

## EC-comparator results

### Setup:

**Date:** 2026-09-23 13:47:21.598091

**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:

d1 = Hamming distance = measures differences of genomic regions presence / absence for s1 and s2

d2 = Cosine distance = measures the copy-number distance between the s1 and s2 using cosine distance

d3 = Min-max distance = measures the copy-number distance between the s1 and s2 using jaccard distance

d4 = Bins distance = measures differences of genomic bins usage

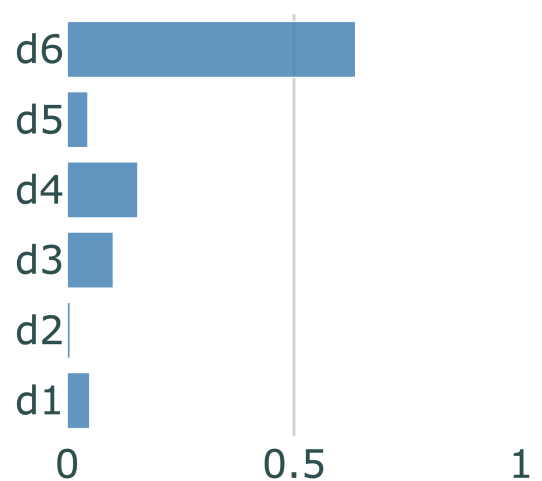
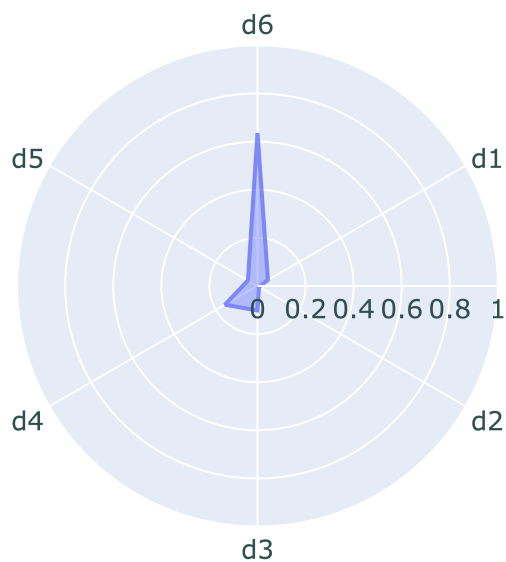
d5 = Paths distance = measures differences of paths decomposition between s1 and s2

d6 = Breakpoint distance = measures differences between the breakpoint junctions profiles 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: 0.9 (0 - highly similar, 5 - dissimilar)**



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 red line.

