



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

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