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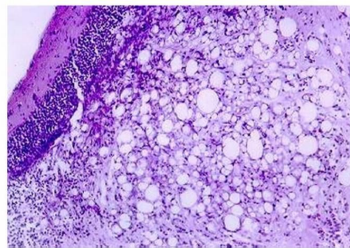
Random subsampling techniques for sea bass mortality prediction

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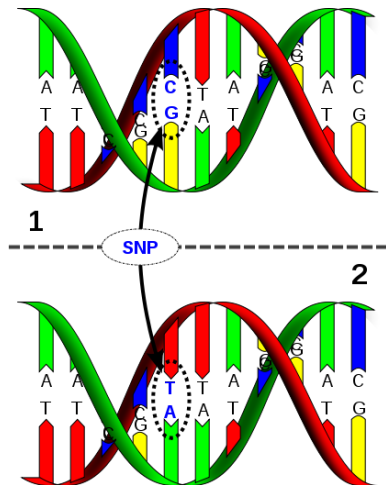
1. Introduction
2. Methodology
 - Datasets description
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 - Uniform subsampling
 - Uniform over chromosomes
 - Annotated subsampling
4. Conclusions

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



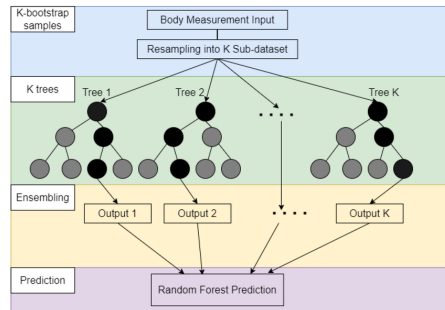
The **genome** might be useful to predict mortality.

SNPs: Single nucleotide polymorphisms.

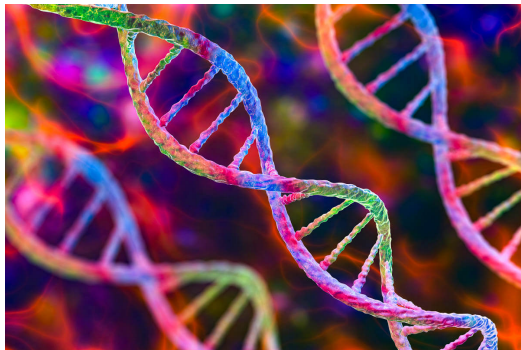
dmlc
XGBoost

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

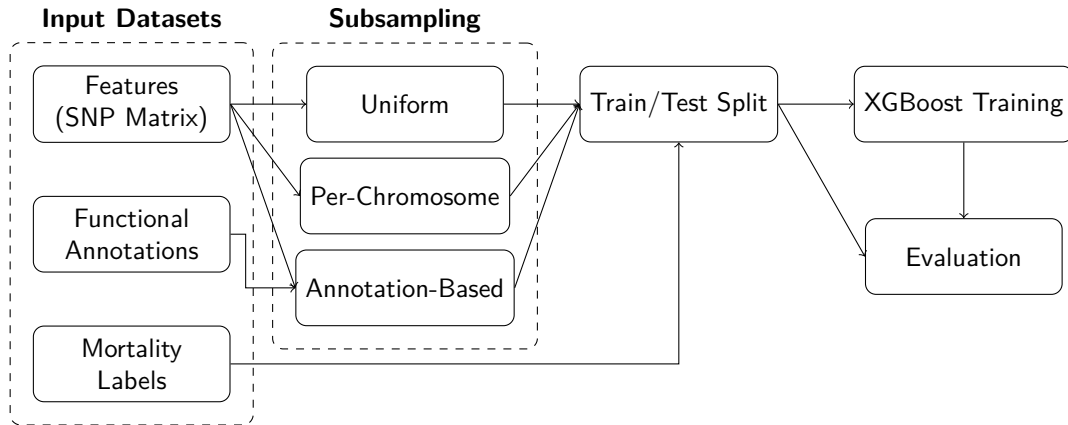
In particular, we use the **XGBoost** classifier.

