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# Mitigating Feature Bias in DL Models for Cervical Cytology

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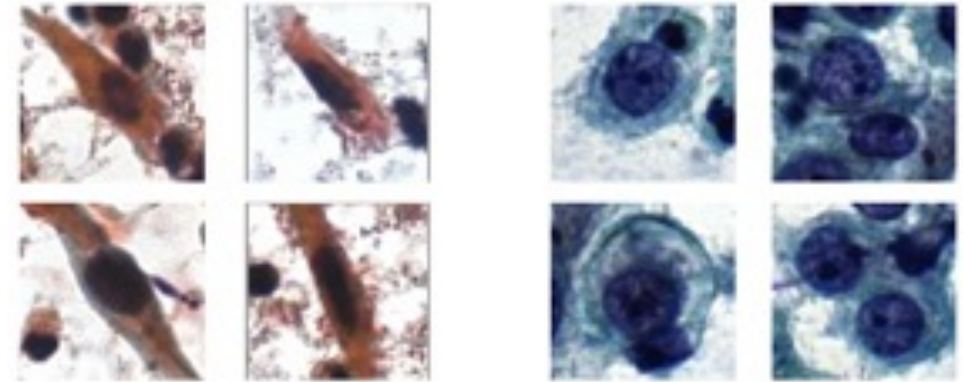
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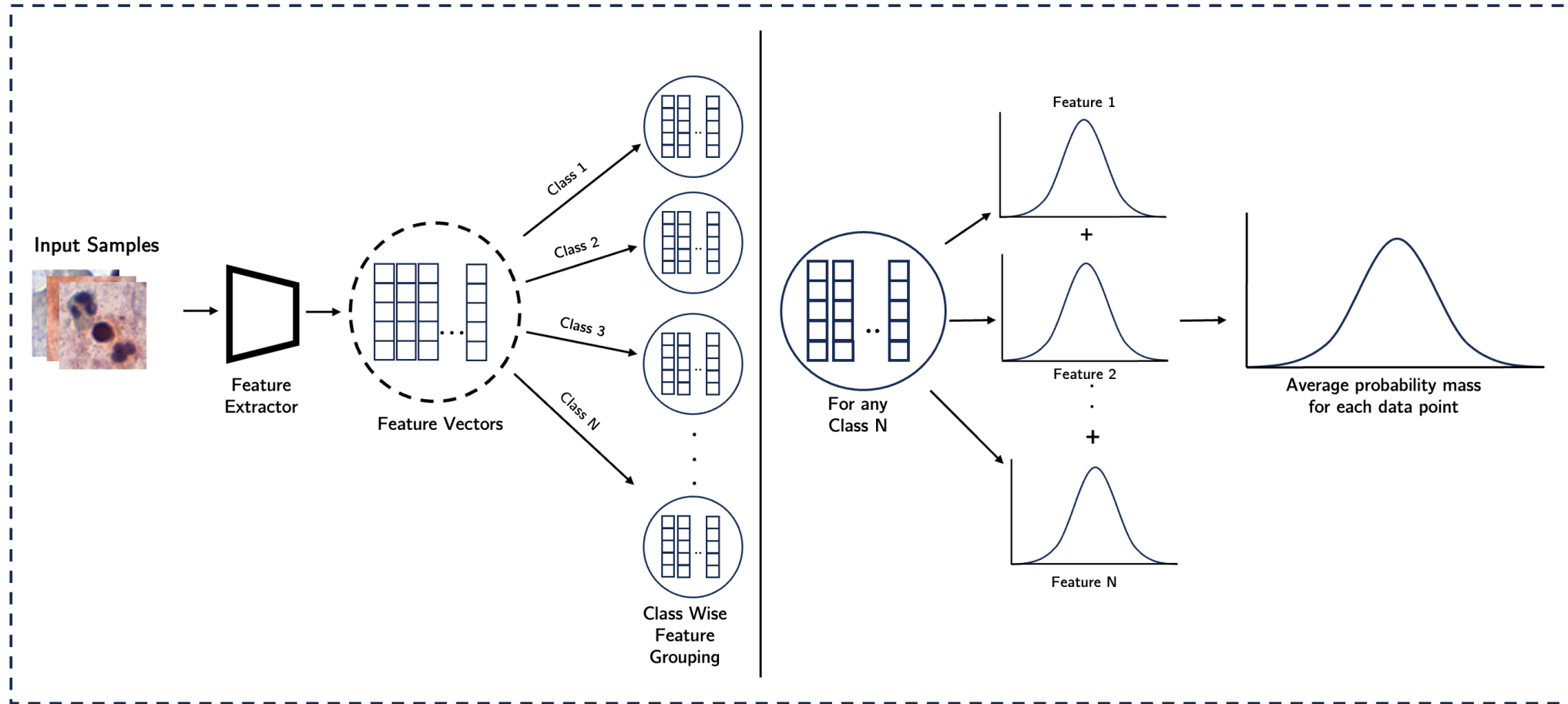
# Motivation

- Clinical datasets often contain inherent feature biases can hinder the practical deployment of these DL models.
- Feature Bias refers to uneven representation of features within same class, leading to inconsistent model performance.
- We introduce an sampling-based feature-bias mitigation method to reduce model skewness and improve performance across feature cohorts.



