



# Introduction to Bioinformatics

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### **Check Galaxy Slides ©**





https://training.galaxyproject.org/training-material/topics/sequence-analysis/tutorials/quality-control/slides.html#1





### **Hands-on and Practical Part**













## Introduction to Bioinformatics

**Application: De novo Genome Assembly** 

Part 2: De Bruijn graph













"tomorrow and tomorrow and tomorrow"

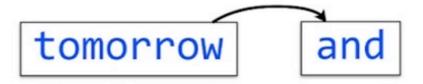
tomorrow

and





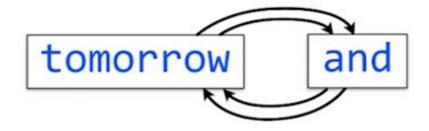


















genome: AAABBBBA







genome: AAABBBBA

3-mers: AAA, AAB, ABB, BBB, BBB, BBA



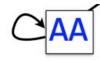




genome: AAABBBBA

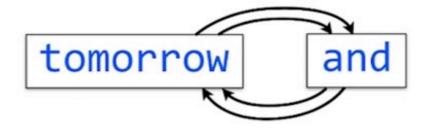
3-mers: AAA, AAB, ABB, BBB, BBB, BBA

L/R 2-mers: AA, AA















genome: AAABBBBA

3-mers: AAA, AAB, ABB, BBB, BBB, BBA

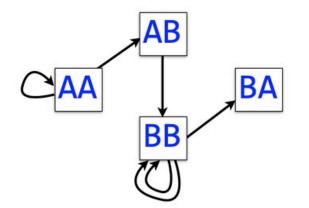
L/R 2-mers: AA, AA







genome: AAABBBBA

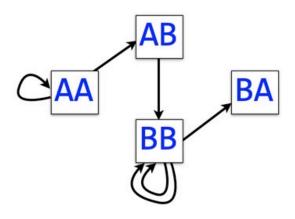


One edge per *k*-mer
One node per distinct *k*-1-mer

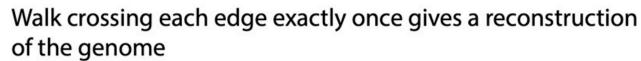






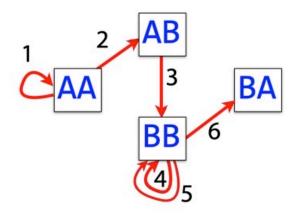












#### **AAABBBBA**

Walk crossing each edge exactly once gives a reconstruction of the genome. This is an *Eulerian walk*.





### **Hands-on and Practical Part**











## **Done with Day 4, Heyyyyy!**

**Thank You!** 



