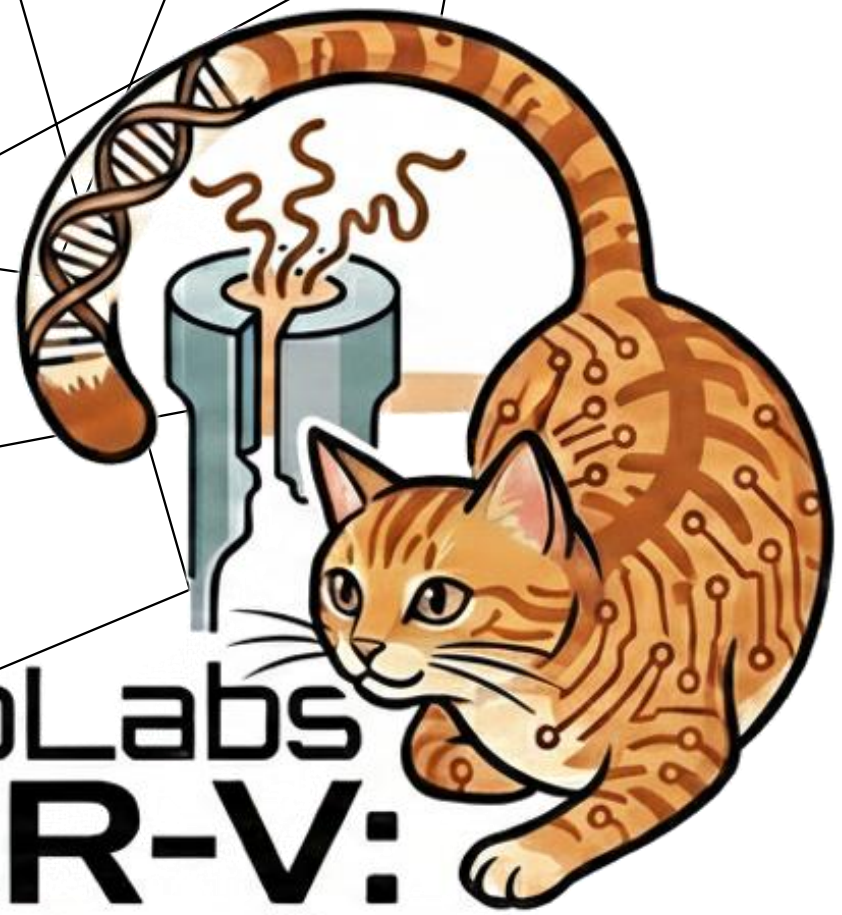


Team: ParaGatoLabs

GINGER-V:

Taming Genomic Basecalling for the Edge

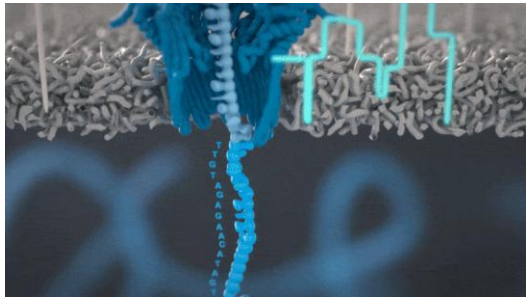
CHIPS
PES UNIVERSITY

PROBLEM STATEMENT AND APPROACH

- Basecalling decodes nanopore ionic current signals (“squiggles”) into DNA/RNA sequences using DNNs.
- Edge deployments of basecalling require: low power, tight memory budgets, sustained throughput matching signal generation rate.
- Key question:
  When and how can genomic basecalling workloads be efficiently executed on FPGAs?

Workload: DNN-based nanopore basecalling models inspired by edge-feasible architectures.

- Acceleration strategy:
  - GEMM-dominant kernels → **RedMulE [1] systolic accelerator** (leveraged from prior work)
  - Non-GEMM operations (control, activations, decoding) → **RISC-V core + custom instructions**
- Methodology:
  - Memory- and throughput-driven **design space exploration.**
  - Analyse tiling, memory traffic, and arithmetic intensity.
- Evaluation metric:
  - Sustained inference throughput vs nanopore signal rate (real-time feasibility).



PROGRESS & STATUS

Basecaller model selection	⏳	*Identifying an edge-feasible CNN-based nanopore basecalling model.*
ONNX -> C conversion	⏳	*Using Deeploy [2] (prior work) for ONNX-to-C compilation for host-side execution.*
RISC-V Host + RedMulE	✅	*Validated heterogeneous execution with CV32E40X RISC-V core orchestrating RedMulE GEMMs. (Simulation)*
Profiling & Custom Instructions	⏳	*Profiling non-GEMM kernels to identify candidates for RISC-V ISA extensions.*
FPGA Deployment (ZCU104)	⏳	*Adapting RedMulE-based system for FPGA realization and integration.*

🟡 **Status:** On track - **accelerator and host validated via simulation**; model integration and FPGA realization in progress.