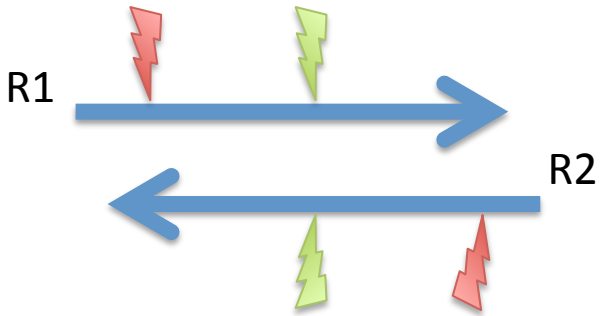
Alternative Library Prep Methods

And Considerations for libraires with less errors

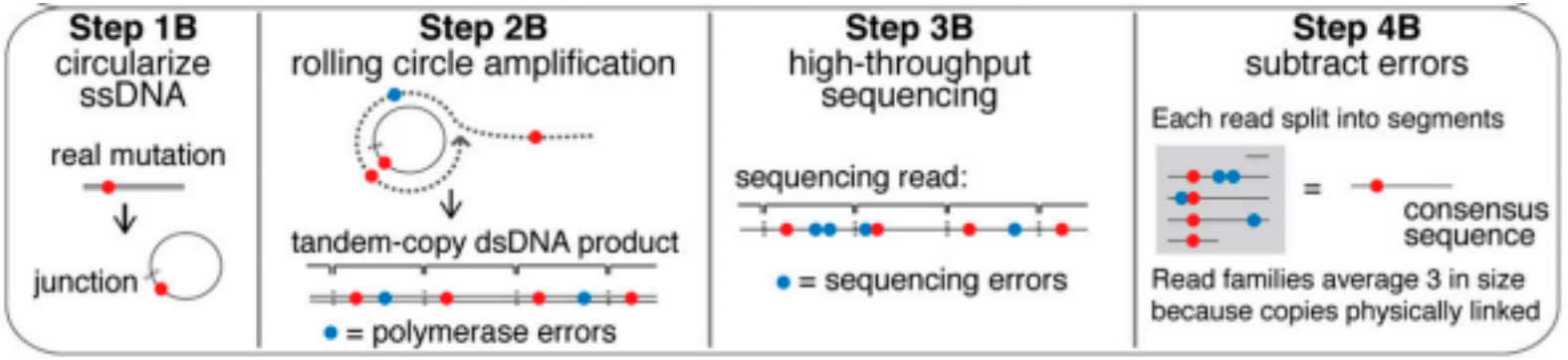
“Double Read” strategy

- Error rates are per base, or sequence specific meaning you can leverage the relationship between read1 and read2 to do error correction.
- Error rate: $1x10^{-4}$ to $1x10^{-6}$ (probably underestimated)



Circle Sequencing

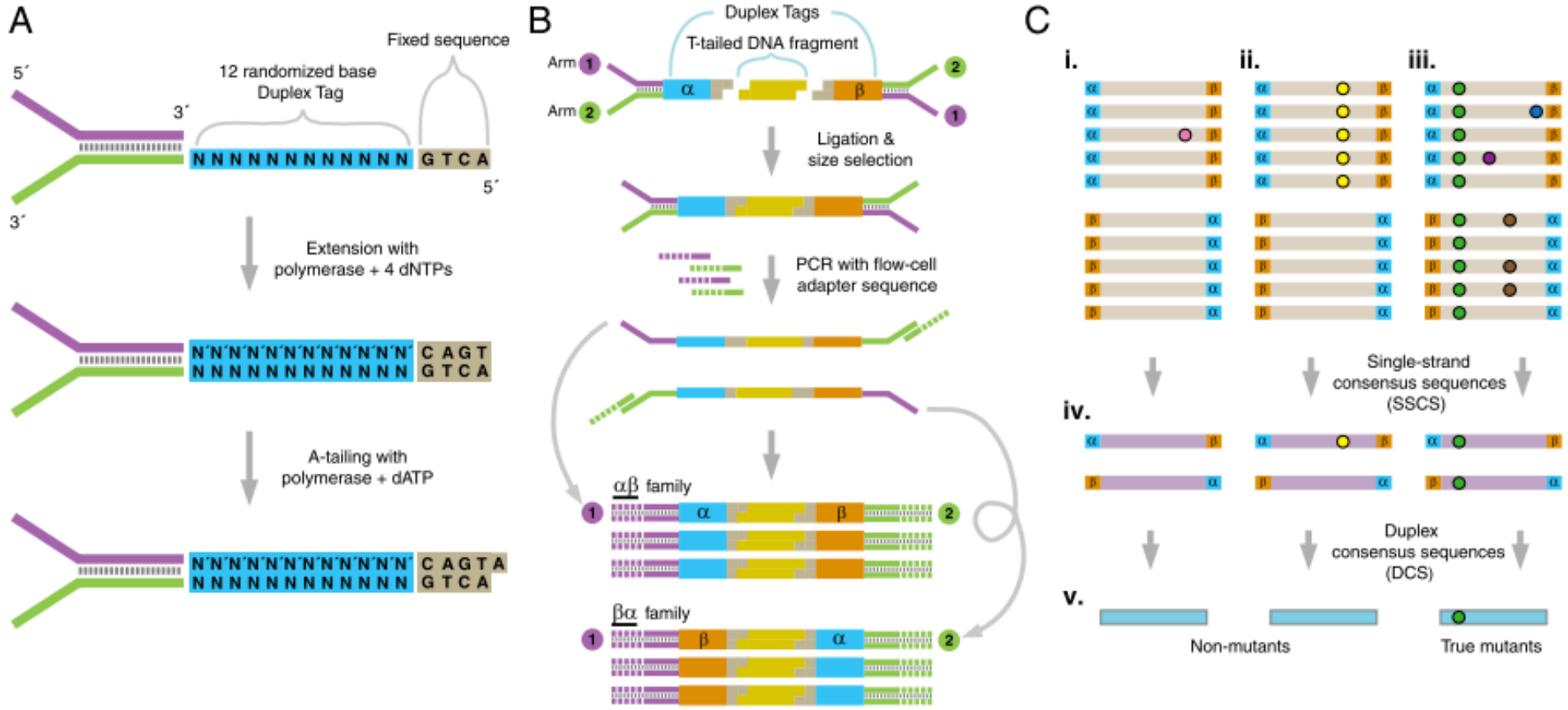
- Circularize smaller fragments of DNA.
- Read each fragment multiple times.
- Discard stochastic errors.
- Error Rate: 7.6×10^{-6}
- Reference: Lou et al 2013



Duplex Sequencing

- Uses a modified adapter which contains a N_{12} region which gets read before the DNA fragment.
- Reads containing the same N_{24} region are stacked together, and discrepancies removed.
- Error Rate: SSCS: 3.4×10^{-5} Duplex Seq: 3×10^{-6}

Duplex Seq Method



Common Features

- All work on the principle that reading the same template multiple times in different ways.
- Each still subject to different types of error.