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Random subsampling techniques for sea bass mortality prediction

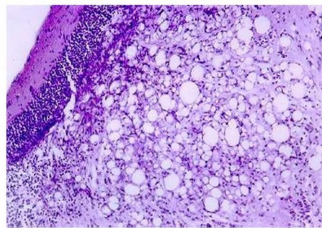
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- Motivation: Identifying impactful SNPs in sea bass mortality
- Dataset: Genomic SNP data, mortality outcomes, and annotations
- Method: Subsampling techniques with XGBoost
- Results: Accuracy/F1 vs. subsampling rate
- Conclusion: Subsampling preserves predictive power

Viral nervous necrosis (VNN) is a highly spread disease among sealife.

We concentrate our efforts on predicting the mortality of a population of **sea basses** affected by VNN.

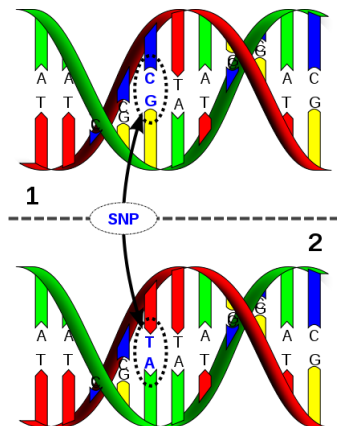


SNPs for predicting mortality



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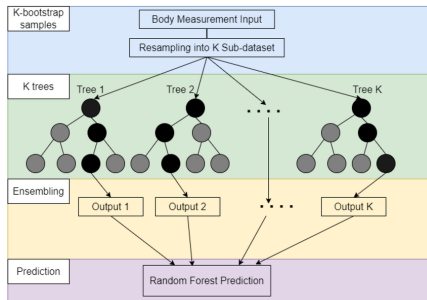
The **genome** might be useful to predict mortality.



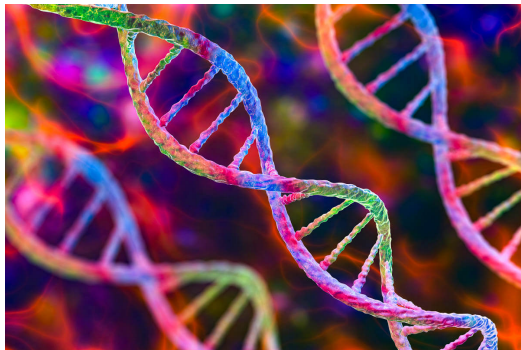
SNPs: Single nucleotide polymorphisms.

Predict if a sea bass will die by watching its genome: **Machine Learning**.

In particular, we use the **XGBoost** classifier.



- Each fish: over **6 million** SNP positions.
- Sample size: only **990** sea bass individuals.
- Traditional models may **overfit** due to high dimensionality.
- We mitigate through **subsampling**.



