Schatzlab Research Projects

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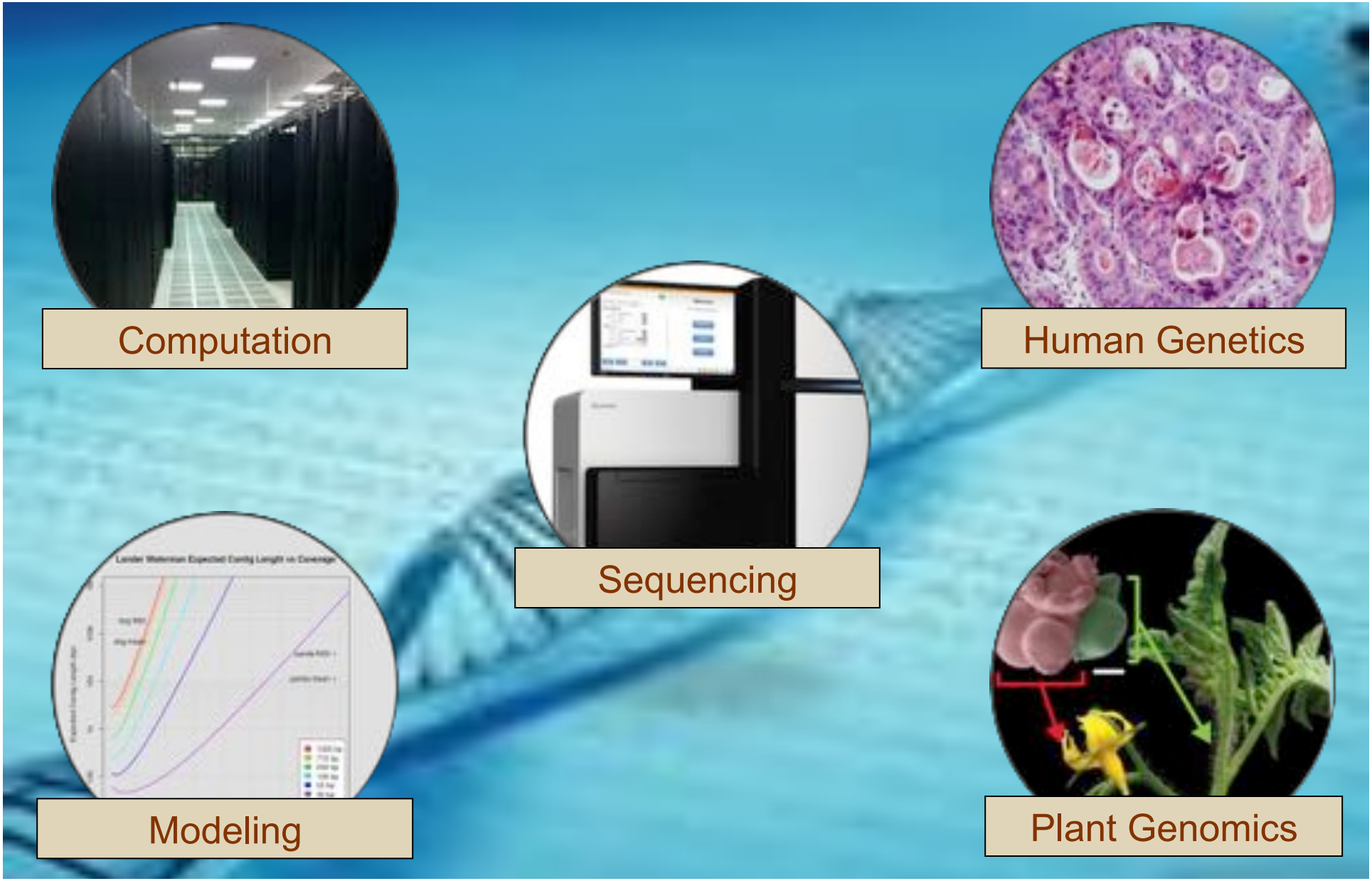
Sept 10, 2014
Research Topics in Biology, WSBS

A Little About Me

Schatz Lab Overview



Unsolved Questions in Biology

- W
- H
- W
- H
- H
- H
- H
- H
- W
- W
- H
- W
- ***Plus thousands and thousands more***

The instruments provide the data, but none of the answers to any of these questions.