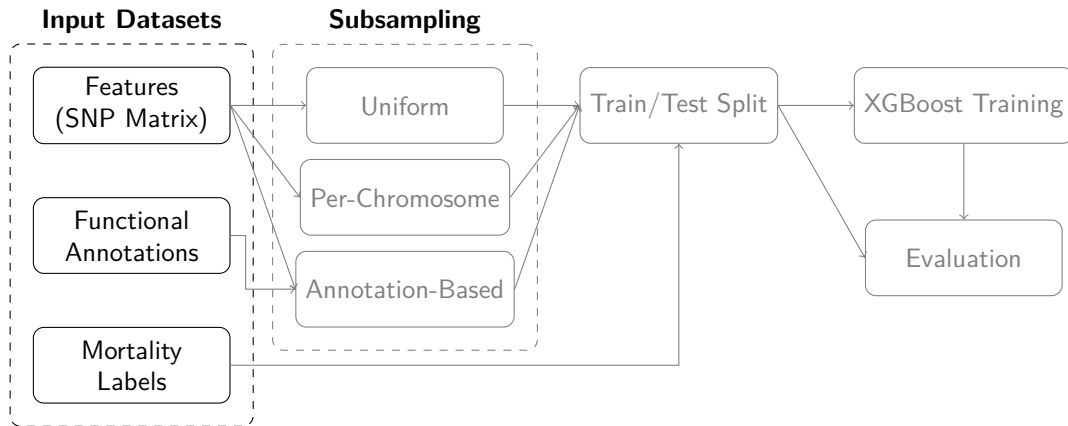


- Each fish: over **6 million** SNP positions.
- Sample size: only **990** sea bass individuals.
- Traditional models may **overfit** due to high dimensionality.
- We mitigate through **subsampling**.



Pipeline Overview





SNP Dataset Structure



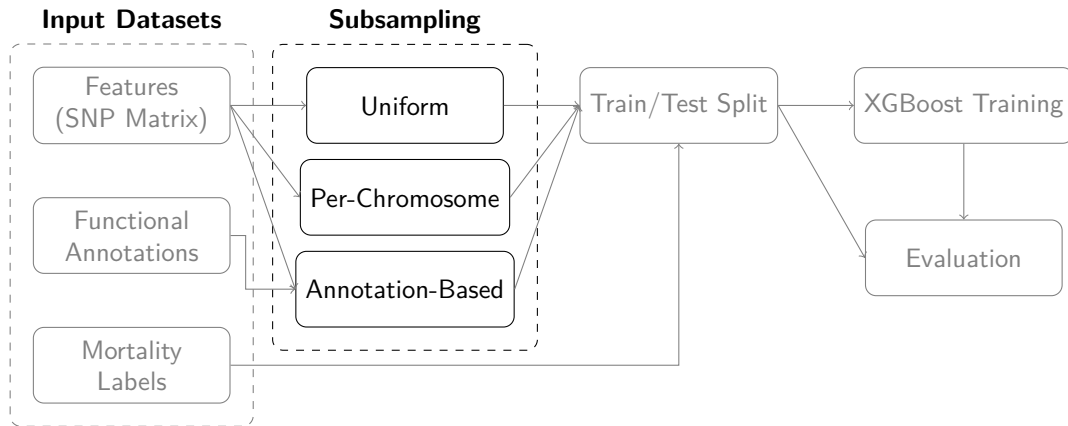
- 990 rows (fish), each with 6,072,853 SNP features.
- SNP values: 0 (no mutation), 1 (heterozygous), 2 (homozygous alt).
- Each fish is paired with a mortality label.

id	mortality
PL06-B12	1
PL06-B06	1
PL06-E06	1
PL08n-B05	0
PL08n-G09	0
⋮	⋮

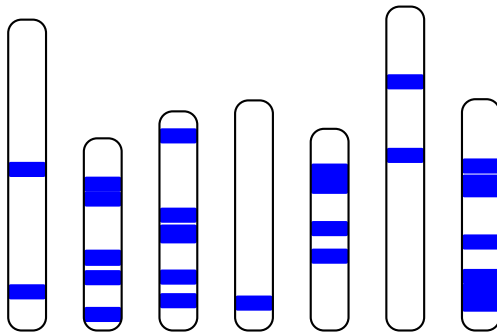
	CAJNNU010000001.1:299	CAJNNU010000001.1:903	CAJNNU010000001.1:986	...
PL04-A06	1	0	0	...
PL04-A08	0	0	1	...
PL04-A09	0	1	1	...
PL04-A10	0	0	0	...
PL04-A11	2	2	1	...
⋮	⋮	⋮	⋮	⋮

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

snp_id	funct	n_tissue
CAJNNU010000001.1:7825	Open_chromatin	10
CAJNNU010000001.1:7865	Open_chromatin	4
CAJNNU010000001.1:8046	Enhancer	21
CAJNNU010000001.1:8084	Open_chromatin	5
CAJNNU010000001.1:8116	Promoter	12
⋮	⋮	⋮



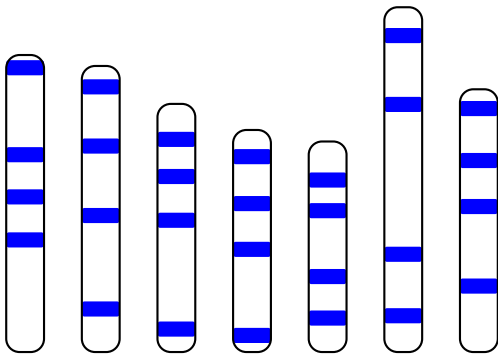
- Randomly sample a fixed proportion p of all SNPs.
- Simple but may cause imbalance across chromosomes.



