SubliMat Verification and Validation Checklist

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Documentation Review

☐ SRS reviewed by domain expert (Junwei Lin)

☐ MG reviewed by instructor (Dr. Spencer Smith)

☐ MIS reviewed by author (Uriel Garcilazo Cruz)

☐ VnV Plan reviewed by all team members

☐ GitHub issues created for all documentation reviews

System Testing

Functional Requirements

Input Validation (R1, R2)

☐ **TC-SubLiMat-1-1**: Valid DNA sequences (ATCG vs ATCG)

☐ **TC-SubLiMat-1-2**: Empty sequence 1

☐ **TC-SubLiMat-1-3**: Empty sequence 2

☐ **TC-SubLiMat-1-5**: Sequences with gaps (A_GC vs ATGC)

☐ **TC-SubLiMat-1-8**: Invalid characters (RTGA)

Matrix Validation (R3)

☐ **TC-SubMat-3-1**: Valid 4x4 matrix

☐ **TC-SubMat-3-2**: Non-square matrix

☐ **TC-SubMat-3-4**: Incorrect dimensions (3x3)

Non-Functional Requirements

Performance (NFR5)

☐ **TC-SubLiMat-4-1**: 10bp sequences ($<$0.1s)

☐ **TC-SubLiMat-4-4**: 500bp sequences ($\sim$25s)

☐ **TC-SubLiMat-4-5**: 5000bp sequences ($>$300s)

Portability (NFR4)

☐ **TC-SCEC-5-1**: Windows compatibility

☐ **TC-SCEC-5-2**: Linux compatibility

☐ **TC-SCEC-5-3**: macOS compatibility

Usability (NFR2)

☐ Survey distributed to 5+ users

☐ Survey results analyzed (Table **??**)

Unit Testing

pairwise_alignment.py

☐ Needleman-Wunsch algorithm validation

☐ Score matrix calculation

☐ Traceback functionality

☐ Edge cases (empty/gapped sequences)

Automation

☐ pytest framework configured

☐ GitHub Actions CI pipeline

☐ Code coverage $>$80% reported

☐ pylint score $>$9.0/10

Additional validation

☐ Domain expert verification session

☐ User testing feedback incorporated

Traceability

☐ All test cases executed and documented

☐ Discrepancies logged in GitHub issues

Final Sign-off

☐ All checklist items completed

☐ Final review by Dr. Spencer Smith

☐ VnV report approved