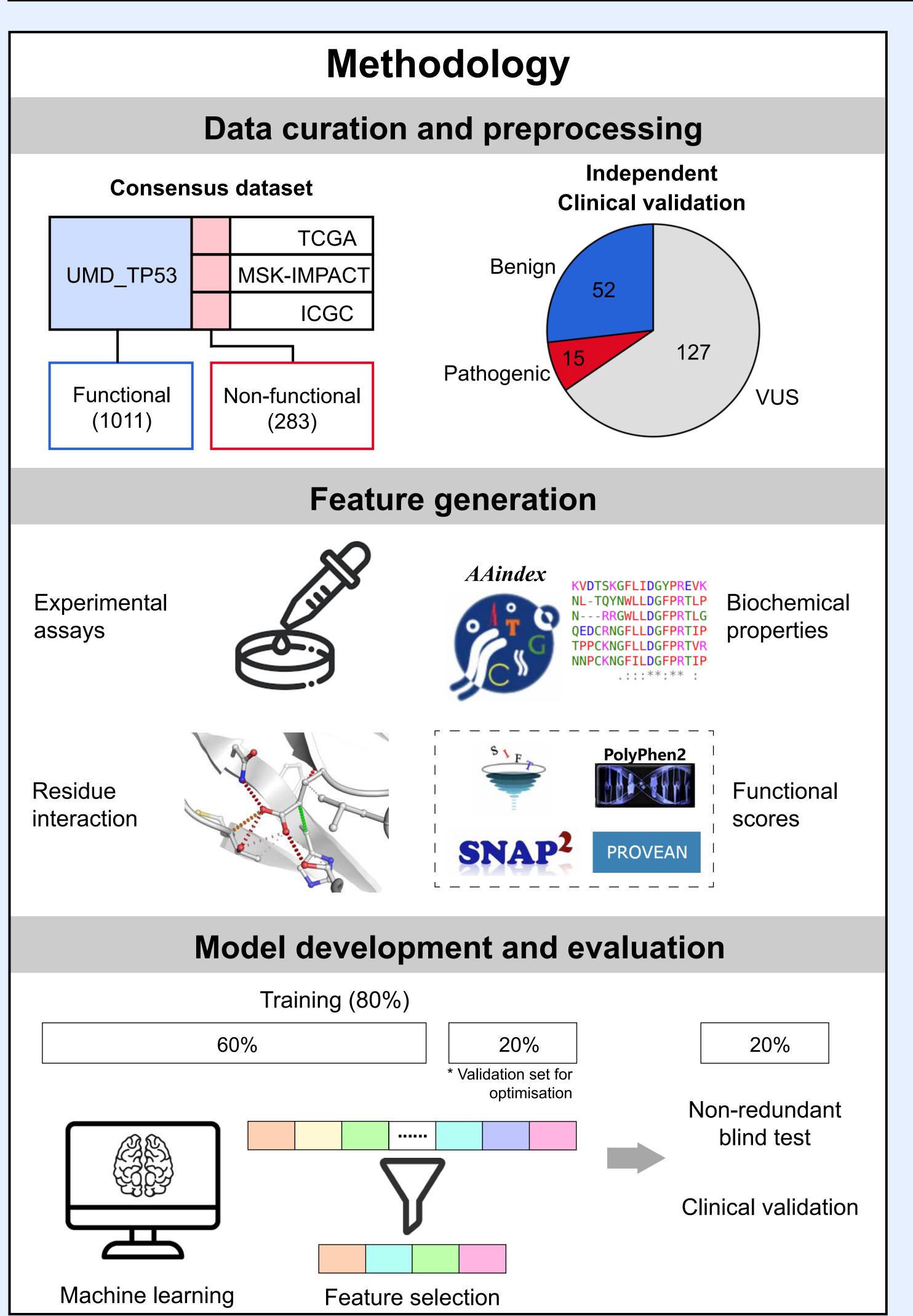
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