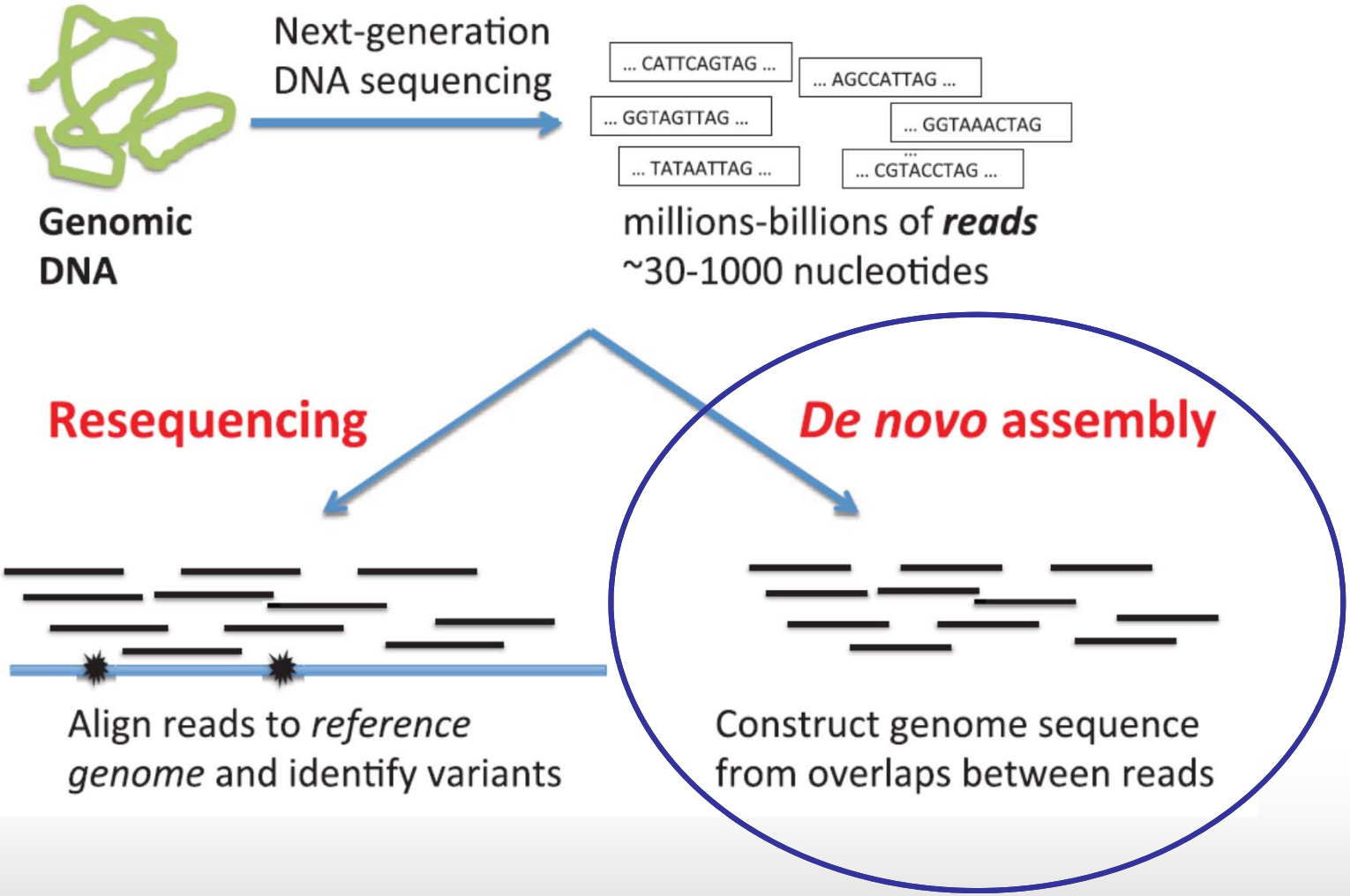
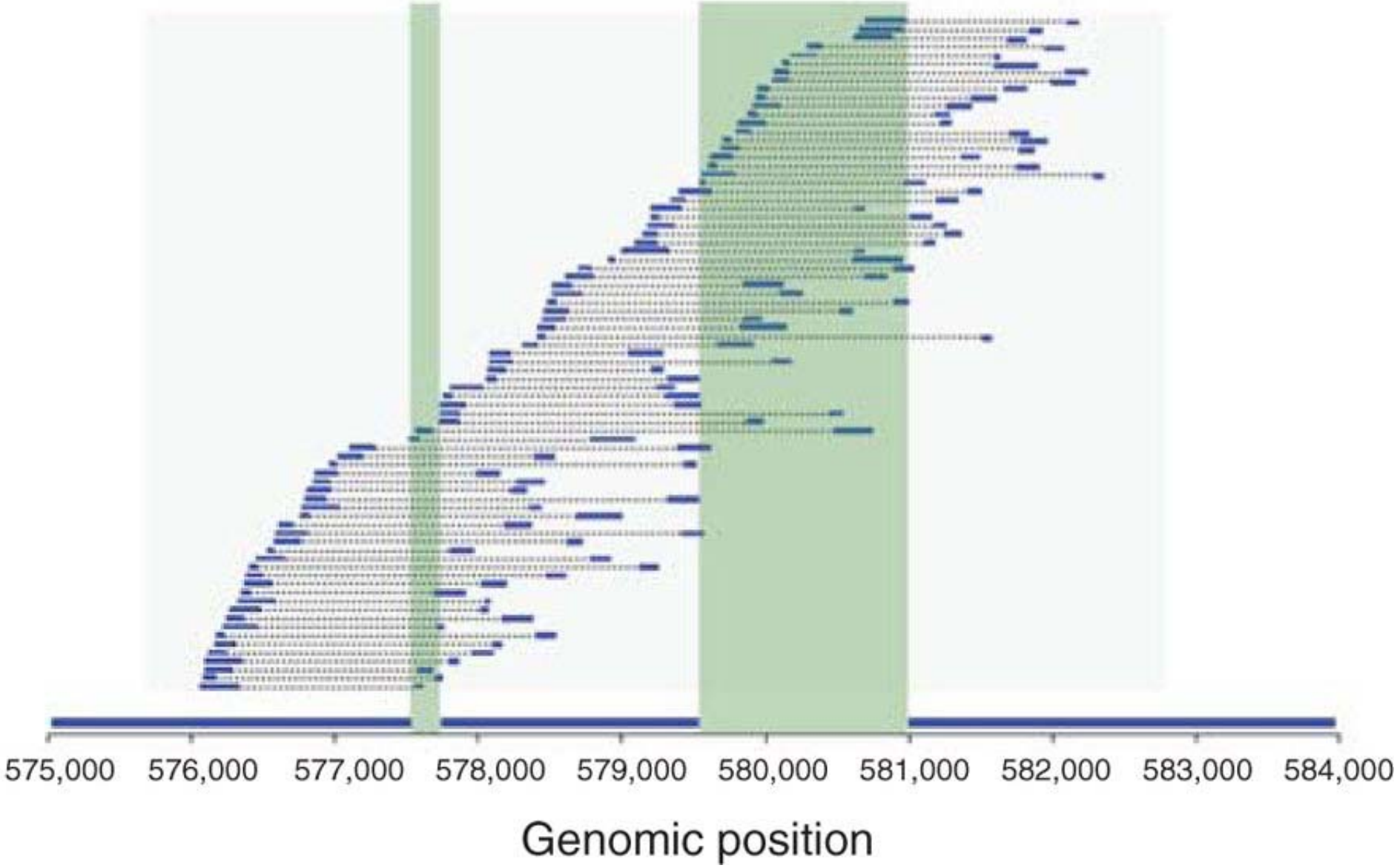
生物信息学