What software and systems will?

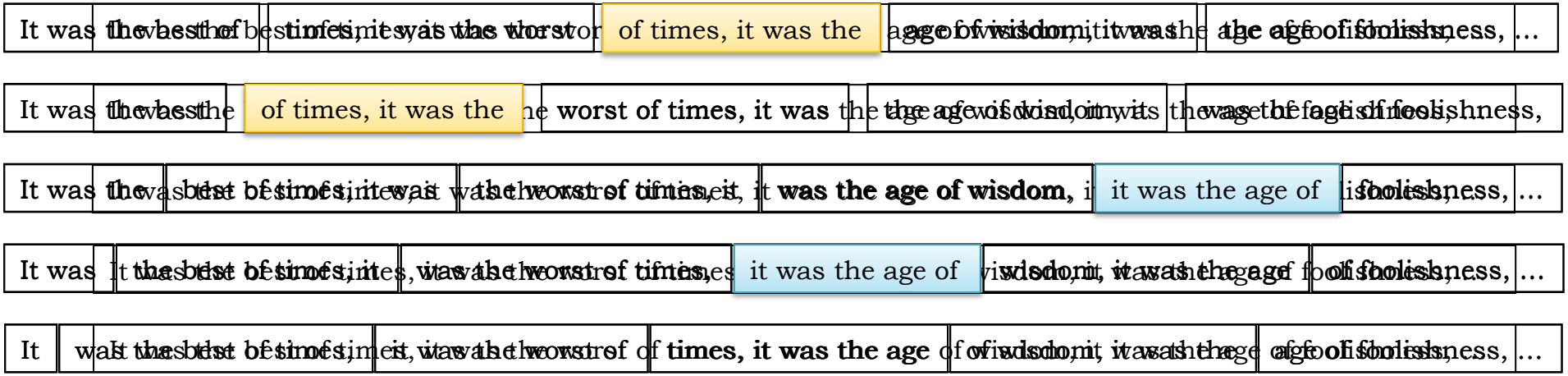
And who will create them?

What is your genome?

Genome of the long-living sacred lotus (Nelumbo nucifera Gaertn.)
Ming, R et al. (2013) Genome Biology 14:R41

Shredded Book Reconstruction

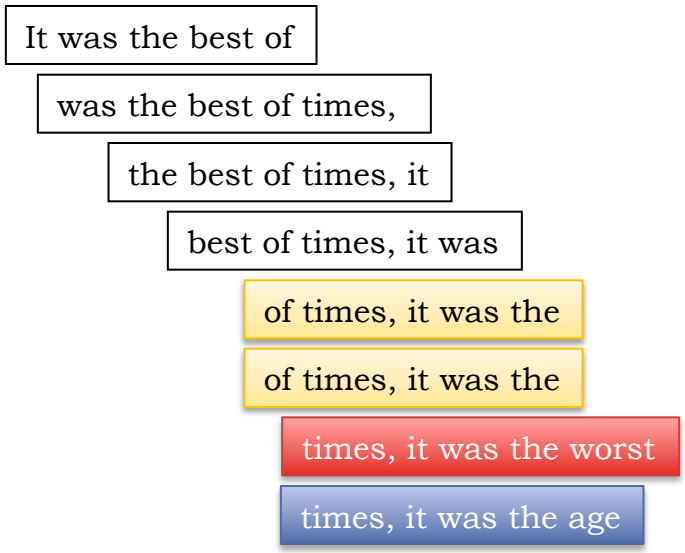
- Dickens accidentally shreds the first printing of A Tale of Two Cities
  - Text printed on 5 long spools



- How can he reconstruct the text?
  - 5 copies x 138, 656 words / 5 words per fragment = 138k fragments
  - The short fragments from every copy are mixed together
  - Some fragments are identical

Greedy Reconstruction

It was the best of
age of wisdom, it was
best of times, it was
it was the age of
it was the age of
it was the worst of
of times, it was the
of times, it was the
of wisdom, it was the
the age of wisdom, it
the best of times, it
the worst of times, it
times, it was the age
times, it was the worst
was the age of wisdom,
was the age of foolishness,
was the best of times,
was the worst of times,
wisdom, it was the age
worst of times, it was