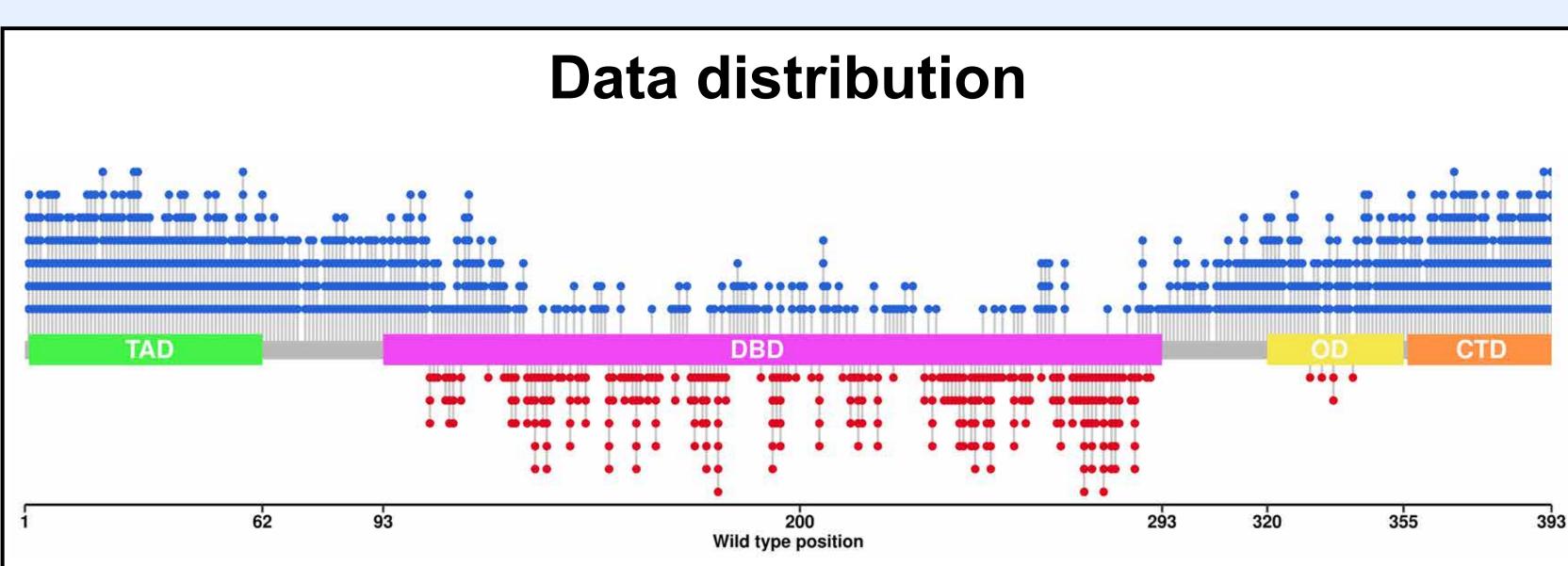


