

# MitoChime: A Machine Learning Pipeline for Detecting PCR-Induced Chimeras in Mitochondrial Illumina Reads

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# Outline

- 1 Introduction
- 2 Problem Statement & Proposed Solution
- 3 Objectives
- 4 Scope and Limitations
- 5 Methodology

## Next Generation Sequencing (NGS)



Source: Illumina, Inc. (n.d.). *iSeq 100 sequencing system* [Image]. Illumina. <https://bit.ly/4iTKQJD>

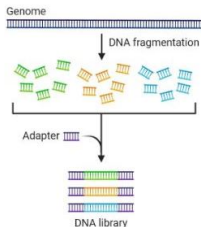


Source: University of the Philippines Visayas. (2022, January 21). *PGC Visayas makes unprecedented acquisition – first of its kind in country* [Image]. University of the Philippines Visayas. <http://bit.ly/44ZMdAN>

## Illumina Seq Workflow

### Step 1. Library Preparation

#### ① Library preparation



Source: Aryal, S. (2024, November 2). *Illumina sequencing steps* [Image]. Microbe Notes. <https://bit.ly/48TOJtu>

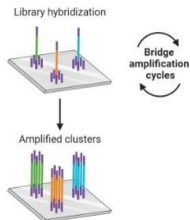


Source: Philippine Genome Center Visayas. (2025, July 23). *Inside internship life: BTS with PGCV interns* [Image]. Facebook. <https://bit.ly/4pC85dV>

## Illumina Seq Workflow

### Step 2. Library Bridge Amplification (PCR)

#### ② DNA library bridge amplification



Source: Aryal, S. (2024, November 2). *Illumina sequencing steps* [Image]. Microbe Notes. <https://bit.ly/48TOJtu>

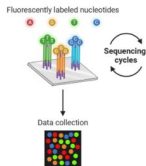


Source: Philippine Genome Center Visayas. (2025, July 23). *Inside internship life: BTS with PGCV interns* [Image]. Facebook. <https://bit.ly/4pC85dV>

# Illumina Seq Workflow

### Step 3. Sequencing and Alignment

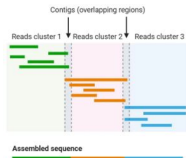
### ③ DNA library sequencing



@H5001123:45:H5TWLBGX:1:11101:12345:1000 1:N:0:ATCG  
GATTGGACTCCATGGTACCGTAATGCGTAGGTATCTATGCGTACCGTATG  
+  
AAAAAFFFFFJJ

Example of one short reads sequence from a FASTA file.

#### ④ Alignment and data analysis



```

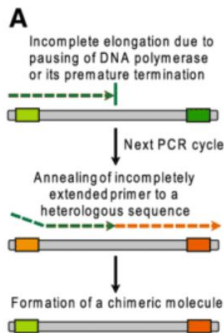
>assembled_mitochondrial_genome
GATCACAGGATCTATACCCATTATACCACTACGCGGAGCTCTCCATCGAT
TTGGTATTTTCGTCTGGGGGGATGACACGCGATAGCATCTCGAGACGCT
AGGCCCTCTAAACACAACAGGAGCAACTGATCATGATGACATTTGGCTCT
TAGGGTCAAGGTAGAGGAGACGCTGGTAGCTAGTAGGACTTGCCTCTGT
GGGCTATTCTCGACGACATATCTCTCAACCTGAGGCTAGTGCTATGAG
ACACTGANGCTCTACGATACGTCAGTCTTACCTGACGATGAGTATAGG
TCTCGTAGCTCGCTTCTAGTCAGTTAAGCTACAGCTTACCTCTACTCT

```

Example of an assemble mitochondrial genome sequence

Source: Aryal, S. (2024, November 2). Illumina sequencing steps [Image]. Microbe Notes. <https://bit.ly/48TO9tu>

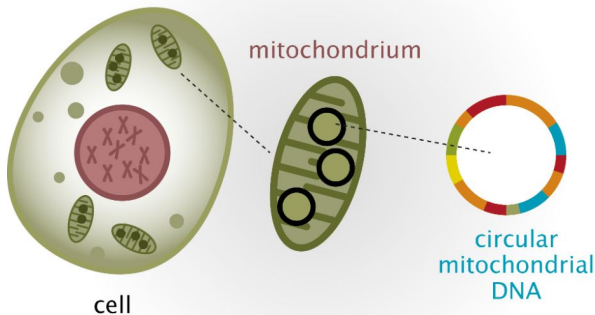
## PCR-Chimera Formation



Source: Omelina, E., Ivankin, A., Letiagina, A., & Pindyurin, A. (2019). *Optimized PCR conditions minimizing the formation of chimeric DNA molecules from MPRA plasmid libraries*. *BMC Genomics*, 20, 536.