Sample Images of various features in Squamous Cell Carcinoma (SCC) class

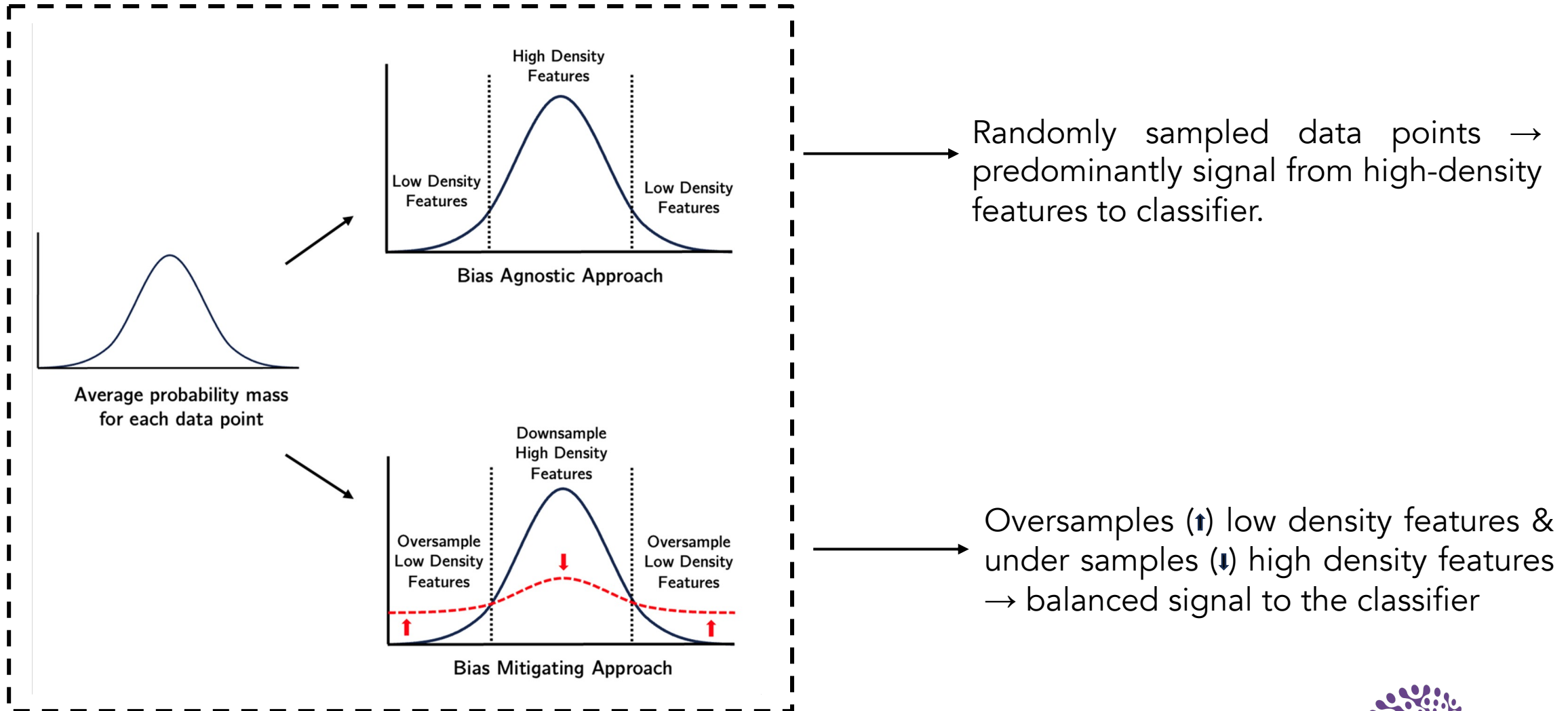
# Our Approach



- Common Workflow for Bias Agnostic & Bias Mitigating Approach :

Feature Extraction & Segregation -> Probability Distribution Computation  
-> Avg. Probability Mass Calculation -> Data Pt Categorization

# Our Approach



Bias Agnostic vs Bias Mitigating Approach

# Methodology

- Setup: We compare this bias mitigation method to a common bias agnostic approach and compare their effectiveness.
- Performance Metric : AUC with 5-Fold Validation
- Model Used: DieT
- Datasets: CRIC cervical cell classification dataset

# Results

	Low Density Cohort (in %)	High Density Cohort (in %)
<b>Bias-Agnostic</b>	$73.89_{\pm 0.33}$	$78.97_{\pm 0.32}$
<b>Bias-Mitigating</b>	$77.38_{\pm 0.59}$	$78.73_{\pm 0.77}$

- Bias-Agnostic approach yields an AUC difference of 5.08% between the two cohorts representing a 73.42% reduction in the AUC difference compared to the Bias-Agnostic approach.

# Summary

1. Feature Bias mitigation is important for medical settings.
2. An effective bias-mitigating approach **reduces the skewness in the model performance** across various feature cohorts.
3. Our bias mitigation approach can mitigates performance gaps between density cohorts, **leading to equitable and robust outcomes in medical applications.**