Functional Specification

NanoOpt- Nanopore Protocol Optimization Toolkit

Overview

- **Project Name:** NanoOpt
- **Objective:** To develop a Python package aimed at optimizing nanopore sequencing protocols, specifically focusing on probe design and sequence validation.

Features

1. Universal Probe Design

Inputs
- Target DNA/RNA sequences
- Constraints (e.g., GC content, melting temperature)

Outputs
- Optimized probe sequence for PCR amplification and nanopore sequencing
- Potential dimerization issues flagged

Functionality
- Utilize algorithms to find the most efficient probe sequences for target sequences.
- Evaluate dimerization risks and suggest mitigation strategies.

2. Sequence Validation

Inputs
- Sequenced fragments (40-100 bases)
- Known reference sequence

Outputs
- Accuracy score
- Mismatches and their locations

Functionality
- Map nanopore sequenced fragments to known reference sequence.
- Calculate and report accuracy metrics.

Workflow

1. Data Input: Import target sequences and constraints.
2. Probe Design: Run the probe design algorithm.
    - Output optimized probe.
    - Check for dimerization risks.
3. Sequencing & Data Collection: Collect nanopore sequence data.
4. Sequence Validation: Import sequenced fragments and known reference.
    - Map fragments to reference.
    - Output accuracy metrics.