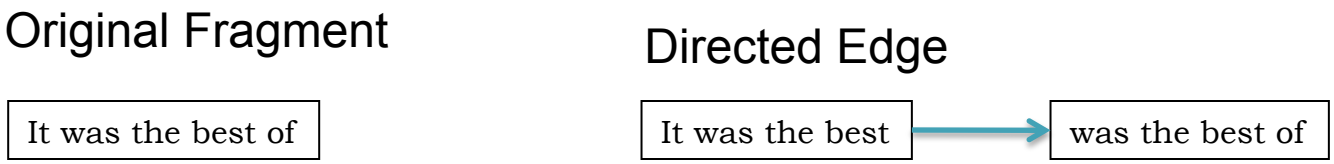
The repeated sequence make the correct reconstruction ambiguous

- It was the best of times, it was the [worst/age]

Model sequence reconstruction as a graph problem.

de Bruijn Graph Construction

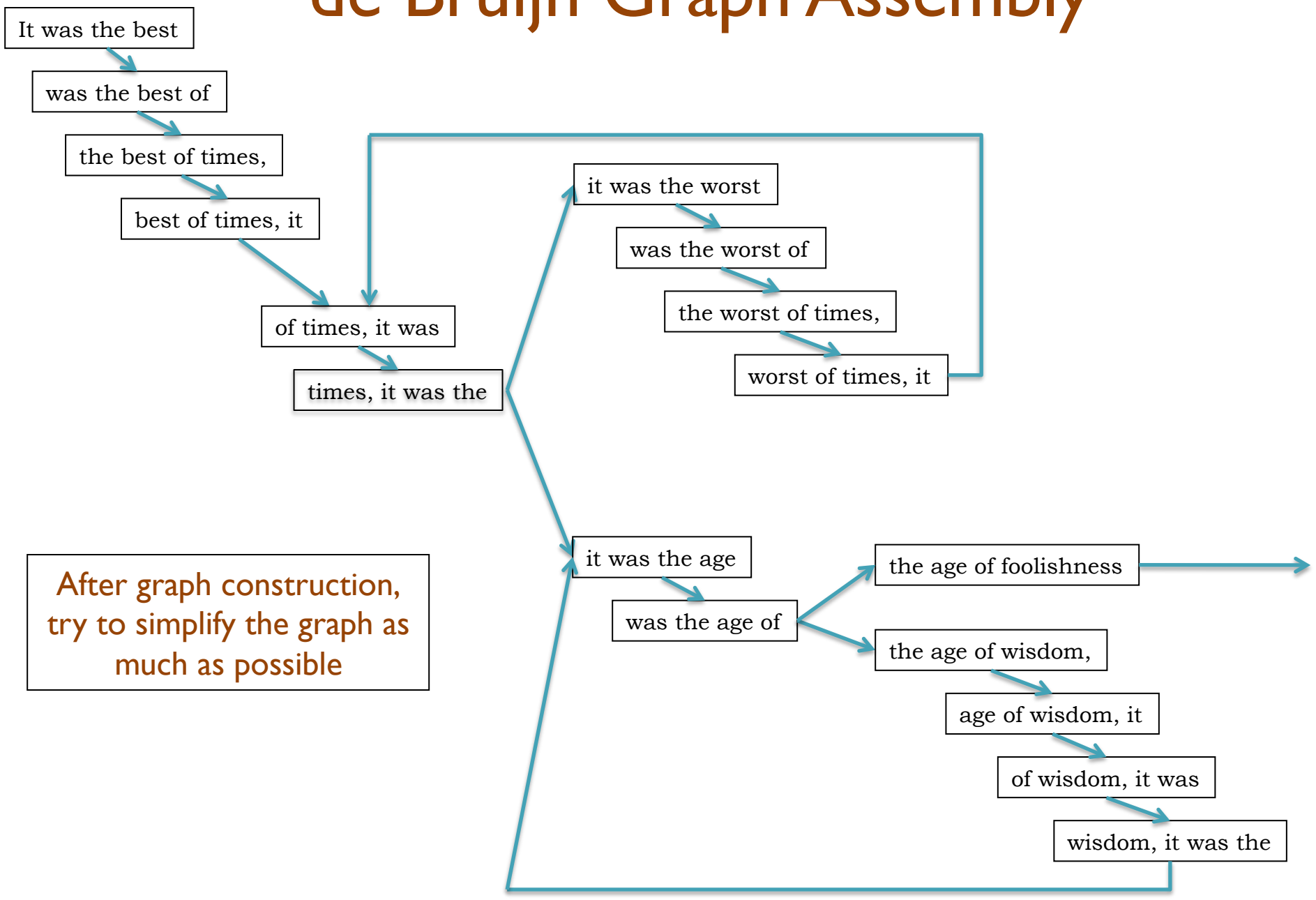
- $D_k = (V,E)$
  - V = All length-k subfragments (k < l)
  - E = Directed edges between consecutive subfragments
    - Nodes overlap by k-1 words