第十章 基因组组装

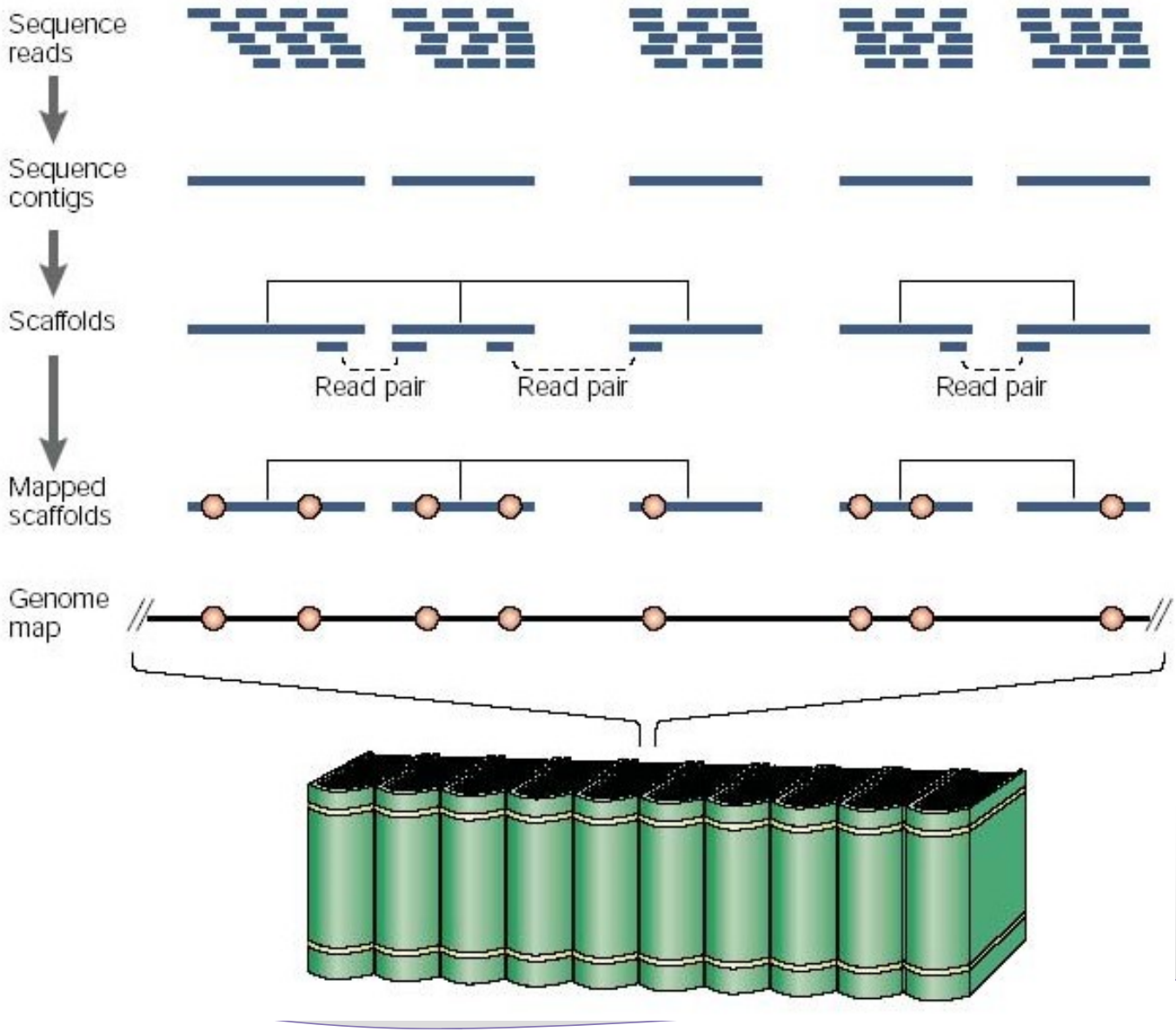
全基因组测序


Next-generation
DNA sequencing
... CATTCAGTAG ...
... AGCCATTAG ...
... GGTAGTTAG ...
... GGTAAACTAG
... TATAATTAG ...
... CGTACCTAG ...
Genomic
DNA
millions-billions of reads
~30-1000 nucleotides
Resequencing
De novo assembly
Align reads to reference
genome and identify variants
Construct genome sequence
from overlaps between reads

读段如何组装成基因组？


575,000
576,000
577,000
578,000
579,000
580,000
581,000
582,000
583,000
584,000
Genomic position

从头测序的基因组组装流程



Contig:
重叠群

Scaffold:
框架

组装

- 全基因组测序：DNA复制和片段化
- “鸟枪法”：全基因组随机片段化

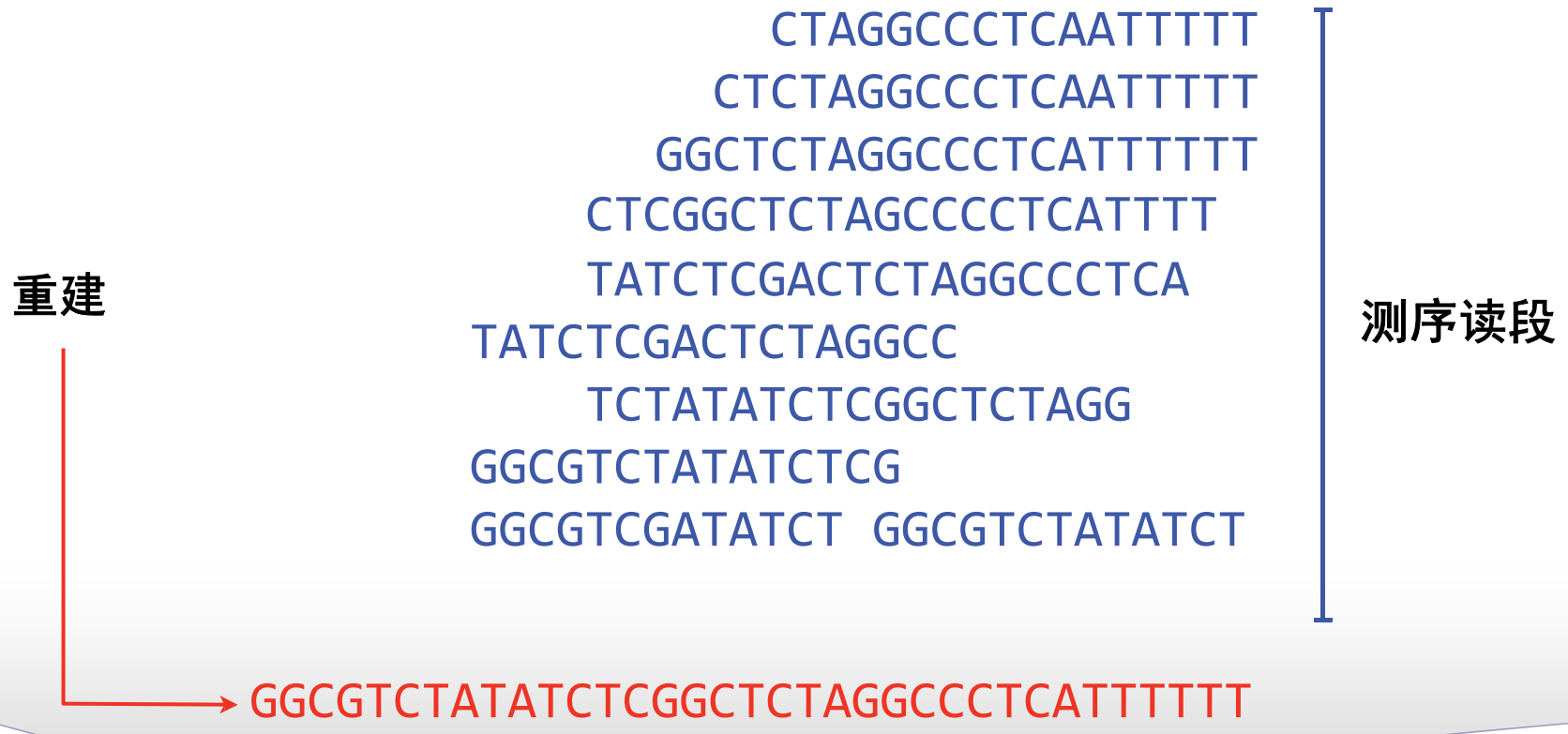
输入：GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

复制：
GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT
GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT
GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT
GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

片段：
GGCGTCTA TATCTCGG CTCTAGGCCCTC ATTTTTT
GGC GTCTATAT CTCGGCTCTAGGCCCTCA TTTTTT
GGCGTC TATATCT CGGCTCTAGGCCCT CATTTTTT
GGCGTCTAT ATCTCGGCTCTAG GCCCTCA TTTTTT