<https://doi.org/10.1186/s12864-019-5847-2>

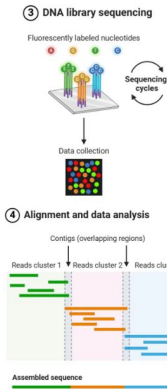
## The Mitochondrial Genome



Source: UZ Brussel. (2020, August 26). *Mitochondrial DNA* [Image]. Vrije Universiteit Brussel. <https://bit.ly/3XTTSg8>



## Disrupts Genome Assembly



```
@HS500123:45:HSTWLBXX:1:11101:12345:1000 1:N:0:ATCG  
GATTGGACTCCATGGTACCGTAATGCTAGGTATCTATGCGTAGCGGTATG  
  
+  
AAAAAFFFFFJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJJ
```

Example of one short reads sequence from a FASTA file.

assembled\_mitochondrial\_genome  
 GAT CACAGGCTAT CACCCTATTAACCAT CACGGGAGCTCTCCATCG  
 TCTGGATTCTGCTGGGGGTGTCACGCCGATGACCTCGAGACGCTG  
 AGCCCTCTCAACACCAACGAGGAAGATGATCATGATGATGATCTTGGCT  
 TAGGGTCAGGTAGAGAGACGCTGGTAGCTCAGTAGGACTTGCTCTGT  
 GGGCTATTCTACGACGGCAATCTCTCAACTGAGGCTAGTGCTCATGGA  
 ACATCGAGCTGACAGCTACTGCTTACCGTACCAAGTATGCGTATAGC  
 TCTCGTAGCTCGCTTCTAGCAAGTAGCTACCGTACCGTACCTCTACG

Example of an assemble mitochondrial genome sequence

Source: Aryal, S. (2024, November 2). Illumina sequencing steps [Image]. Microbe Notes. <https://bit.ly/48TOjtu>

**Table:** Comparison of Chimera Detection Approaches and Tools

Method / Tool	Core Approach	Key Limitations
<b>Reference-based Detection</b>	Compares each query sequence against curated databases of verified, non-chimeric sequences to identify mosaic similarity patterns.	Dependent on database completeness; poor performance for novel taxa or missing parents; limited sensitivity for low-divergence chimeras.
<b>De novo Detection</b>	Detects chimeras using internal dataset structure, abundance hierarchy, and compositional similarity without external references.	Assumes true sequences are more abundant; fails under amplification bias; unreliable when parents have similar abundance or high similarity.
<b>UCHIME</b>	Alignment-based method that partitions queries into segments, identifies parent candidates, and computes a chimera score via three-way alignment.	Reduced accuracy for very closely related parents ( $<0.8\%$ divergence); sensitive to incomplete references; de novo mode requires abundant parents.
<b>UCHIME2</b>	Enhanced UCHIME with improved benchmarking and sensitivity/specificity presets.	Fake models limit theoretical accuracy; genuine variants may resemble chimeras; not ideal as a

# Problem Statement & Proposed Solution

- **Problem Statement:** Chimeric sequencing reads can disrupt mitochondrial genome assembly, but current assembly pipelines assume artifact-free input and existing chimera detection tools are not designed specifically for organellar, particularly mitochondrial datasets, leaving assemblies vulnerable to undetected artifacts.
- **Proposed Solution:** A machine-learning pipeline designed to detect PCR-induced chimeric reads using both alignment-based and sequence-derived features to improve the quality and reliability of downstream mitochondrial genome assemblies.

# General Objective

- Develop and evaluate a machine-learning pipeline (MitoChime) to detect PCR-induced chimeric reads in *S. lemuru* mitochondrial sequencing data to improve downstream assembly quality.