- Locally constructed graph reveals the global sequence structure
  - Overlaps between sequences implicitly computed

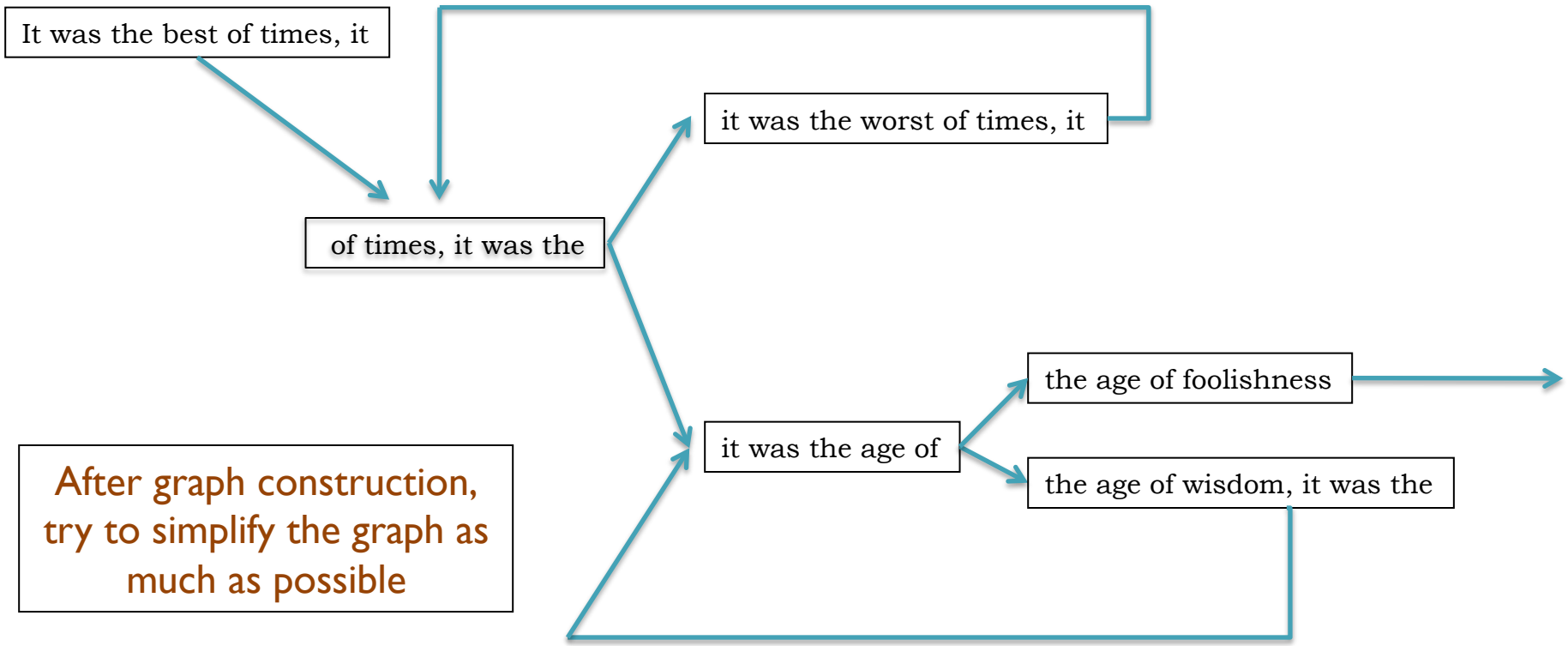
de Bruijn, 1946
Idury and Waterman, 1995
Pevzner, Tang, Waterman, 2001