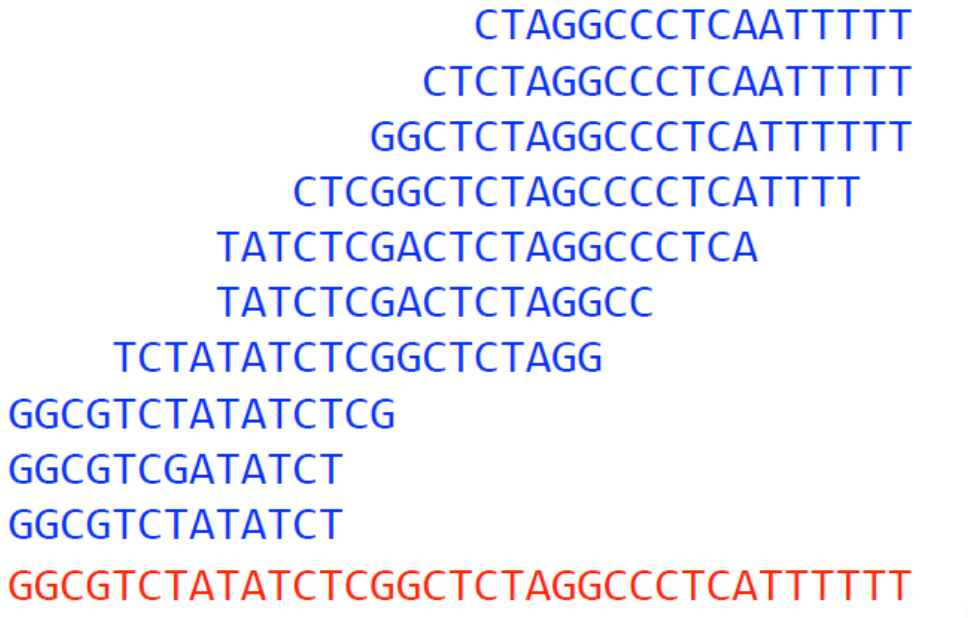
组装

- 测序：如果基因组上每个位置都有许多读段覆盖
- 问题：读段在基因组上哪个位置？



组装

- 覆盖率 (*Coverage*, *C*)：
  - 一般指平均覆盖率
  - 基因组上每一个位置平均覆盖读段的条数



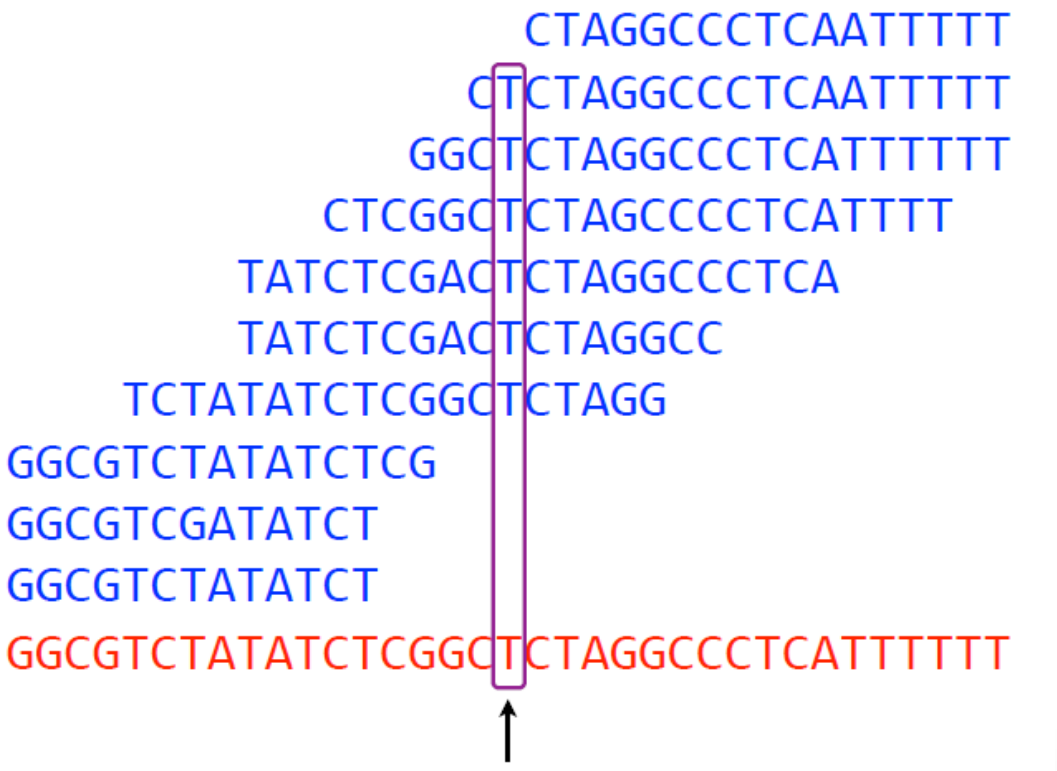
177个碱基

35个碱基

平均覆盖率 = 177 / 35 ≈ 7x

组装

- 也可以表示特定位置的覆盖率



该位置覆盖率 = 6

组装：基本原则

- 一条读段的后端与另一条读段的前端越相似，则

```
      TATCTCGACTCTAGGCC
      ||||||| |||||||
TCTATATCTCGGCTCTAGG
```

- 则两条读段越有可能在基因组上重叠

```
      TATCTCGACTCTAGGCC
TCTATATCTCGGCTCTAGG
GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT
```

组装

- 如果两条读段的确来自基因组上重叠的位置，为何会不同？

  - 测序错误
  - 不同染色体拷贝上的差异：例如人是双倍体，来自父亲和母亲的拷贝可能有差异

来自母亲的读段 TATCTCGACTCTAGGCC

来自父亲的读段 TCTATATCTCGGCTCTAGG

母亲的参考序列 TCTATATCTCGACTCTAGGCC

父亲的参考序列 TCTATATCTCGGCTCTAGGCC

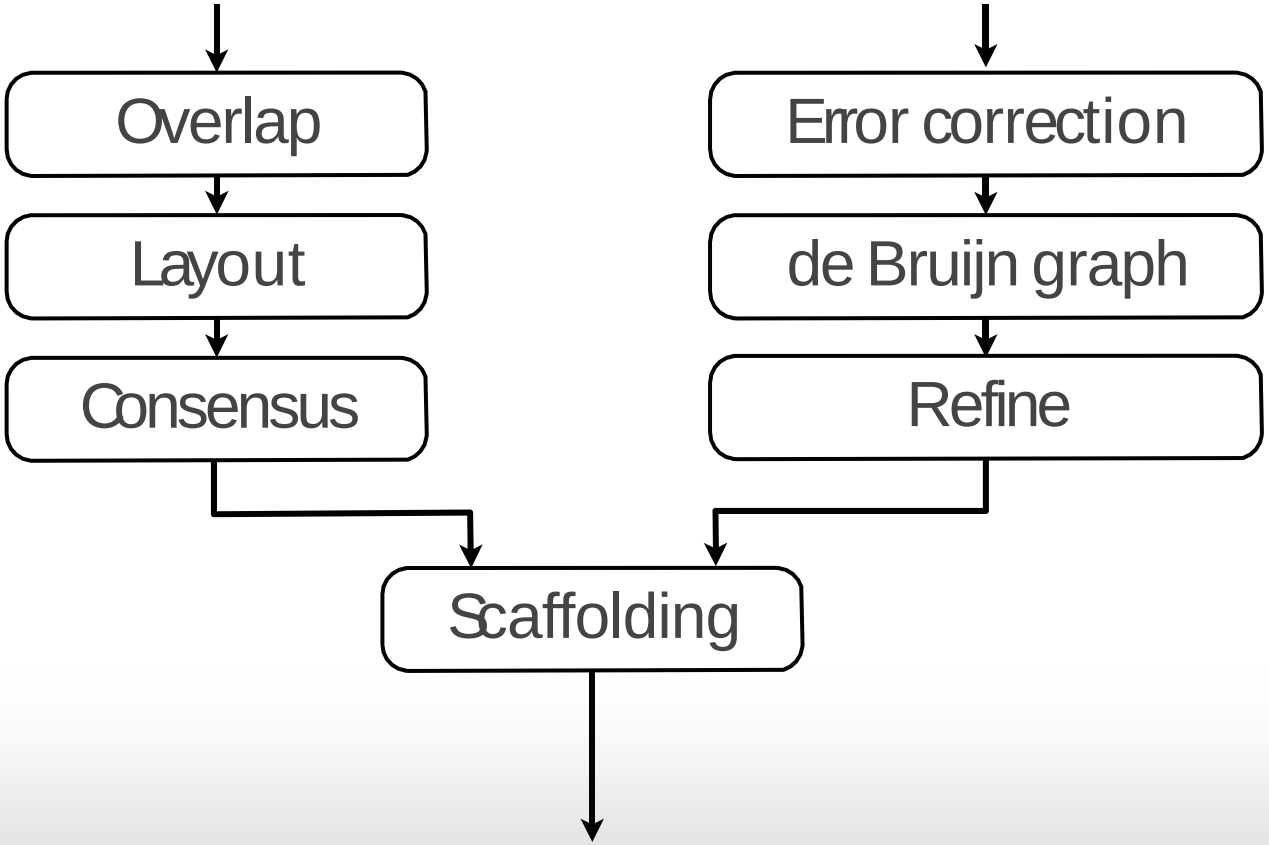
Genotype & SNP calling

两大类组装算法

- OLC: Overlap-Layout-Consensus
  - String Graph Assemblers
  - 根据读段直接构建重叠图
  - 去除冗余读段，寻找组装的路径
  - 工具：SGA, Fermi
- DBG: De Bruijn graph
  - 根据读段构建*k*-mer图，丢弃原始读段
  - 寻找组装的路径
  - 工具：Velvet, ABySS, SOAPdenovo2
- 重复片段（Repeat）的影响
  - 破坏基因组组装：Contig
  - 两类算法不考虑重复片段