# Specific Objectives

- 1 Construct simulated *Sardinella lemuru* Illumina paired-end datasets containing both clean and PCR-induced chimeric reads.
- 2 Extract alignment-based and sequence-based features such as k-mer composition, microhomology, and split-alignment counts from both clean and chimeric reads
- 3 Train, validate, and compare supervised machine learning models for classifying reads as clean or chimeric.
- 4 Determine feature importance and identify indicators of PCR-induced chimerism.
- 5 Integrate the optimized classifier into a modular and interpretable pipeline deployable on standard computing environments at PGC Visayas.

# Scope of the Study

- Focuses on PCR-induced chimeric reads in *Sardinella lemuru* mitochondrial sequencing data to:
  - to limit interspecific variation in mitochondrial genome size, GC content, and repetitive regions so that differences in read patterns can be attributed more directly to PCR-induced chimerism
  - to align the analysis with relevant *S. lemuru* sequencing projects at PGC Visayas
  - to take advantage of the availability of *S. lemuru* mitochondrial assemblies and raw datasets in public repositories such as the National Center for Biotechnology Information (NCBI), which facilitates reference selection and benchmarking
  - to develop a tool that directly supports local studies on *S. lemuru* population structure and fisheries management produce tools applicable to local population and fisheries studies

# Scope of the Study

- Uses wgsim-based simulations and selected empirical mitochondrial datasets
- Analysis targets low-dimensional alignment and sequence features (k-mers, GC content, clipping, split alignments) to maintain interpretability and computational accessibility
- Long-read platforms and other taxa are not included

# Key Exclusions

- Naturally occurring chimeras
- NUMTs
- Large-scale nuclear genome rearrangements
- High-dimensional deep learning embeddings



# Other Limitations

- No simulations with variable sequencing error rates
- No testing of alternative parameter settings (k-mer length, microhomology windows)
- Reliance on supervised machine learning may limit detection of novel/unknown chimeric patterns

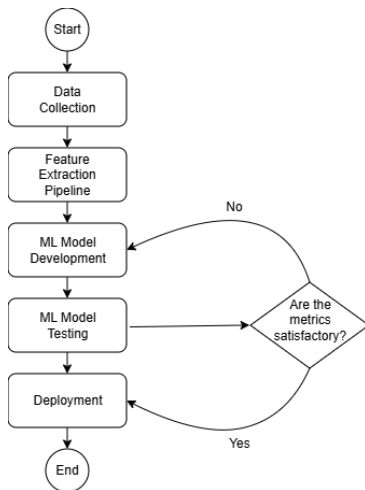


Figure: Process Diagram of the Special Project

The *S. lemur* mitochondrial reference genome (NCBI: NC\_039553.1) was downloaded in FASTA format and used as the basis for generating simulated reads.

# Data Preprocessing

- A Python script was used to generate the reads.
- Clean reads were produced with wgsim from the reference genome with error rate set to 5%.
- A chimeric reference was created by creating a custom script to combine non-adjacent segments with microhomology
- Chimeric reads were simulated with wgsim.
- All reads were mapped with minimap2 to extract alignment information.
- SAM/BAM files were converted, sorted, and indexed with samtools.

- Final dataset: 40k reads, roughly balanced between clean and chimeric (19,984 clean reads and 20,000 chimeric).
- Some of the clean reads failed to align due to the set error rate.

# Data Preprocessing

```
NC_039553.1_3_540_8:0:0_6:0:0_ef2      163      NC_039553.1      3      60      150M
TGGTGTAGCTTAAACAAAGCATAAACTGAAGATGTTACGATGGGCCGTGATAAGCCCCACACGCACTGAAAGGTTT
.....
AS:i:220      nn:i:0      tp:A:P      cm:i:8      s1:i:164      s2:i:0      de:f:0.0533
NC_039553.1_4_430_13:0:0_11:0:0_243d      163      NC_039553.1      4      60      150M
GGTGTAGCTTAAACAAAGCATAAACTGCAGATGATCCGCTGGGCCGTGATAAGCCGCAGCAGGAGTGAAAGTTTTG
.....
AS:i:170      nn:i:0      tp:A:P      cm:i:9      s1:i:135      s2:i:0      de:f:0.0867
```