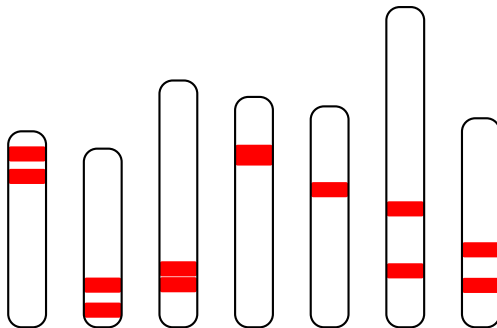
Per-Chromosome Subsampling

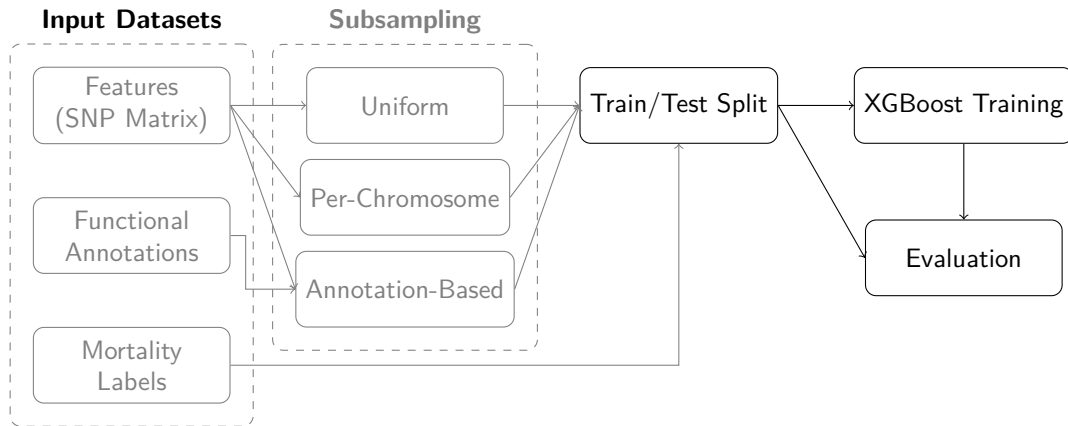


- Ensures balanced representation from each chromosome.
- Randomly sample same number of SNPs per chromosome.



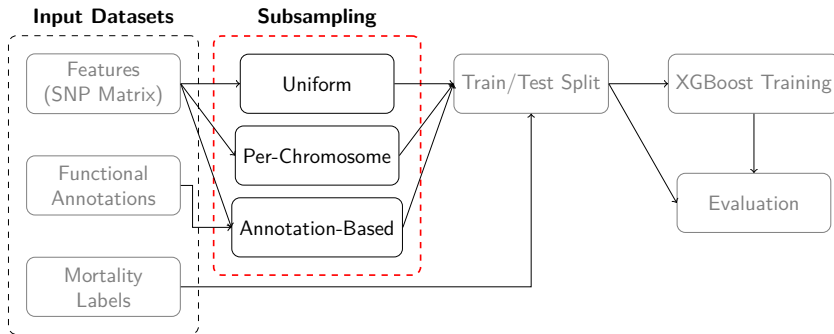
- Filter SNPs by biological annotation.
- Then apply uniform subsampling to relevant regions.





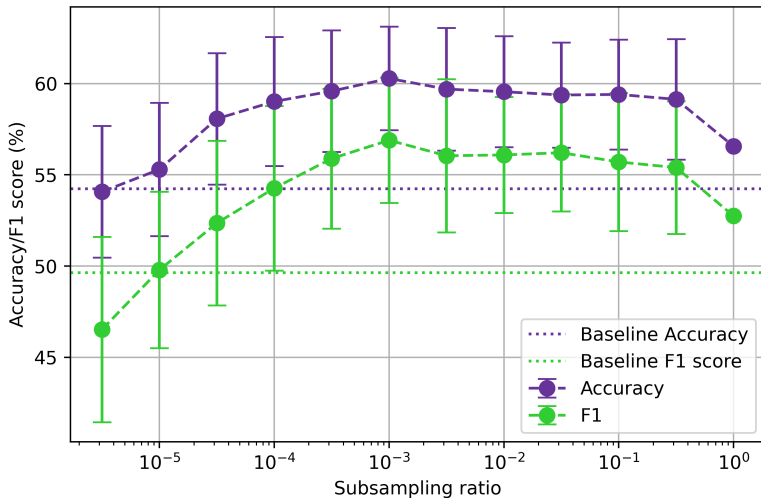
In order to limit the variance of results we impose:

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

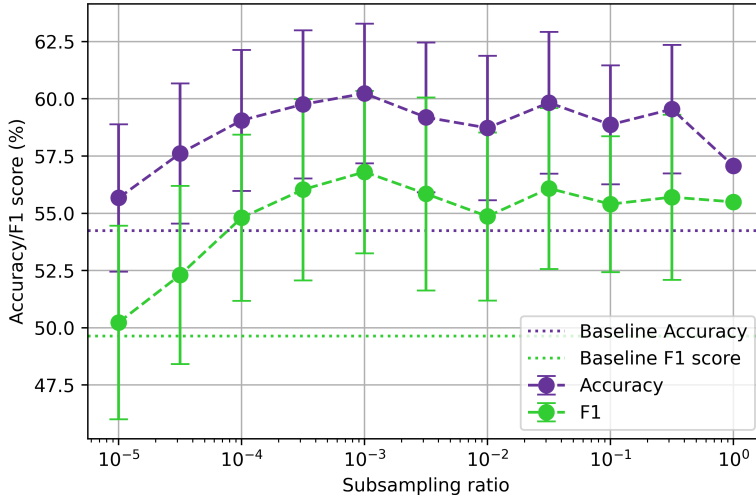


- Subsampled with multiple p values: log-spaced varying from the whole genome to few SNPs.
- Trained model for each combination of model and subsample rate.
- Multiple runs for each pair of parameters.
- Comparison with **baseline results** from a "dumb" classifier, always guessing the most common class.

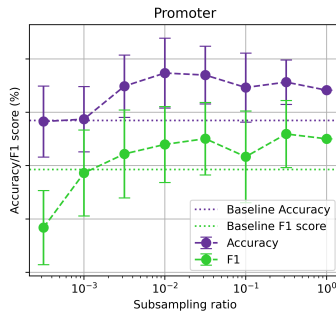
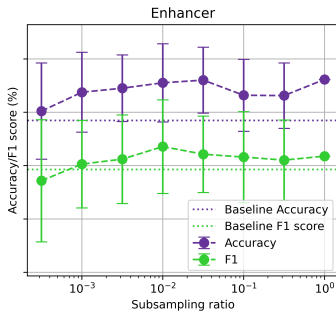
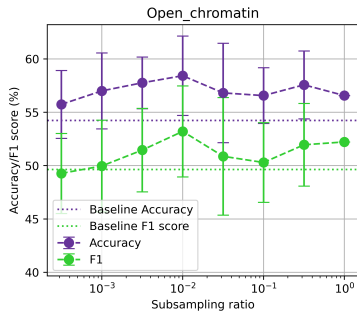
Results: uniform subsampling



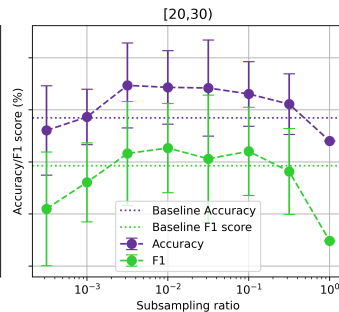
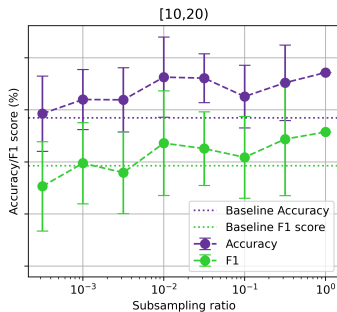
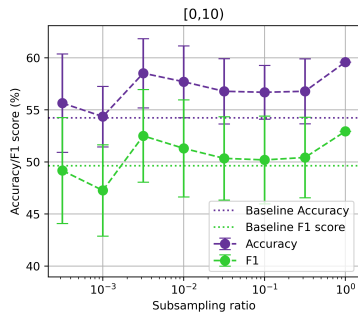
Results: uniform subsampling on each chromosome



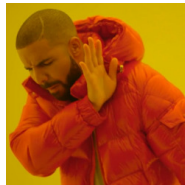
Results: annotated subsampling (function)



Results: annotated subsampling (tissue number)



- 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

Thank You!