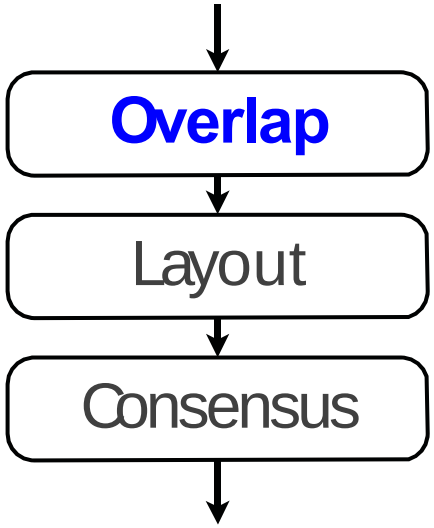
两大类组装算法

- OLC: Overlap-Layout-Consensus
- DBG: De Bruijn graph



Overlap-Layout-Consensus

❒ OLC: Overlap-Layout-Consensus



构建重叠图

将重叠图收束成contigs

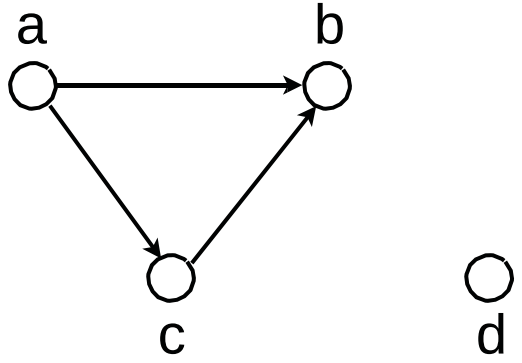
每一个contig选择最有可能的核苷酸序列

Overlap

- 发现所有重叠：
  - 建立一个有向图 (directed graph)
  - 结点 (vertex, node) 为读段
  - 有向边 (directed edge) 连接结点

有向图

- 有向图G(V, E)
  - 一系列结点V
  - 一系列有向边E
- 有向边：有序的结点对
  - (source, sink)
  - 节点：圆圈
  - 边：连接两个圆圈的线



$V = \{a, b, c, d\}$

$E = \{(a, b), (a, c), (c, b)\}$

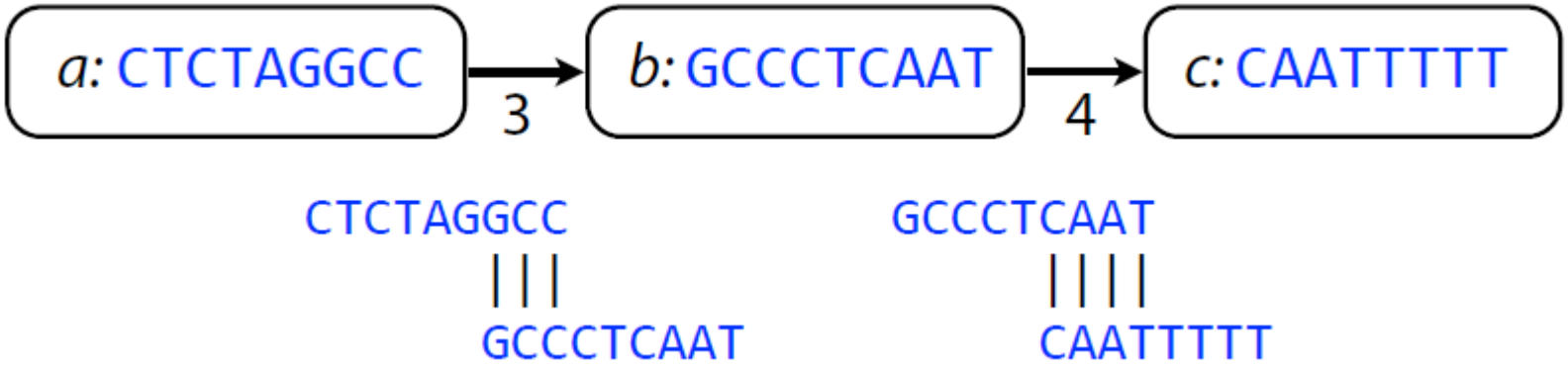
发起　　接收

重叠图

- 例如，后缀/前缀至少3个字符重叠
- 结点为读段，有向边为发起的后缀和接收的前缀重叠数

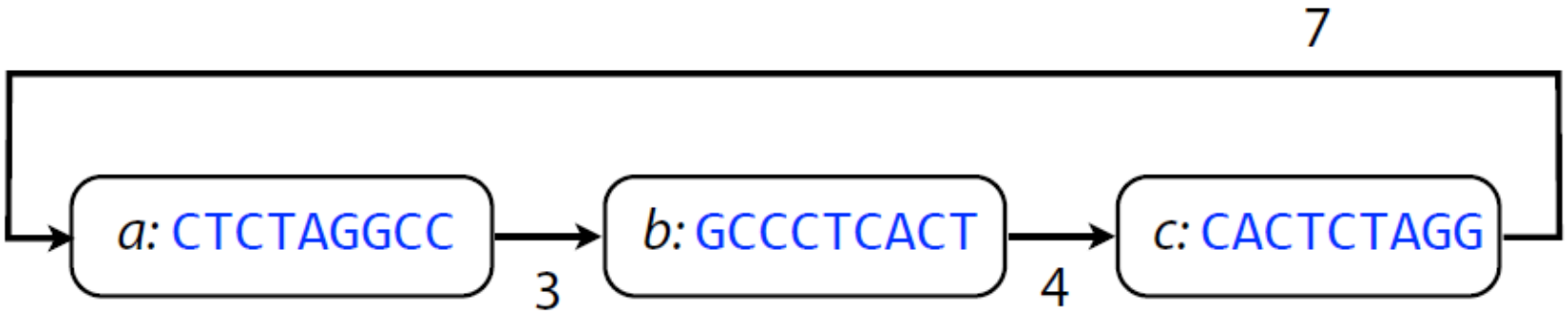
结点　{ *a:* CTCTAGGCC, *b:* GCCCTCAAT, *c:* CAATTTTT }

