

AmpliconComparison results

Setup:

Date: 2023-08-30 10:23:24.395363

Sample s1: ../examples/ecdna1/true.bed

Sample s2: ../examples/ecdna1/reconstructed.bed

Output directory: ../examples/ecdna1/output

Results:

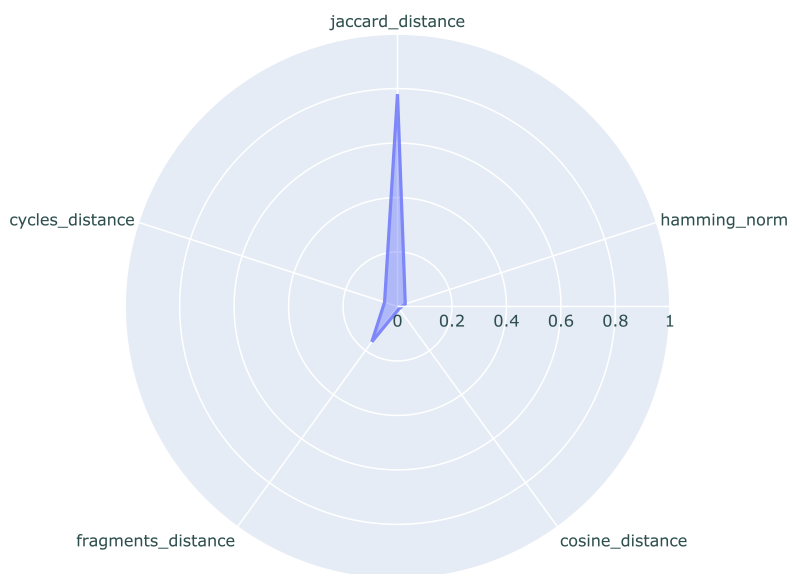
Here we compute the cycle distance between `s1` and `s2`.

Distance description:

1. cosine_distance = measures the distance between the s1 and s2 normalized coverage profiles
2. hamming_norm = measures the amount of dissimilar genomic bins usage for s1 and s2
3. fragments_distance = measures the amount of fragment usage per genomic bin which is dissimilar between s1 and s2
4. cycles_distance = measures the amount of cycles usage per genomic bin which is dissimilar between s1 and s2
5. jaccard_distance = measures how many breakpoints-pairs could not be matched between s1 and s2

The radial plot shows all these distances, with values between 0 (low cost, high similarity) and 1 (high cost, low similarity). The more colorful the more distant are `s1` and `s2`.

Total cost: 1.03 (0 - highly similar, 5 - dissimilar)



Distance	Value
hamming_norm	0.03
cosine_distance	0.01
jaccard_distance	0.78
fragments_distance	0.16
cycles_distance	0.05
total_cost	1.03

Coverage (gray track) and breakpoint-pairs matches for s1 (green) and s2 (blue). Unmached breakpoint-pairs are displayed in gray. The $\log_2(s1/s2)$ is displayed in black. The zero reference is displayed as dotted read line.

