old sequencing technologies → short reads

→ problem with repeats

→ tangled assembly graph → fragmented assembly

new technologies → long reads

→ problem solved ?

→ no : problem errors in reads and repeats which are longer than the reads

We want to assemble correctly and resolve repeats correctly to get a ~~better~~ and contiguos assembly.

How do we do that ?

by first ignoring the repeats which we want to resolve

Really ?

→ yes

We create these fast disjointigs, which already include the genomic structure by there reads because the reads should cover the genome equally.

→ dot plot

→ repeat

→ results

If you want to learn more about our methods, results from other datasets and know about the improvement from our algorithm since the initial version make sure to visit our posts.