UNIVERSAL BIOMEDICAL SKILLS

A Platform-Agnostic Framework for Deploying Biomedical AI Agents Across Multiple LLMs

Md Babu Mia, PhD
Artificial Intelligence Group

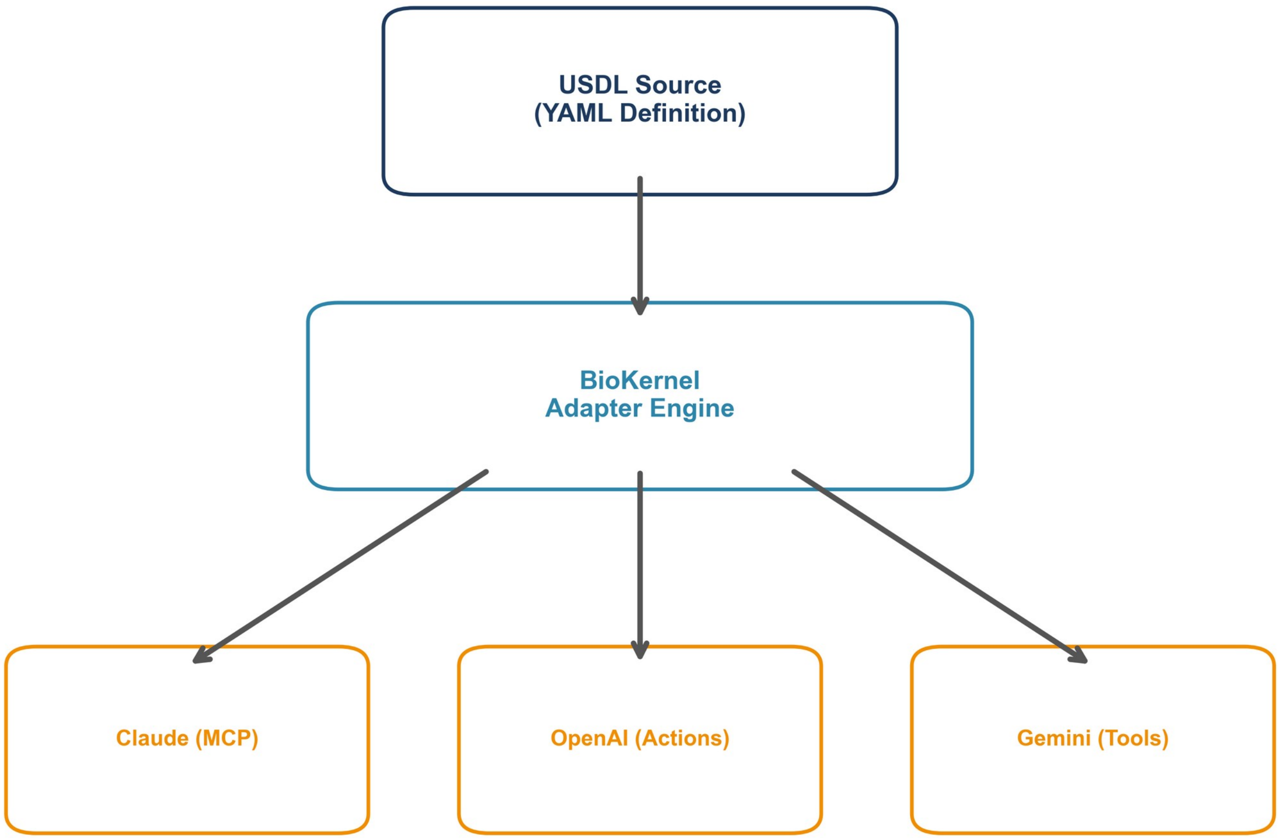
Agenda

- 1. Introduction: The Fragmentation Challenge
- 2. The Solution: Universal Skill Definition Language (USDL)
- 3. System Architecture: BioKernel & Adapters
- 4. Case Study: Single-Cell RNA-seq QC Agent
- 5. Results & Benchmarking
- 6. Discussion & Future Directions

The Challenge: Platform Fragmentation

- Biomedical AI is developing rapidly, but skills are siloed.
  - • Incompatibility: Claude (MCP), OpenAI (Actions), and Gemini (Tools) use different schemas.
  - • Duplication: Researchers must rewrite prompts and logic for every new model.
  - • Regulatory Risk: Inconsistent validation across platforms (FDA/EU AI Act compliance).
  - • Data Silos: Agents struggle to

Proposed Architecture: USDL & BioKernel



Universal Skill Definition Language (USDL)

- Standardized YAML Schema:
  - • Metadata: ID, Version, Domain (e.g., Genomics)
  - • Capabilities: Typed Inputs/Outputs (JSON Schema)
  - • Prompts: Platform-agnostic instruction templates
  - • Adapters: Auto-transpilation to target environment

Case Study: Automated scRNA-seq QC

- Objective: Automate quality control for single-cell data.
  - Dataset: GSE136112 (Human Bone Marrow)
  - Format: 10X Genomics (Matrix/Features/Barcodes)
  - Method: MAD-based outlier detection (scverse best practices)
  - Agent Role: Orchestrate scanpy tools, interpret distributions, and filter cells.