有向边　{ (*a*, *b*), (*b*, *c*) }

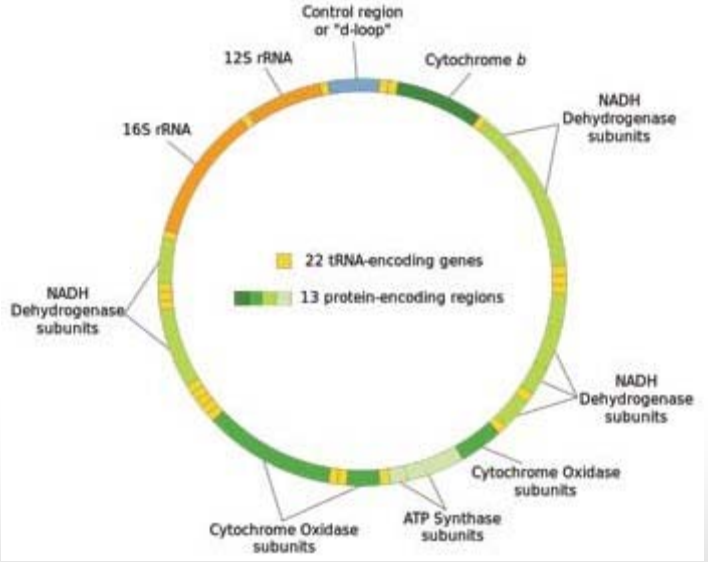


重叠图

- 重叠图可以是环形，起点和终点是同一个结点



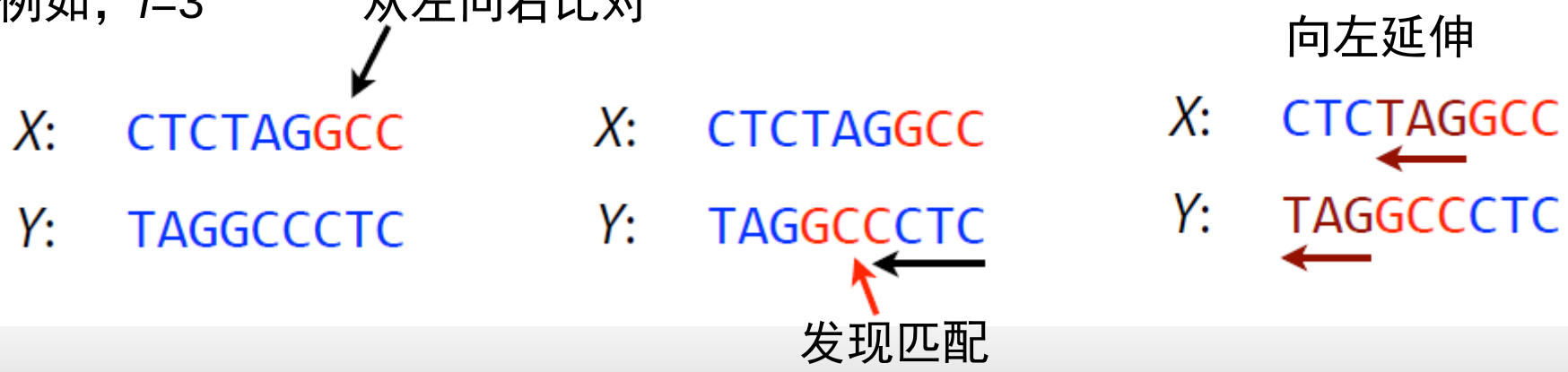
- 环形DNA链
  - 细菌基因组一般为环形
  - 线粒体DNA为环形
  - DNA的重复序列



重叠搜索

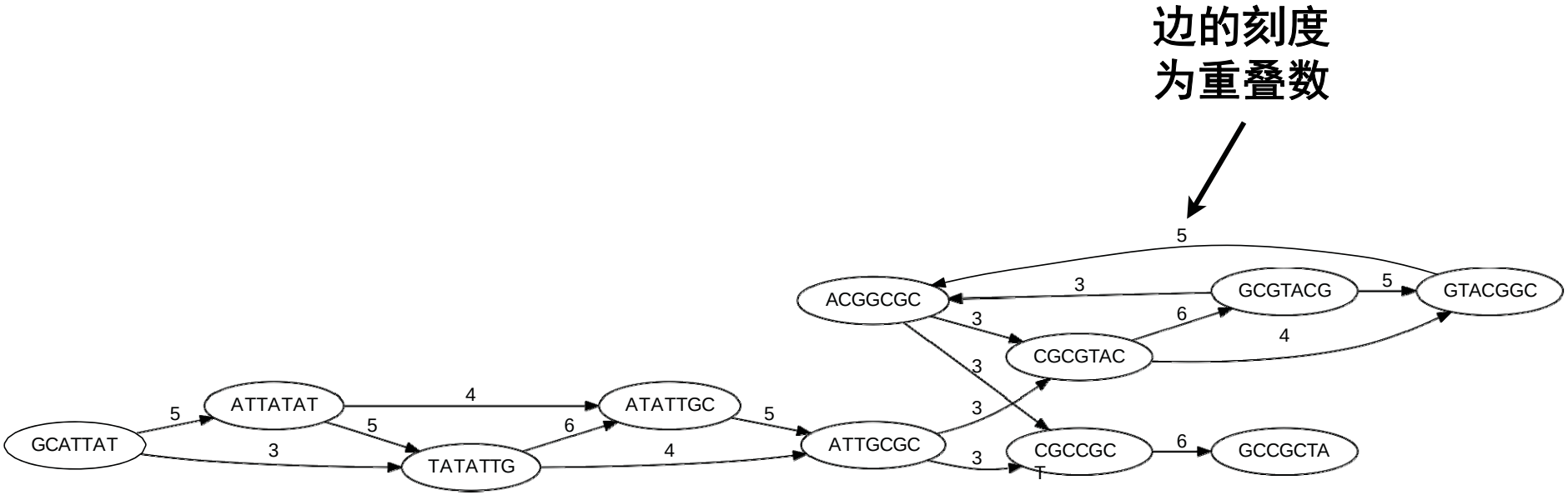
- 如何建立重叠图？
  - 两条读段*X*, *Y*，长度为*k*
  - *X*后缀精确匹配*Y*前缀的长度≥ *l*
- 思路：
  - 利用FM索引，在*Y*里搜索长度为*l*的*X*后缀
  - 若匹配则向左延伸，确认*Y*的前缀是否都可以匹配

例如，*l*=3　　从左向右比对



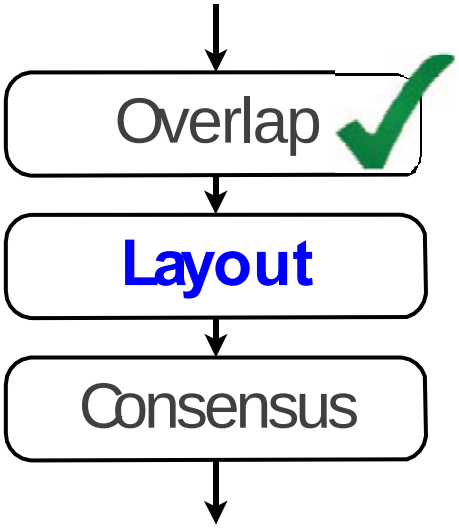
重叠搜索

- 重叠图*l* = 3



原始序列：GCATTATATATTGCGCGTACGGCGCCGCTACA

Overlap-Layout-Consensus



构建重叠图

将重叠图收束成contigs

每一个contig选择最有可能的核苷酸序列

Shortest common superstring

- **SCS：基因组组装**
  - 给定一系列读段S，寻找SCS(S)，保证
  - 所有读段S都是其子串，并且最短
- **若无“最短”的限制：直接合并所有读段**

