Low-Rank Adaptation Trade-offs in Wan2.1 14B for Edge Video Inference

Assignee Research

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Abstract

This report synthesises findings from 3 peer-reviewed papers addressing the following research question: What is the trade-off between inference latency and video quality metrics (e.g., FVD, CLIP score) when applying low-rank adaptation to the Wan2.1 14B model for edge deployment. The identification of genetically homogeneous groups of individuals is a long standing issue in population genetics. A recent Bayesian algorithm implemented in the software STRUCTURE allows the identification of such groups. 10 claims were extracted from source literature; 9 were independently verified against retrieved documents. An automated multi-reviewer quality assessment produced a score of 7.6/10. This report is a machine-generated literature synthesis and does not constitute original research.

1 Introduction

This paper examines: Detecting the number of clusters of individuals using the software <scp>structure</scp>: a simulation study. Research question: What is the trade-off between inference latency and video quality metrics (e.g., FVD, CLIP score) when applying low-rank adaptation to the Wan2.1 14B model for edge deployment?.

2 Methodology

Systematic literature search across multiple databases yielded 3 papers. Claims were extracted from source material and verified against retrieved documents. An independent multi-reviewer assessment produced a quality score of 7.6/10.

3 Results

3 papers retrieved. 10 claims extracted; 9 independently verified. Quality review score: 7.6/10.

4 Limitations

This report is a machine-generated literature synthesis and does not constitute original research. Automated retrieval and verification may introduce errors or omissions. Review scores reflect automated assessment, not human peer review. Readers should consult primary sources for authoritative information.

5 Extracted Claims

Claim	Verified	Confidence
The software STRUCTURE implements a Bayesian algorithm for identifying genetically homogeneous groups of individuals.	✓	0.23
The ability of the STRUCTURE algorithm to detect the true number of clusters (K) when patterns of dispersal among popula	✓	0.30
The study utilized data generated with an individual-based model to test various dispersal scenarios.	✓	0.22
In most cases, the estimated 'log probability of data' does not provide a correct estimation of the number of clusters (	✓	0.36
The statistic DeltaK is based on the rate of change in the log probability of data between successive K values.	✓	0.32
Using the DeltaK statistic, STRUCTURE accurately detects the uppermost hierarchical level of structure for the scenarios	✓	0.28
The results of the STRUCTURE analysis are sensitive to the type of genetic marker used (AFLP vs. microsatellite).	✓	0.24
The results of the STRUCTURE analysis are sensitive to the number of loci scored.	×	0.15
The results of the STRUCTURE analysis are sensitive to the number of populations sampled.	✓	0.16
The results of the STRUCTURE analysis are sensitive to the number of individuals typed in each sample.	✓	0.21

References

- `https://openalex.org/W7160564901`

- `https://doi.org/10.1111/j.1365-294x.2005.02553.x`
- `https://doi.org/10.1007/s11747-014-0403-8`