de Bruijn Graph Assembly



After graph construction, try to simplify the graph as much as possible

de Bruijn Graph Assembly



After graph construction, try to simplify the graph as much as possible

The full tale

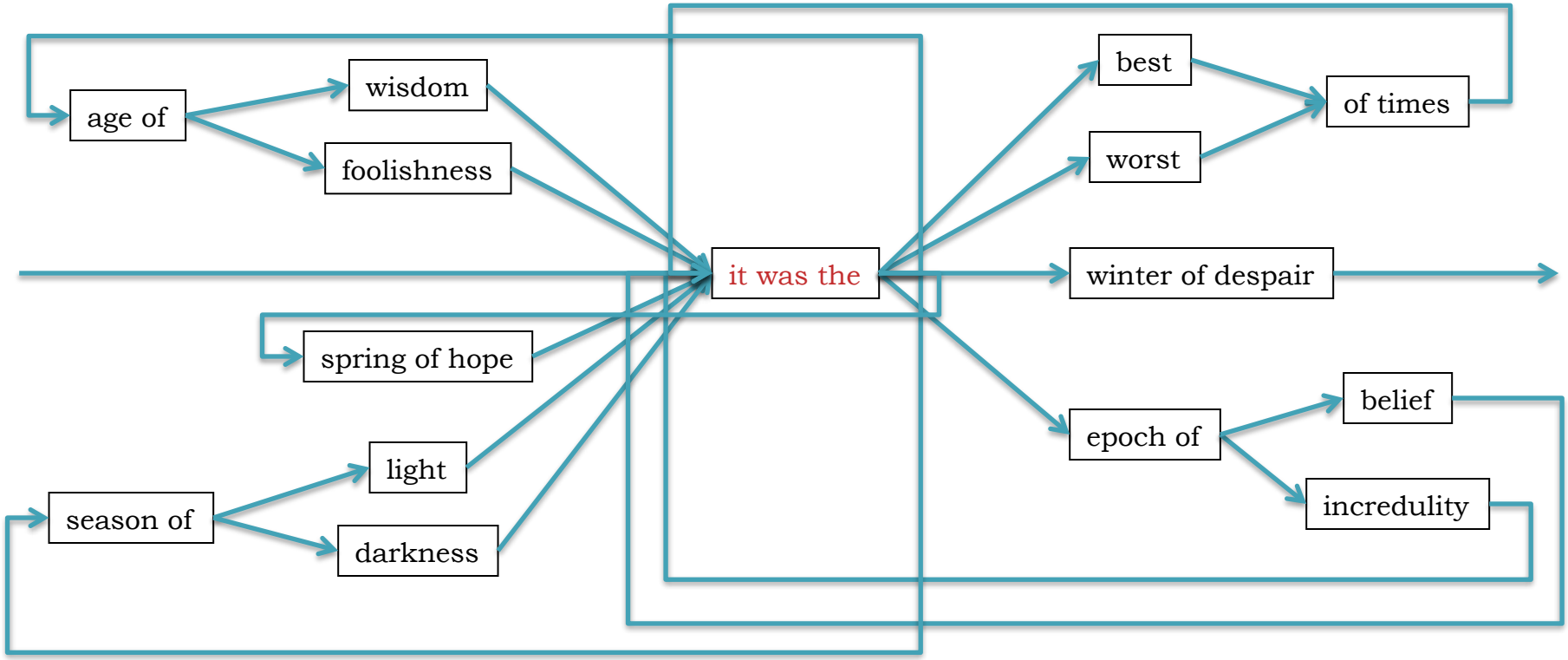
… it was the best of times it was the worst of times …

