

# Lorentz Center workshop Life Sciences with Industry

November 2021

## Super-Pangenomes for breeding even better vegetables

Until recently plant breeders were already very content if they would have one high quality reference genome sequence for every crop they are working on. Now for more and more crops this wish is becoming a reality but also a lot of them are still under development. The “reference genomes” for these crops are still in a rudimentary state with a lot of gaps making them suboptimal as a tool in genomics and breeding. The ideal reference genome consists of chromosome level assemblies.

While we are still working to get good reference genomes there is already a new kid on the block. Now just having one reference genome sequence is not sufficient any more. You should have a basket full of them and preferable also the genomes of many related species. The more genomes the better and the way to organize all of these data is in Pangenomes or Super-pangenomes. But that means that we as seed companies will have to invest again quite substantially in next generation sequencing and bioinformatics. But how should we do this and when should we start?

### Questions for the participants in the Lorentz Workshop to answer:

- Why do we need a reference genome in plant breeding? Why is this useful?
- Why do we need a (super-) pangenome in plant breeding?
- How should we make such a pangenome or super-pangenome?
- How should we choose the plant material (lines, types, species) to put in there?
- Which information, knowledge should be added to the pangenome?
- How can we apply this knowledge in plant breeding?
- What is the added value of such a pangenome or super-pangenome for plant breeding? (Return on investment?).

This WS Life Sciences is interesting for people with a background in plant breeding, bioinformatics, plant biology, biochemistry, etc.