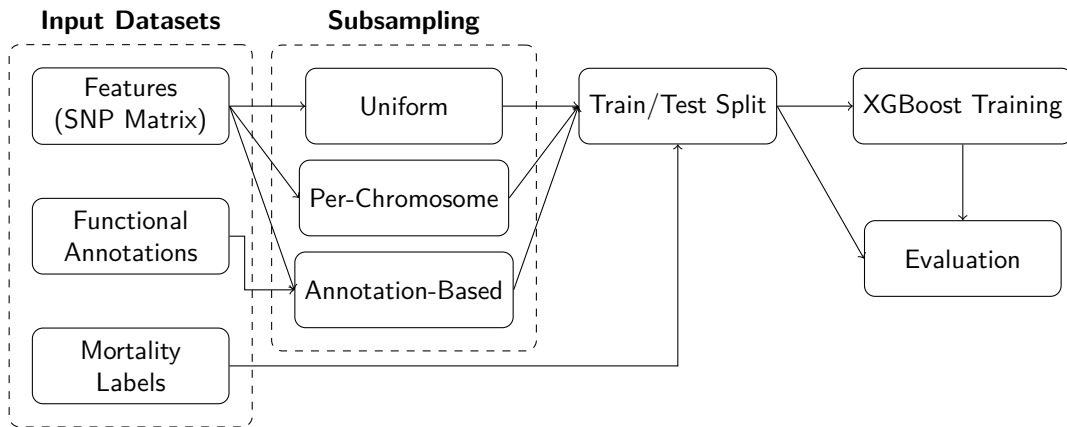


Figure: Pipeline of the model training after subsampling of the data

- 990 rows (fish), each with 6,072,853 SNP features.
- SNP values: 0 (no mutation), 1 (heterozygous), 2 (homozygous alt).
- Each fish is paired with a mortality label.

- Annotations include function: Promoter, Enhancer, Open Chromatin.
- Tissue number (0–25) indicates location-specific relevance.

- Randomly sample a fixed proportion p of all SNPs.
- Simple but may cause imbalance across chromosomes.

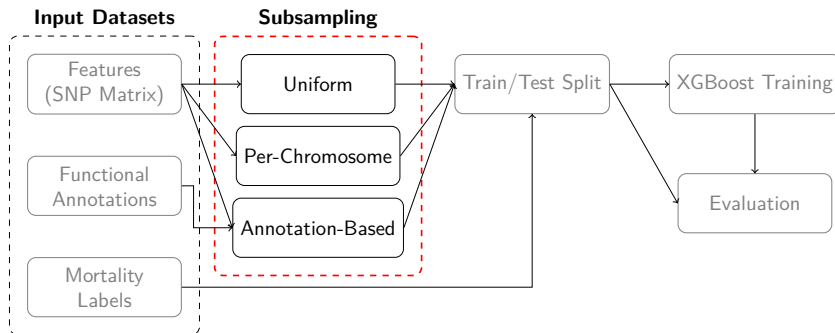
- Ensures balanced representation from each chromosome.
- Randomly sample same number of SNPs per chromosome.

- Filter SNPs by biological annotation.
- Then apply uniform subsampling to relevant regions.

- Trade-offs in simplicity, biological interpretability, and balance.
- Aim: maximize predictive power while reducing dimensionality.

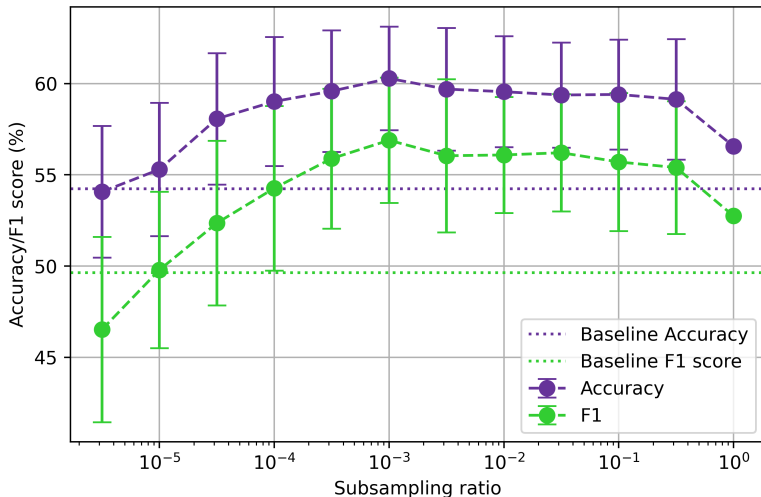
In order to limit the variance of results we impose:

- XGBoost random seed, train-test split fixed
- Subsampling is the only random component varying between experiments.