… it was the age of wisdom it was the age of foolishness …

… it was the epoch of belief it was the epoch of incredulity …

… it was the season of light it was the season of darkness …

… it was the spring of hope it was the winder of despair …



Introductions

Tyler Garvin

CNV and transcriptome analysis of single cells

Giuseppe Narzisi

Indels related to Autism and other human diseases

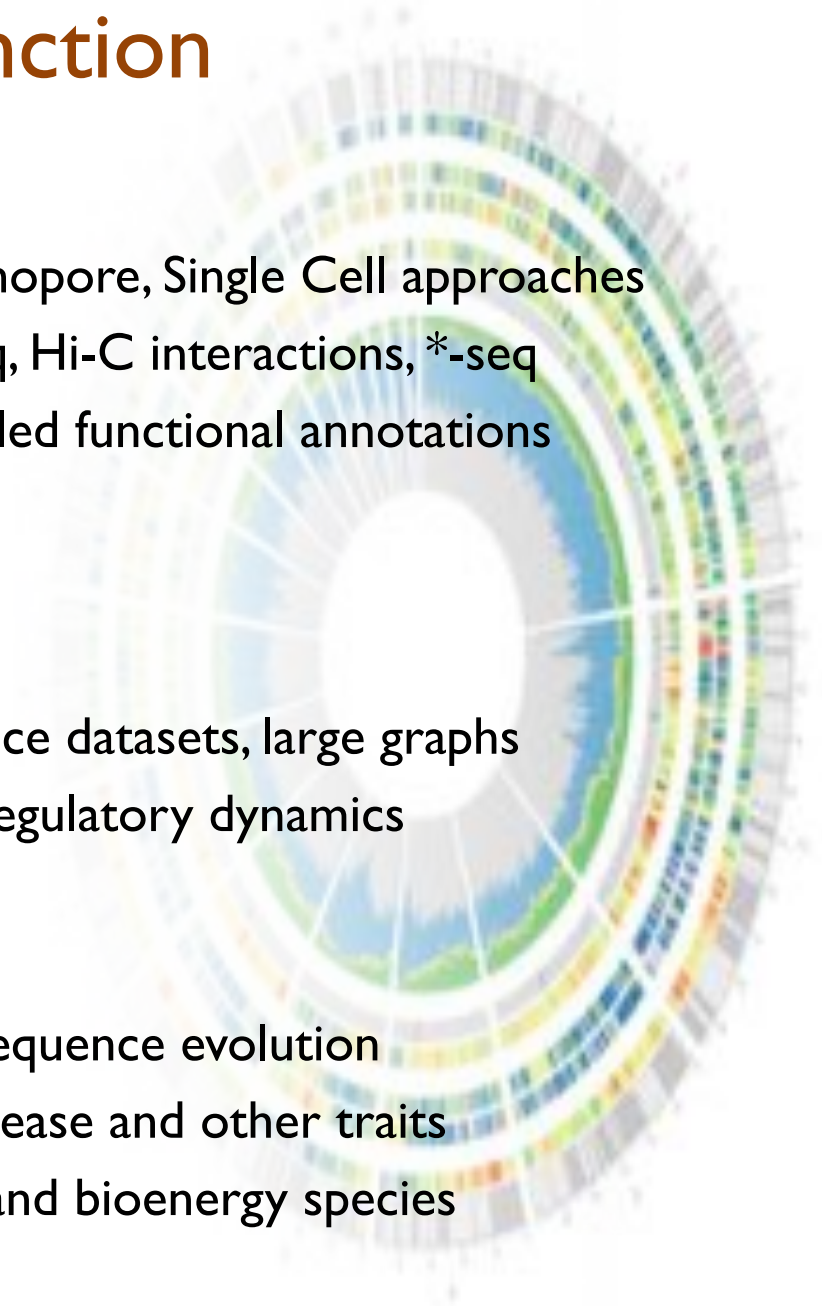
Maria Nattestad

Hi-C Chromatin Interactions within plants

Hayan Lee

Modeling of genome assembly performance

Understanding Genome Structure & Function



Biotechnology

- Sequencing: Illumina, PacBio, Oxford Nanopore, Single Cell approaches
- Biochemical assays: RNA-seq, Methyl-seq, Hi-C interactions, *-seq
- More accurate sequencing & more detailed functional annotations

