inStrain·····

·····BAM··inStrain profile·compare·····
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inStrain·····SNV·····FASTA·BAM·····
·····compare·····profile·compare·····
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·····BAM··

profile····FASTA·····BAM·FASTA·····BAM·····
··FASTA·····reads·····
·····BAM·····bin·····scaffold·bin·····scaffold·····

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··FASTA | ·BAM····· | ·····

BAM | ····· | ·····SNV··

···· | Illumina·HiFi·Nanopore·· | ·····

···· | profile·compare····· | ·····ANI·····

·····profile···

·····BAM·····FASTA·····`-p`·····4·····
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```
#!/usr/bin/env bash
set -euo pipefail
ref=/data/dereplicated_references.fna
bam1=/data/sample1.sorted.bam
bam2=/data/sample2.sorted.bam
root="$PWD/instrain-pilot-001"
for f in "$ref" "$bam1" "$bam2"; do test -s "$f"; done
test ! -e "$root" || { echo "output exists: $root" >&2; exit 2; }
mkdir -p "$root"
inStrain --version > "$root/version.txt" 2>&1
inStrain profile "$bam1" "$ref" -o "$root/sample1.IS" -p 4   > "$root/sample1.log" 2>&1
inStrain profile "$bam2" "$ref" -o "$root/sample2.IS" -p 4   > "$root/sample2.log" 2>&1
inStrain compare -i "$root/sample1.IS" "$root/sample2.IS"    -o "$root/compare.IS" -p 4 > "$root/compare.log" 2>&1
test -d "$root/sample1.IS"
test -d "$root/sample2.IS"
test -d "$root/compare.IS"
sha256sum "$ref" "$bam1" "$bam2" > "$root/inputs.sha256"
```

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·····reads·····SNV·

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inStrain····Illumina·····Q30·····SNV·····Nanopore·
·····profile·compare·····HiF
i·····Q30·····Nanopore·····

compare·····FASTA·profile·····popANI·coverage overlap·SNV·····map
ping·····
····scaffold·····FASTA·····bin·····scaffold-to-bin·····

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·····BAM···profile·····compare·····
·····profile·····profile·····BAM·····
·····FASTA···

·····BAM·····
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inStrain·····profile·compare https://instrain.readthedocs.io/en/latest/user_manual.html

inStrain····· https://instrain.readthedocs.io/en/latest/important_concepts.html