Figure: SAM File of Clean Reads

# Data Preprocessing

```
era_1_A9831-10051_B14983-15061_MH0_105028_105471_0:0:0_0:0:0_e2e 2129 NC_039553.1
ATCACCCACTTGACAAGCCCCACCGCCTGTACAATTGCCGTTACAGCTCTAGCACTCA IIIIIIIIIIIIIIIIIIIIIII
ms:i:116 AS:i:116 nn:i:0 tp:A:P cm:i:10 s1:i:55 s2:i:0 de:f:0 SA:Z
era_1_A9831-10051_B14983-15061_MH0_105008_105480_0:0:0_0:0:0_e5a 2193 NC_039553.1
ATCACCCACTTGACAAGCCCCACCGCCTGTACAATTGCCGTTACAGCTCTAGCACTCAAGATTGGCC
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII NM:i:0 ms:i
cm:i:11 s1:i:57 s2:i:0 de:f:0 SA:Z:NC_039553.1,98,-,87M63S,60,0; rl:i:0
```

Figure: SAM File of Chimeric Reads

# Feature Extraction Pipeline

- BAM files were processed with a Python script (`extract_features.py`) to build a TSV feature matrix.
- Used Pysam for parsing alignments and NumPy for computation.



# Feature Extraction Pipeline

- Focused on three features linked to PCR-induced chimeras:
  - ① **Supplementary Alignment (SA)**: Detects split alignments; counts and metrics extracted from SA tags
  - ② **K-mer Composition Difference**: Breakpoints inferred; left/right segments compared using cosine and JS metrics.
  - ③ **Microhomology**: Overlap at junction quantified (length + GC content) within a defined window.
- Pipeline design and outputs to be validated by experts.

# Feature Extraction Pipeline

read_id	label	read_length	mean_base	ref_name	ref_start_1	strand	mapq	cigar	has_sa	sa_count	num_seg	sa_diff_cor
NC_03955	0	150	13	NC_03955	3	0	60	150M	0	0	1	0
NC_03955	0	150	13	NC_03955	4	0	60	150M	0	0	1	0
NC_03955	0	150	13	NC_03955	5	0	60	150M	0	0	1	0
NC_03955	0	150	13	NC_03955	6	0	60	150M	0	0	1	0
NC_03955	0	150	13	NC_03955	9	0	60	150M	0	0	1	0

Figure: TSV Dataset showing Clean Reads

# Feature Extraction Pipeline

read_id	label	read_len	mean_b	ref_name	ref_start	strand	mapq	cigar	has_sa	sa_count	num_seg	sa_diff
chimera_1	1	150	40	NC_03955	40	1	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	53	0	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	65	0	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	65	0	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	67	0	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	67	1	60	118M32S	1	1	2	0
chimera_1	1	150	40	NC_03955	69	1	60	150M	0	0	1	0
chimera_1	1	150	40	NC_03955	76	0	60	109M41S	1	1	2	0

Figure: TSV Dataset showing Chimeric Reads

# Dataset construction and split

- Simulated feature tables:
  - Clean reads (label 0)
  - PCR-induced chimeras (label 1)
- `build_datasets.py`:
  - Concatenate tables
  - Shuffle rows (avoid file-order artefacts)
- 80/20 **stratified** train-test split
- Test set held out and used **only once** at the end

# Validation strategy

- Layer 1: 80/20 stratified train–test split
- Layer 2: 5-fold stratified cross-validation on training set
  - Train on 4 folds, validate on 1
  - Rotate so each fold is validation once
- Layer 3: Final evaluation on held-out test set
- Hyperparameter tuning:
  - RandomizedSearchCV inside CV for top models
- Goal: stable estimates and **unbiased** test performance

# Model zoo and preprocessing pipeline

- **Baseline:** dummy majority-class classifier
- **Linear models:** logistic regression, calibrated linear SVM
- **Tree ensembles:**
  - Random Forest, Extra Trees
  - Gradient Boosting, XGBoost, LightGBM, CatBoost
- **Others:** bagging trees, k-NN, Gaussian NB, shallow MLP
- Common scikit-learn pipeline:
  - Median imputation (numeric missing values)
  - Standardisation (zero mean, unit variance)
- Ensures a **fair comparison** across models