读段S集合　BAA AAB BBA ABA ABB BBB AAA BAB

直接合并　BAAAABBBAABAABBBBBAAABAB

24

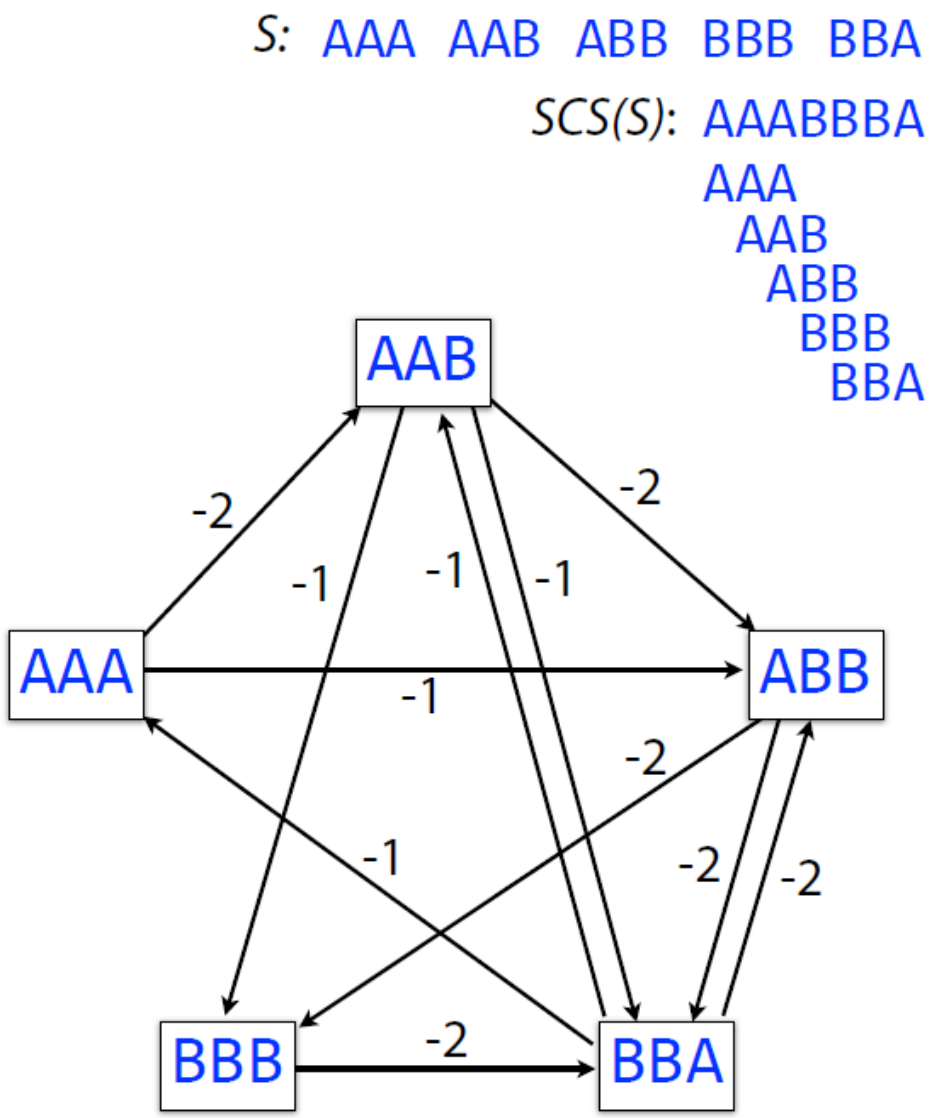
SCS(S)　AAABBBABAA

10

AAA
AAB
ABB
BBB
BBA
BAB
ABA
BAA

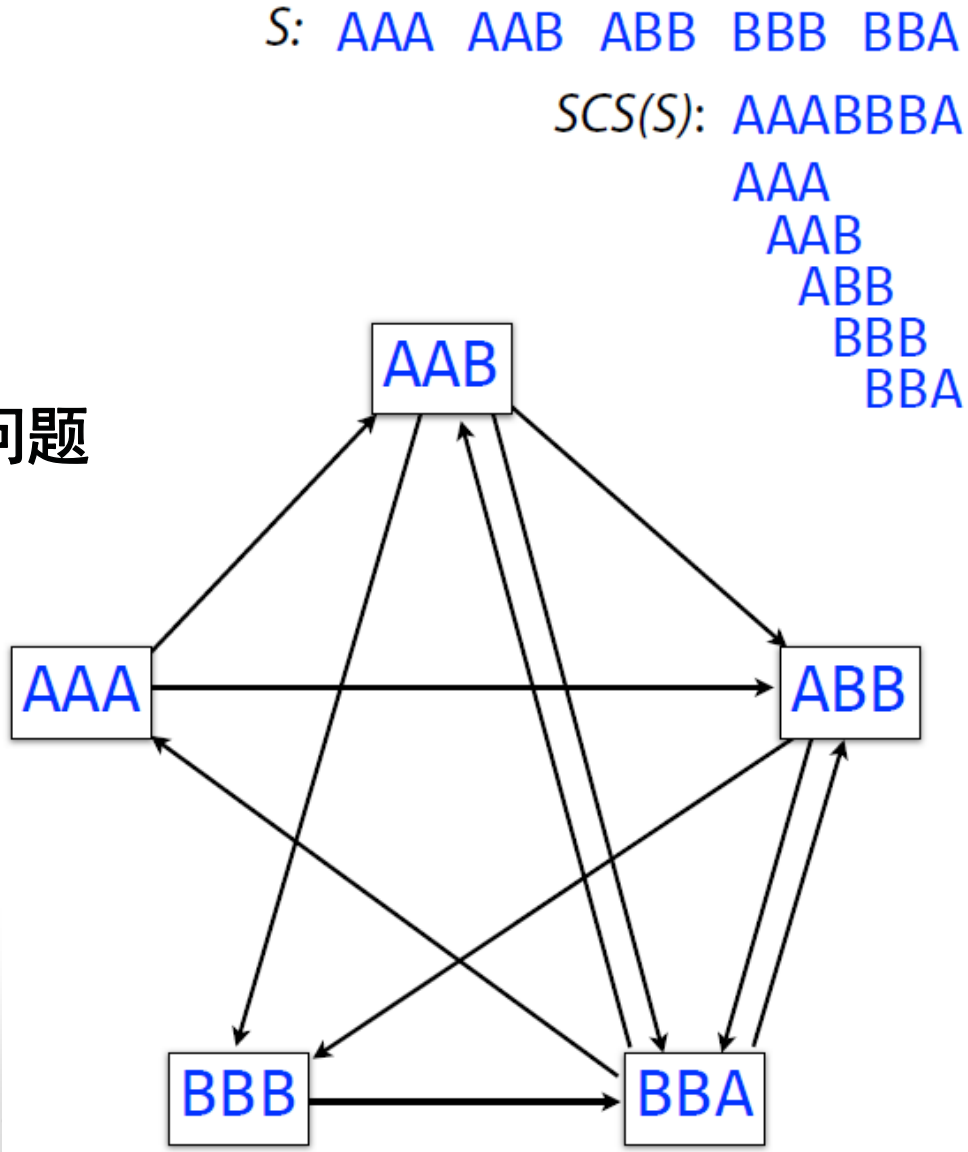
Shortest common superstring

- 如何求解SCS(S)?
  - 考虑边的权重 = -重叠长度
- SCS：
  - 走代价最小的路径
  - 访问每个结点仅一次
  - Traveling Salesman Problem (TSP)
  - NP-hard



Shortest common superstring

- 不考虑边的权重
- Hamiltonian Path problem: NP-complete
  - NP完全问题
  - 既是NP问题又是NP-hard问题
  - 需要启发式算法



SCS：贪心算法

- 选择最长的重叠，合并发起和接收：不保证最优

Greedy-SCS algorithm (l = 1):

输入读段

ABA ABB AAA AAB BBB BBA BAB BAA

2 BAAB ABA ABB AAA BBB BBA BAB

2 BABB BAAB ABA AAA BBB BBA

2 BBAAB BABB ABA AAA BBB

2 BBBAAB BABB ABA AAA

2 BBBAABA BABB AAA

2 BABBBAABA AAA

1 BABBBAABAAA

BABBBAABAAA

Superstring

每一行合并一次

第一列：合并字符的长度

红色读段合并后进入下一轮

贪心算法:
BABBBAABAAA

真实的SCS：
AAABBBABAA

SCS：贪心算法

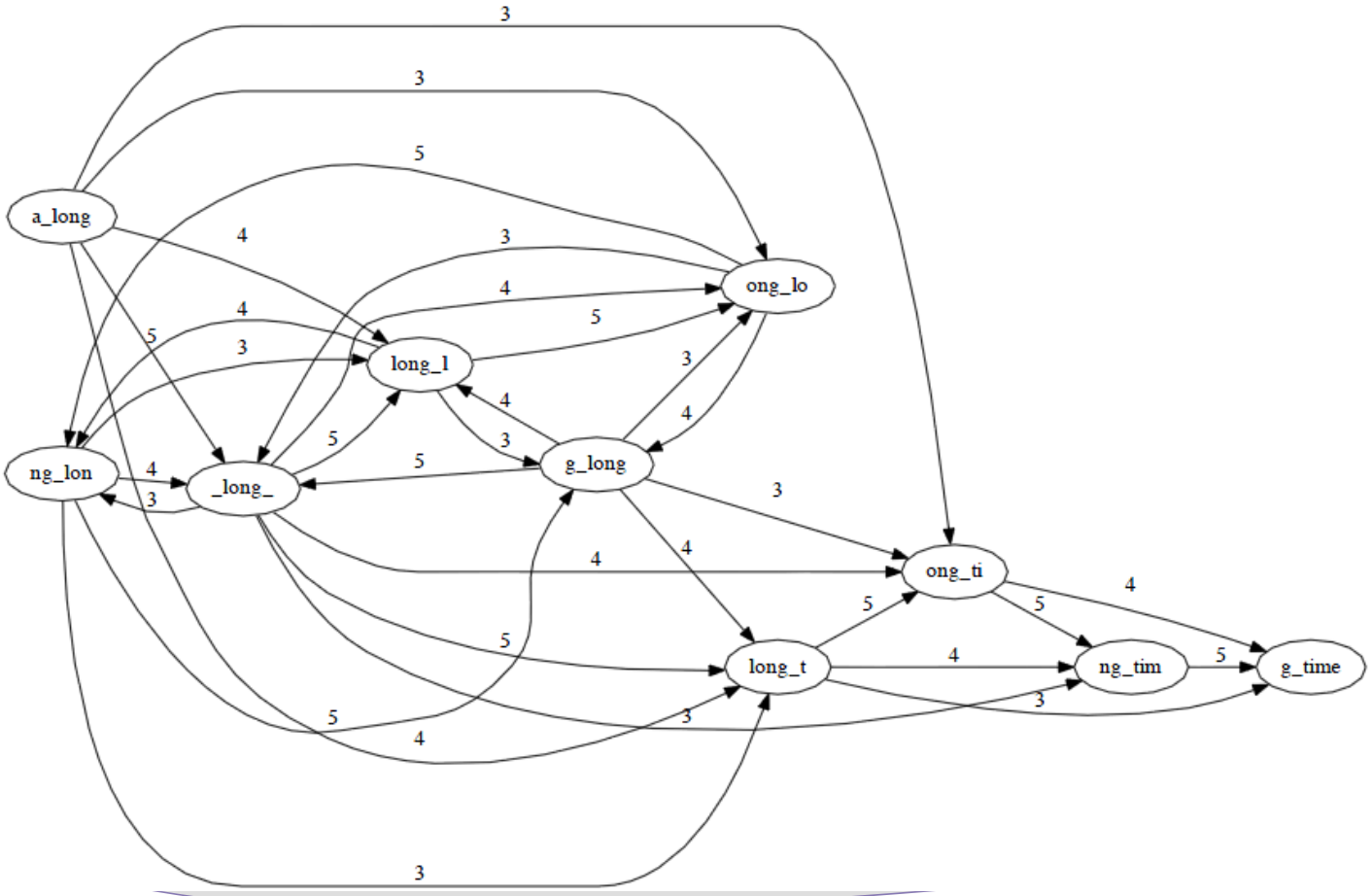
- Greedy-SCS算法 ($k = 6, l = 3$):
  - a_long_long_long_time

```
  ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long g_time ng_tim
5 ng_time ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long
5 ng_time g_long_ ng_lon a_long long_l ong_ti ong_lo long_t
5 ng_time long_ti g_long_ ng_lon a_long long_l ong_lo
5 ng_time ong_lon long_ti g_long_ a_long long_l
5 ong_lon long_time g_long_ a_long long_l
5 long_lon long_time g_long_ a_long
5 long_lon g_long_time a_long
5 long_long_time a_long
4 a_long_long_time
  a_long_long_time
```