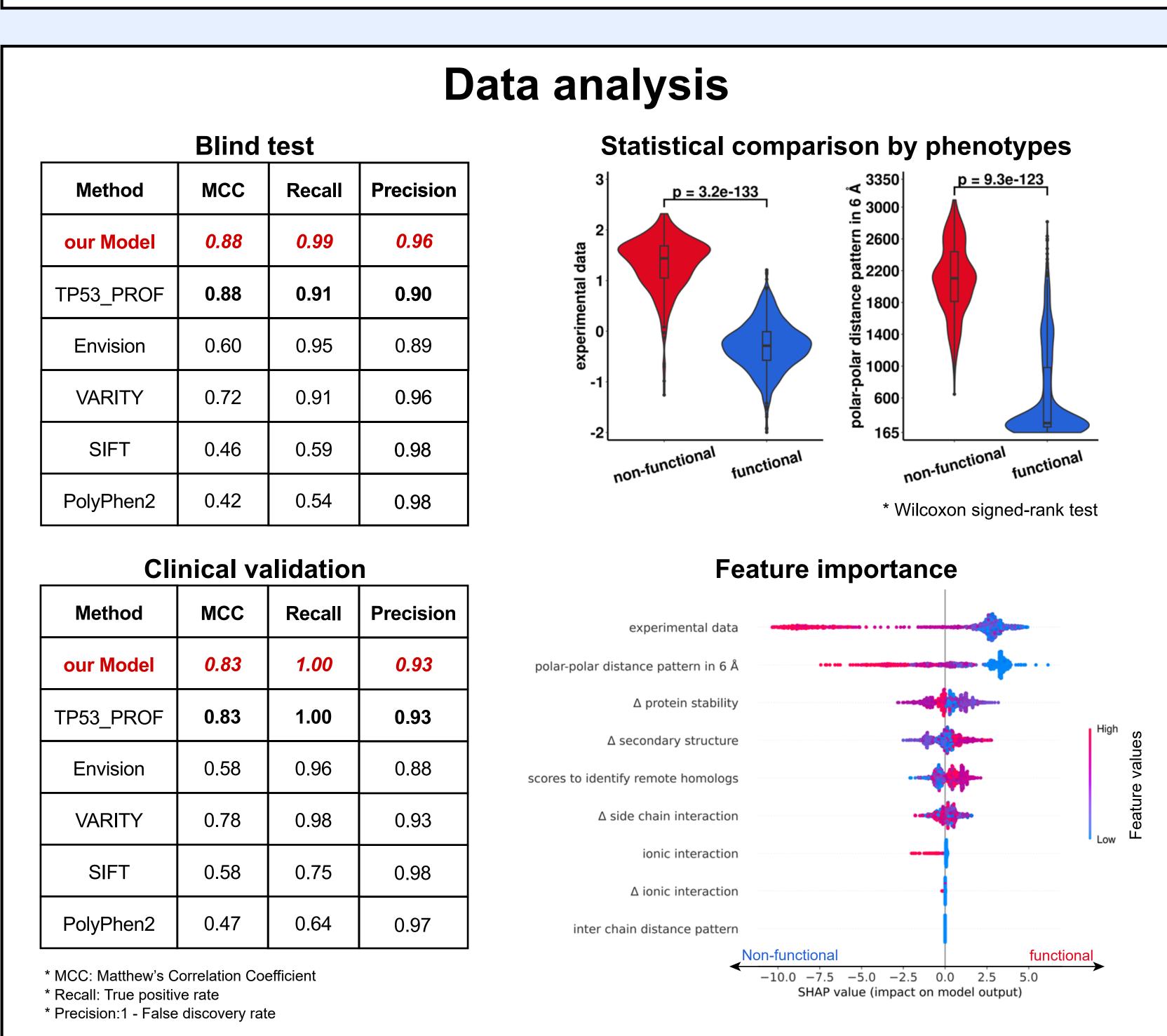
Background

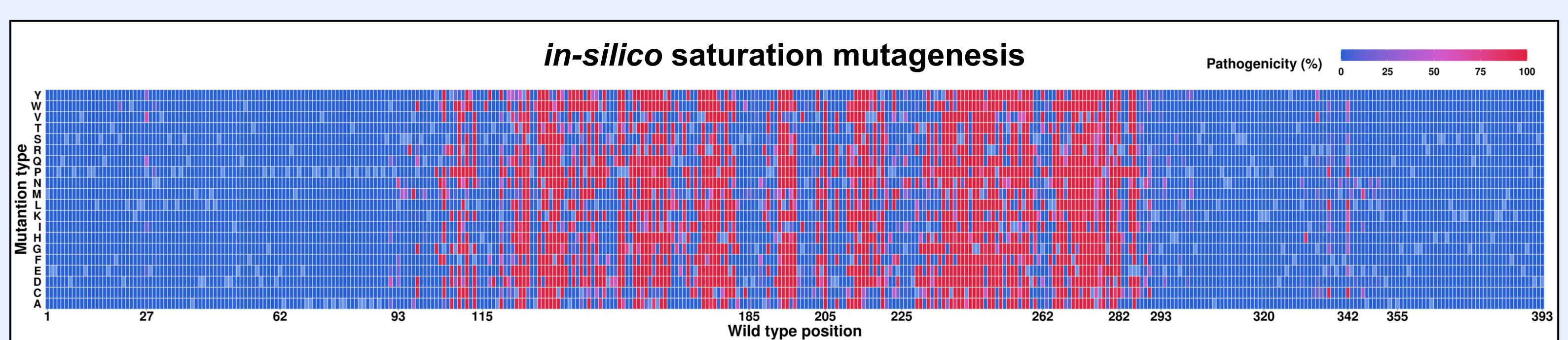
- Over 50% of cancers are associated with the missense mutations in tumour suppressor protein p53.
- p53 plays a crucial role in DNA damage-induced activation by repairing erroneous replication and activating cellular apotosis.
- It is time-consuming and labour intensive to experimentally elucidate all the possible effects of all missense variants.

Aim: we aimed to accurately identify deleterious missense mutations in p53 by leveraging computational biophysical tools and employing a machine learning analysis.









Conclusion

- Our structure-based model **accurately characterises** the oncogenic effects of **all possible missense mutations** in p53, with a comparable performance to state-of-the-art methods.
- Feature interpretation reveals that intact p53 function is strongly reliant on experimental residue activity, the number of polar residues within 6 Å, and the change of protein stability upon mutation.
- This work offers clinical diagnostic utility, which is crucial for patient monitoring, and the development of personalised cancer treatment.