# Effect of hyperparameter tuning

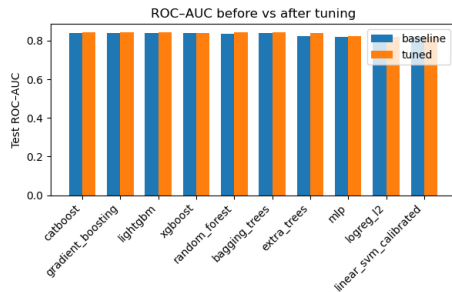
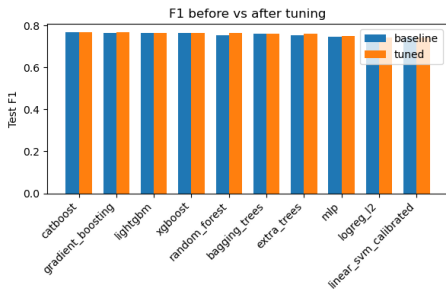
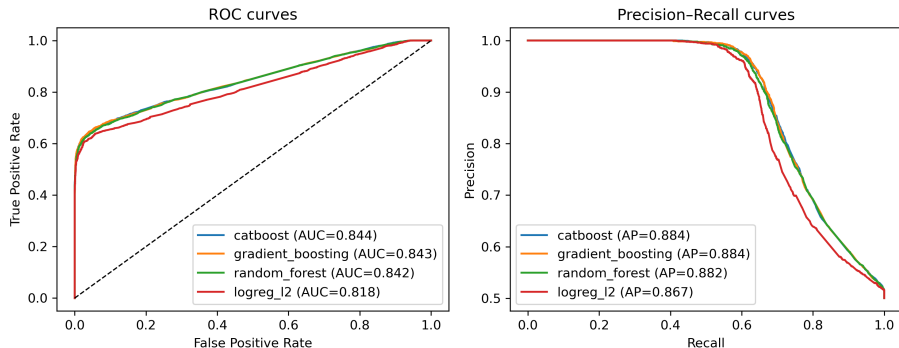


Figure: Test F1: baseline vs tuned.

Figure: Test ROC-AUC: baseline vs tuned.

- Tuning done with RandomizedSearchCV on training set
- Small but consistent gains ( $\Delta F1$ ,  $\Delta AUC \approx 0.001-0.01$ )
- Top-ranked models remain the same (CatBoost, Gradient Boosting, LightGBM)

# ROC and precision–recall curves



**Figure:** ROC (left) and PR (right) curves for CatBoost, Gradient Boosting, Random Forest, and logistic regression.

- Ensembles: ROC–AUC  $\approx 0.84$ ; logreg:  $\approx 0.82$
- Average precision  $\approx 0.88$  for ensembles
- Precision  $> 0.9$  up to recall  $\approx 0.5$ – $0.6$



# Confusion matrix: CatBoost (test set)

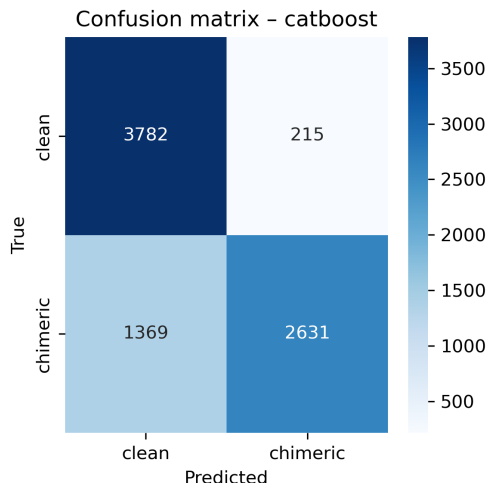
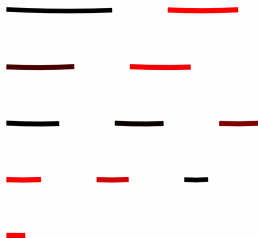
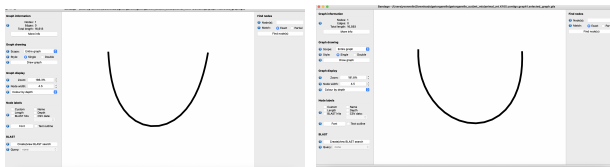


Figure: Confusion matrix heatmap for CatBoost.

