



Figure 1: Schematic of the transformation used to scale the positions in the genome to the origin of replication and account for bidirectional replication. Circle (A) represents the original replicon genome without any transformation. Circle (B) represents the same replicon genome after the transformation. The origin of replication is denoted by “*oriC*” and the terminus of replication is denoted by “*ter*”. The dashed line represents the two halves of the replicon separate by replication. The replicon genome in this example is 100 base pairs in length. Every 10 base pairs is denoted by a tick on the genome. The origin in (A) is at position 20 in the genome and is transformed in (B) to become position 1. The terminus is at position 60 in (A) and position 60 and 40 in (B). The terminus has two positions in (B) depending on which replicon half is being accounted for. If the replication half to the right of the origin is considered, the terminus will be at position 40. If the replication half to the left of the origin is considered, the terminus will be at position 60. Position 40 in (A) becomes position 20 in (B). Position 80 in (A) becomes position 40 in (B), because of the bidirectional nature of bacterial replication.