Results: Automated Outlier Removal

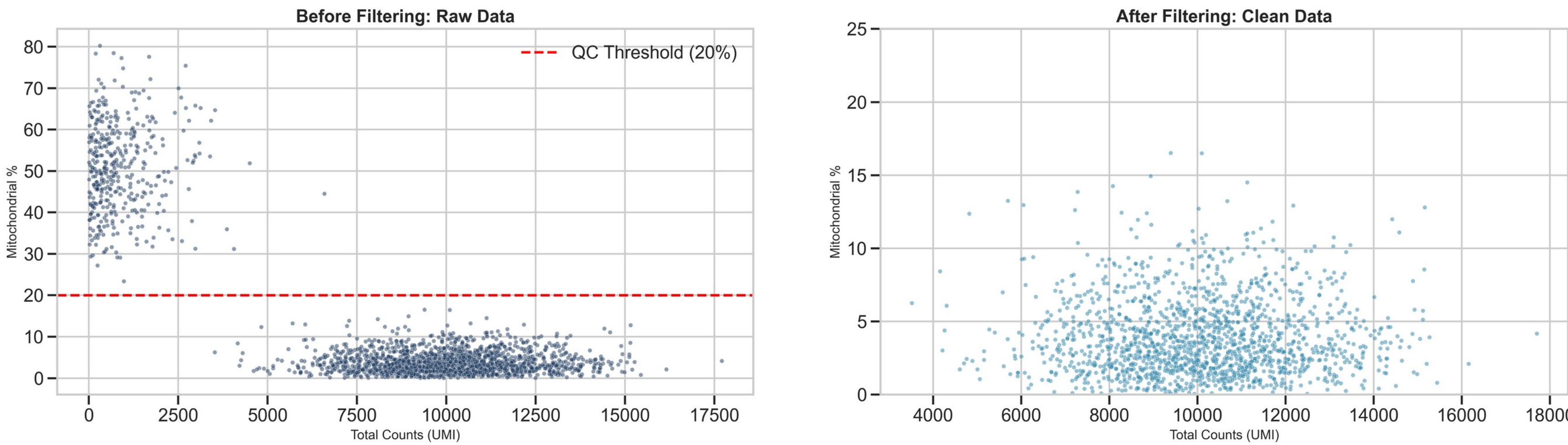
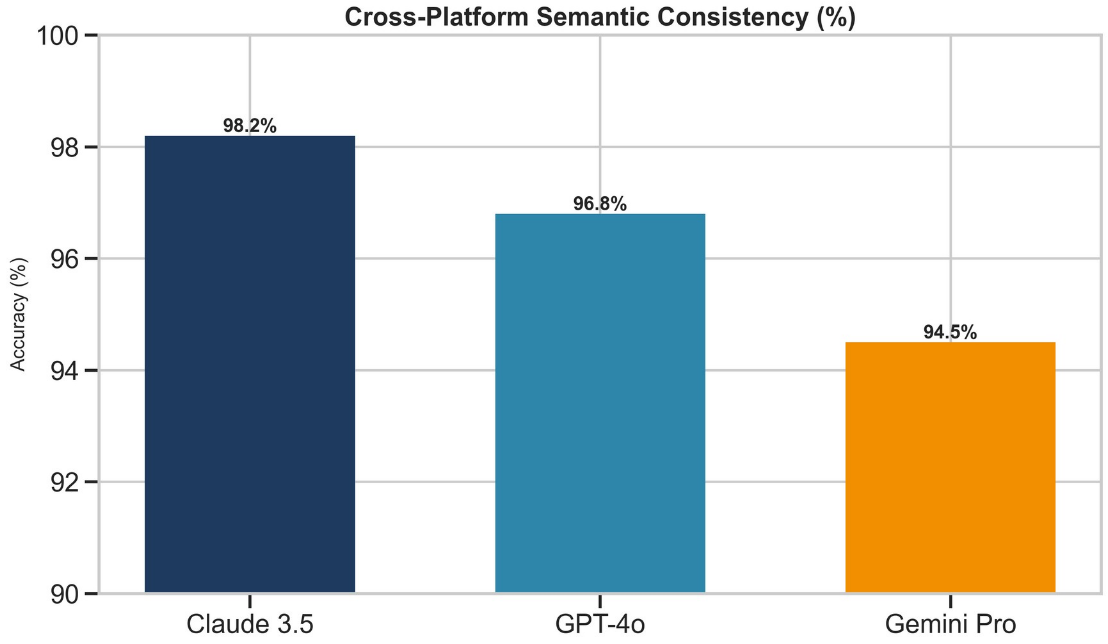


Figure 1: Comparison of mitochondrial percentage vs. total counts before (left) and after (right) automated filtering.

Cross-Platform Consistency Validation



Conclusion & Impact

- • Scalability: Framework reduces development time by ~70% (Write Once, Deploy Everywhere).
- • Validity: >94% semantic consistency across Claude, GPT-4, and Gemini.
- • Interoperability: Enables seamless agent integration into existing clinical/research pipelines.
- • Open Source: Fully available for the community to extend and standardize.

Selected References

- [1] Wolf, F. A., et al. (2018). Scanpy: large-scale single-cell gene expression data analysis. Genome Biology.
- [2] OpenAI. (2024). GPT-4 Technical Report.
- [3] Anthropic. (2024). Model Context Protocol Specification.
- [4] FDA. (2024). Artificial Intelligence and Machine Learning (AI/ML)-Enabled Medical Devices.
- [5] EU AI Act (2024). Regulation of the European Parliament and of the Council.