



Figure 2: results for the simulated read tests. For 10 reference genome sequences, we simulated both short and long reads. The read sets were then assembled with Unicycler (hybrid assembly), Flye (long-read-only assembly), Flye+Pilon (hybrid assembly), Tricycler (long-read-only assembly) and Tricycler+Pilon (hybrid assembly).

Each assembled chromosome was aligned back to the reference chromosome to determine the mean assembly identity (A) and the worst identity in a 100 bp sliding window (B). For long-read-only assembly, Tricycler consistently achieved higher accuracy than Flye. Tricycler+Pilon achieved the highest accuracy and did better than alternative hybrid approaches (Unicycler and Flye+Pilon).