Algorithmics

- Highly scalable algorithms and systems
- Indexing and analyzing very large sequence datasets, large graphs
- Constructing Pan-genomes & inferring regulatory dynamics

Comparative Genomics

- Cross species comparisons, models of sequence evolution
- Identifying mutations associated with disease and other traits
- Genotype-to-phenotype of agricultural and bioenergy species

Acknowledgements

Schatz Lab

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Alejandro Wences

CSHL

Hannon Lab
Gingeras Lab
Jackson Lab
Hicks Lab
Iossifov Lab
Levy Lab
Lippman Lab
Lyon Lab
Martienssen Lab
McCombie Lab
Tuveson Lab
Ware Lab
Wigler Lab

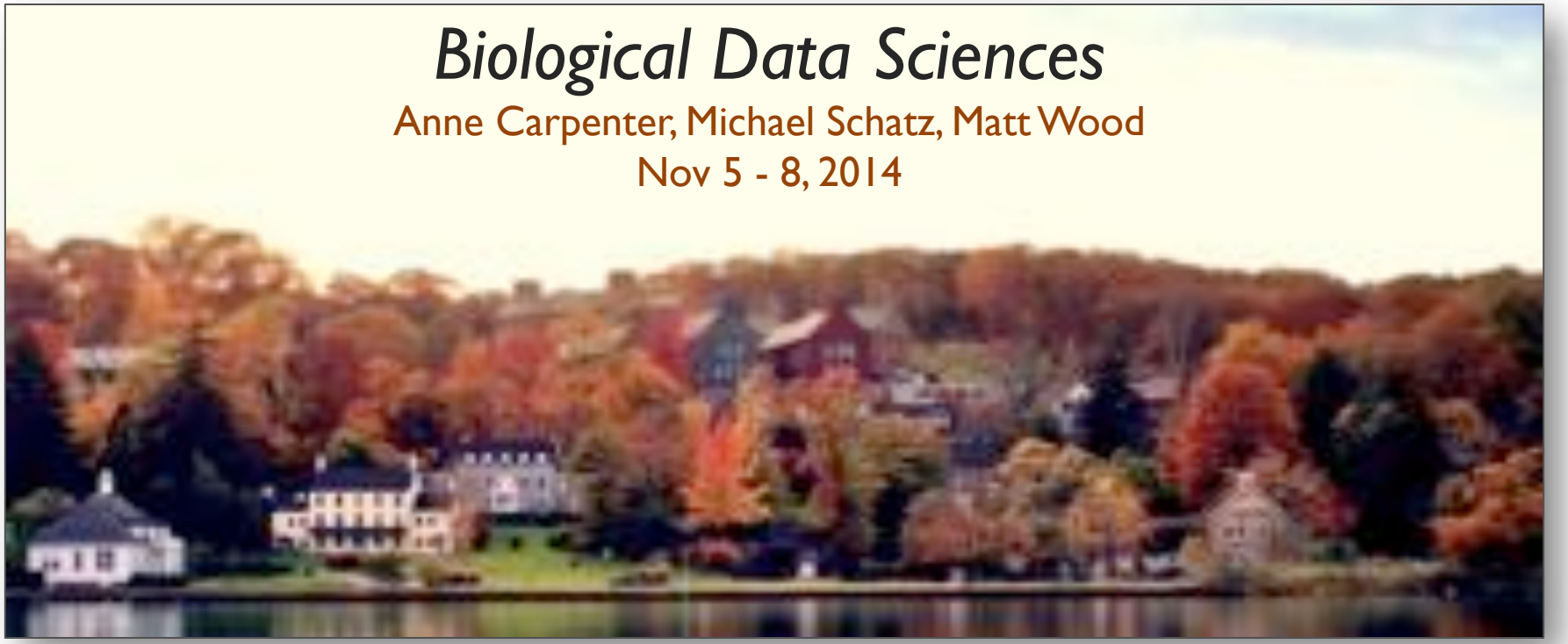
Pacific Biosciences
Oxford Nanopore

NSF

National Human Genome Research Institute

U.S. DEPARTMENT OF ENERGY

SFARI
SIMONS FOUNDATION AUTISM RESEARCH INITIATIVE



Thank you

http://schatzlab.cshl.edu

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