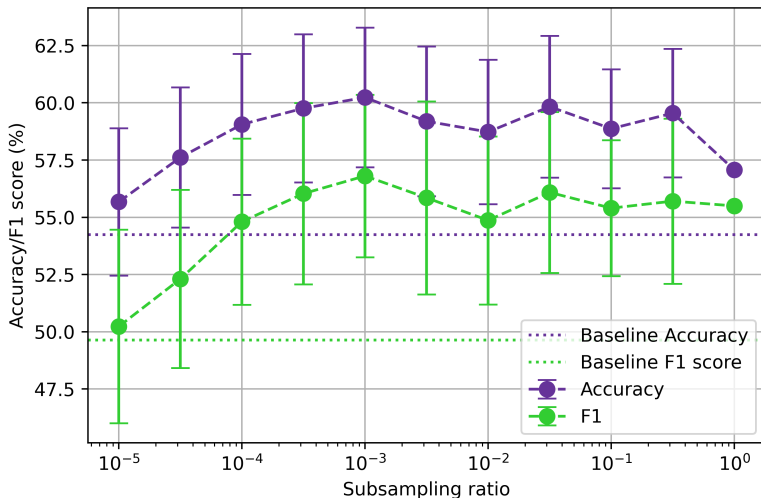


- Subsampled with multiple p values: log-spaced varying from the whole genome to few SNPs.
- Trained model for each combination of model and subsample rate.
- Multiple runs for each pair of parameters.
- Comparison with **baseline results** from a "dumb" classifier, always guessing the most common class.

Results: uniform subsampling



Results: uniform subsampling on each chromosome



Results: annotated subsampling (function)

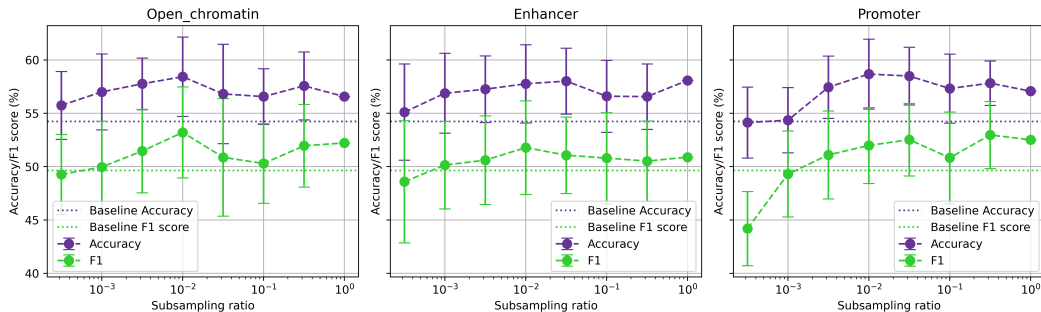


Figure: Plot of accuracy and F1 scores when subsampling uniformly on each chromosome.

Results: annotated subsampling (tissue number)

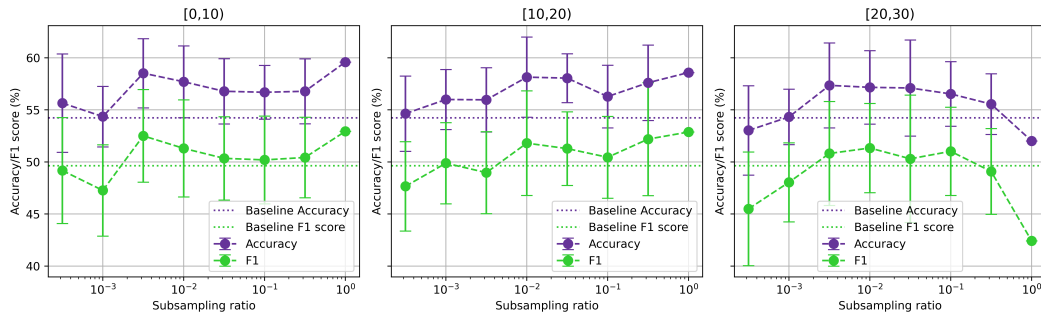
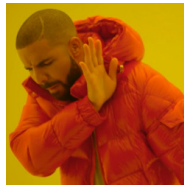


Figure: Plot of accuracy and F1 scores when subsampling uniformly on each chromosome.

- Random SNP subsampling retains model effectiveness.
- No strong trend between rate and accuracy (outside extremes): this may be good.
- There doesn't seem to be specific regions of the genome containing the information determining the disease effects.



The results don't show any meaningful trend



We showed that subsampling allows the use of more complex models

End



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Thank You