NanoOpt- Nanopore Protocol Optimization Toolkit

Functional Specification

Background

Nanopore sequencing is predominantly employed for long-read sequencing tasks. However, its application for short-read sequencing, particularly for tuberculosis (TB) sequences ranging from 40 to 100 bases, remains under-explored. Optimizing the process requires specialized probe designs for PCR amplification and rigorous validation against known reference sequences. There is an unmet need for a computational tool to facilitate these optimization steps.

User Profile

- Lab Members in a Bioengineering Research Lab
- Domain Knowledge: Expertise in bioengineering, molecular biology, and DNA sequencing. Focused on global health solutions such as point-of-care diagnosis for HIV and TB.
- Computing Skills: people in my lab have relatively minimum knowledge in nanopore sequencing or bioinformatics in general. The project should output an easy result.

Use Cases

1. Universal Probe Design

- Objective: To design a probe that can be used for PCR amplification and nanopore sequencing, avoiding dimerization issues.

- Expected Interactions:
  1. User inputs target DNA/RNA sequence and any constraints.
  2. System outputs optimized probe sequence and flags for potential dimerization.

2. Sequence Validation

- Objective: To validate the accuracy of nanopore-sequenced fragments against a known reference sequence.

- Expected Interactions:
  1. User inputs sequenced fragments and a known reference sequence.
  2. System outputs accuracy metrics and identifies mismatches.