- Clean reads (*negative class*):
  - Specificity  $\approx 0.95$  ( $TN = 3782 / 3997$ )
  - False positive rate  $\approx 0.05$  ( $FP = 215 / 3997$ )
- Chimeric reads (*positive class*):
  - Precision  $\approx 0.92$  ( $TP = 2631 / (2631 + 215)$ )
  - Recall  $\approx 0.66$  ( $TP = 2631 / 4000$ )
- Behaviour at default threshold:
  - **Conservative chimera filter:** low FP, higher FN
  - Misses  $\sim 34\%$  of chimeras ( $FN = 1369 / 4000$ )

# Downstream impact of residual chimeras (GetOrganelle)



- **Clean:** 1 contig (16,613 bp)
- **Mixed 50%:** 1 contig (16,593 bp)
- **Chimera-only:** 11 contigs ( $\sim 39.7\%$  mapped)
- **Implication:** missed chimeras can degrade assembly completeness/contiguity.

Figure: Clean, 50% mixed, and chimera-only assemblies.

# Top features for CatBoost

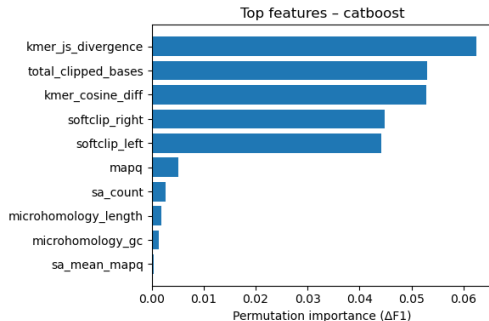
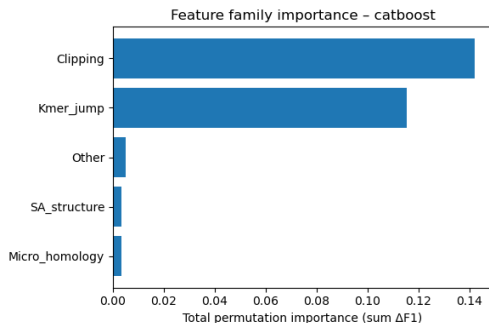


Figure: Permutation importance ( $\Delta F1$ ) for CatBoost.

- Strongest predictive signals:
  - kmer\_js\_divergence (within-read composition shift)
  - total\_clipped\_bases (junction-like clipping)
  - kmer\_cosine\_diff (windowed k-mer change)
- Also informative:
  - Left/right soft-clipping
  - Mapping quality (MAPQ)
  - SA count (supplementary alignments)
- Consistent with PCR chimera breakpoints and split mappings

# Feature family importance



**Figure:** Aggregated permutation importance by feature family (CatBoost).

- Aggregated importance:
  - **Clipping** features dominate
  - **K-mer jump** features are also strong
- Smaller contributions:
  - SA structure
  - Micro-homology
  - Other alignment context
- Similar ranking observed for Gradient Boosting and Random Forest

# Summary of findings

- Tree-based ensembles (CatBoost, Gradient Boosting, LightGBM) outperform linear baselines.
- Best performance on held-out reads:
  - $F1 \approx 0.77$
  - $ROC-AUC \approx 0.84$
- Most predictive signals match chimera junction patterns:
  - within-read k-mer composition shifts (*k-mer jump*)
  - extensive soft-clipping / clipped bases
- At the default threshold, CatBoost is **conservative**:
  - specificity  $\approx 0.95$  (keeps clean reads)
  - recall  $\approx 0.66$  (misses some chimeras)

# Next steps

- **Error analysis:** characterize FP vs FN cases (focus on false negatives).
- **Calibration:** adjust threshold / use cost-sensitive objective to increase recall while controlling FP.
- **Biological validation:** compare assemblies before vs after filtering (contig count, length, coverage).
- **Exploratory extension:** sequence models (CNN / Transformer / RNN) for subtle breakpoint patterns.

# Thank you!