组装结果：a_long_long_time?　　丢失：_long

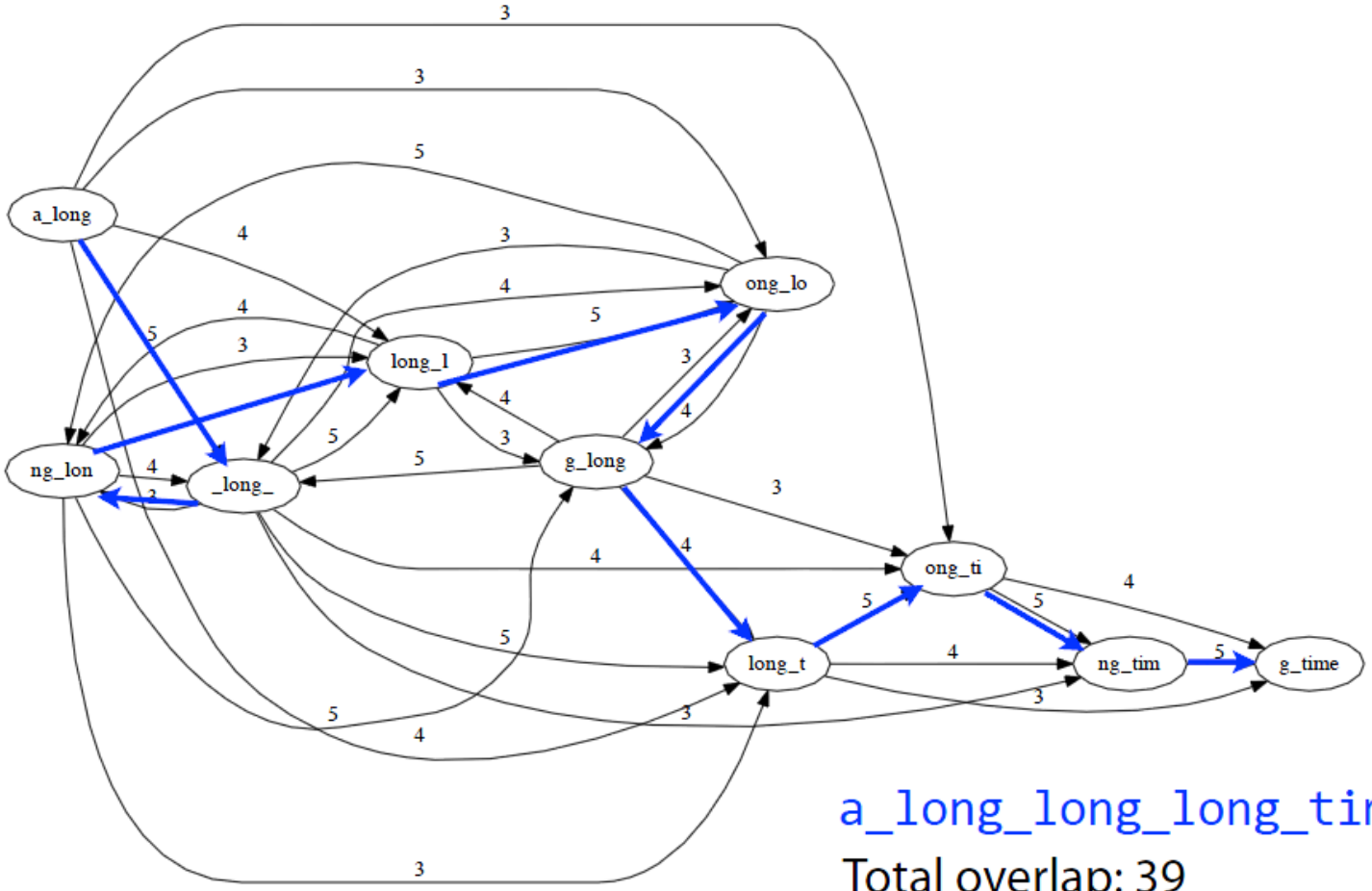
SCS：贪心算法

- Greedy-SCS算法 ($k = 6, l = 3$):
  - a_long_long_long_time



SCS：贪心算法

- Greedy-SCS算法 ($k = 6, l = 3$):
  - a_long_long_long_time

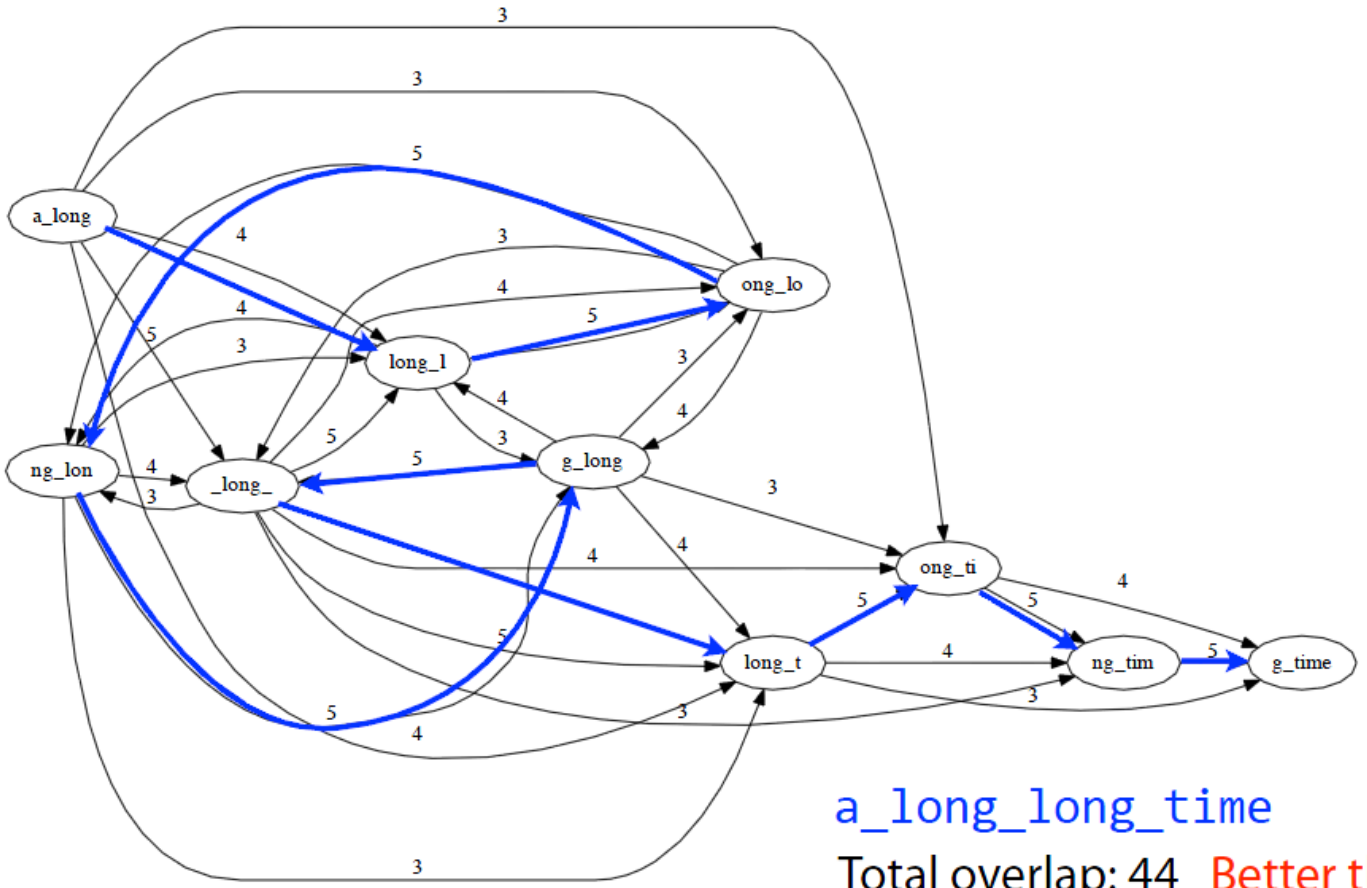


a_long_long_long_time

Total overlap: 39

SCS：贪心算法

- Greedy-SCS算法 ($k = 6, l = 3$):
  - a_long_long_long_time



a_long_long_time

Total overlap: 44 Better than the correct path!

SCS：贪心算法

❒ Greedy-SCS算法 (k = 8, l = 3):

- a_long_long_long_time

```
  long_lon ng_long_ _long_lo g_long_t ong_long g_long_l ong_time a_long_l _long_ti long_tim
7 long_time long_lon ng_long_ _long_lo g_long_t ong_long g_long_l a_long_l _long_ti
7 _long_time long_lon ng_long_ _long_lo g_long_t ong_long g_long_l a_long_l
7 _long_time a_long_lo long_lon ng_long_ g_long_t ong_long g_long_l
7 _long_time ong_long_ a_long_lo long_lon g_long_t g_long_l
7 g_long_time ong_long_ a_long_lo long_lon g_long_l
7 g_long_time ong_long_ a_long_lon g_long_l
7 g_long_time ong_long_l a_long_lon
7 g_long_time a_long_long_l
3 a_long_long_long_time
  a_long_long_long_time
```

组装结果：a_long_long_long_time

SCS：贪心算法

- $k = 8$的读段可以正确识别三个_long
  - 一个读段横跨三个_long

a_long_long_long_time

g_long_l

- 重复序列：破坏组装
  - 读段长度增加：解决重复序列的问题
  - 算法不能解决重复序列

a_long_long_long_time

collapse

a_long_long_time

人类基因组~50%为重复序列

重复序列：破坏组装

- **Greedy-SCS算法，不同的*k*，*l*值**

输入　　it_was_the_best_of_times_it_was_the_worst_of_times

输出

l, *k*	output
3, 5	the_worst_of_times_it_was_the_best_o
3, 7	s_the_worst_of_times_it_was_the_best_of_t
3, 10	_was_the_best_of_times_it_was_the_worst_of_tim
3, 13	it_was_the_best_of_times_it_was_the_worst_of_times

重复序列：it_was_the_长度为11

重复序列：破坏组装

Greedy-SCS算法，不同的k , l 值

输入　swinging_and_the_ringing_of_the_bells_bells_bells_bells_bells

输出

l, k	output
3, 7	swinging_and_the_ringing_of_the_bells_bells
3, 13	swinging_and_the_ringing_of_the_bells_bells_bells
3, 19	swinging_and_the_ringing_of_the_bells_bells_bells_bells_b
3, 25	swinging_and_the_ringing_of_the_bells_bells_bells_bells_bells

子串越长越有可能正确识别重复序列

k = 25

e_bells_bells_bells_bells

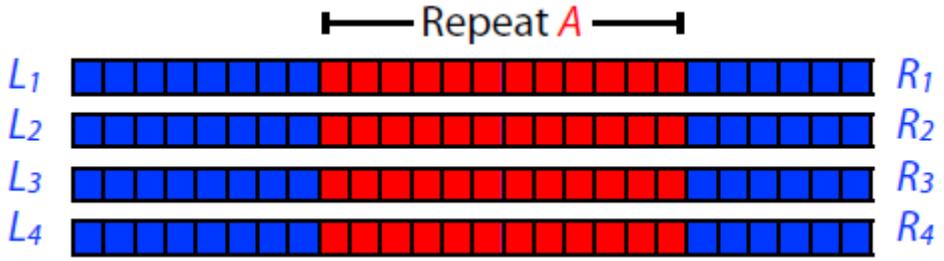
_bells_bells_bells_bells_

bells_bells_bells_bells_b

重复序列

❒ 关于重复序列*A*的重叠图

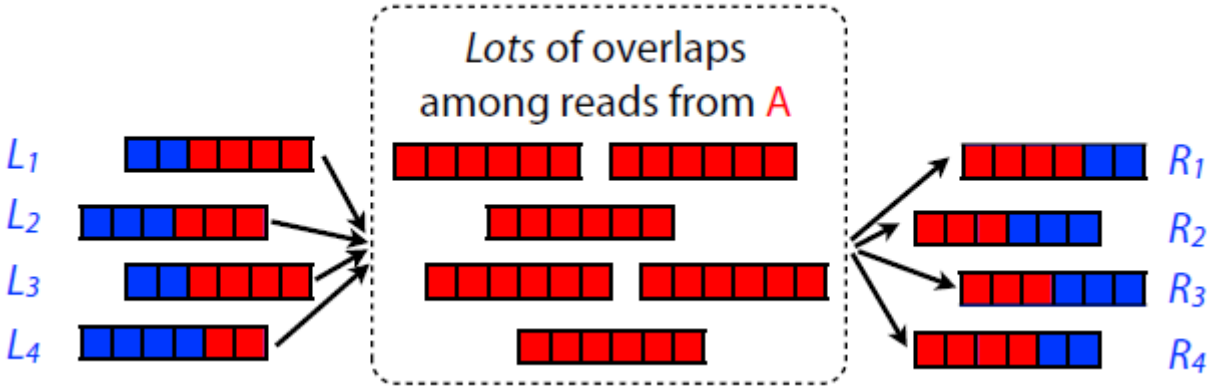
基因组序列



A比读段长

❒ 不能确定重复序列的路径

读段

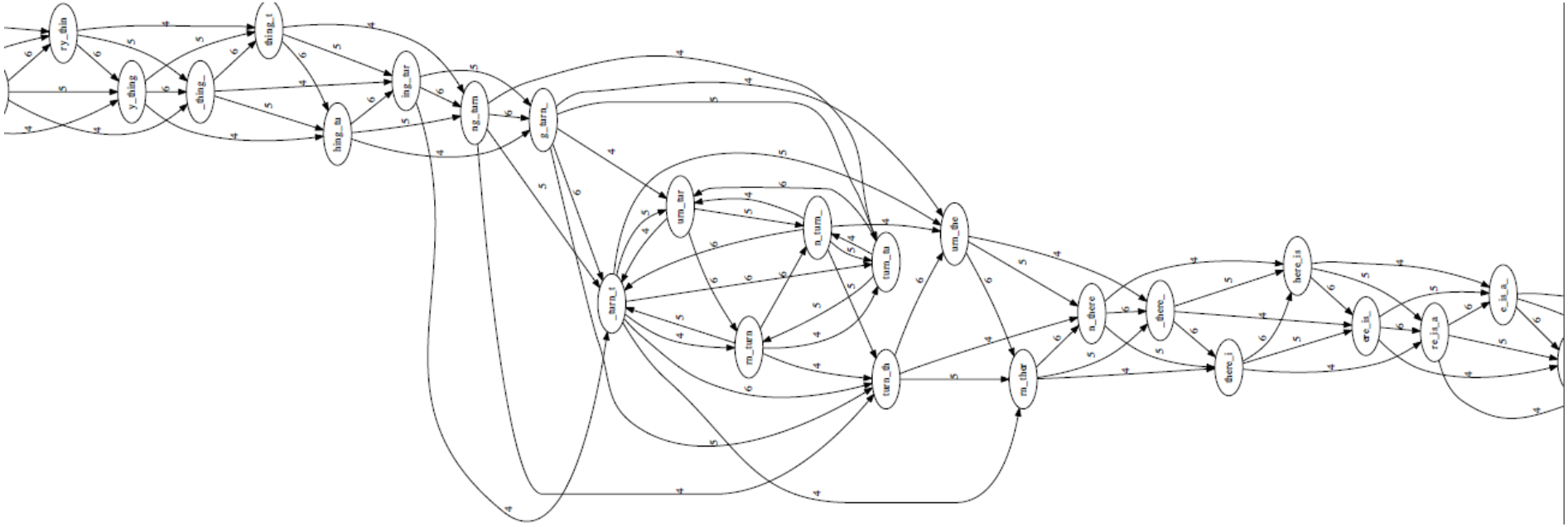


Layout

- Greedy-SCS算法的缺陷
  - 不能发现最优的SCS
  - 存在重复序列时得到错误的路径
- 若不考虑重复序列，如何从重叠图获得Contigs？

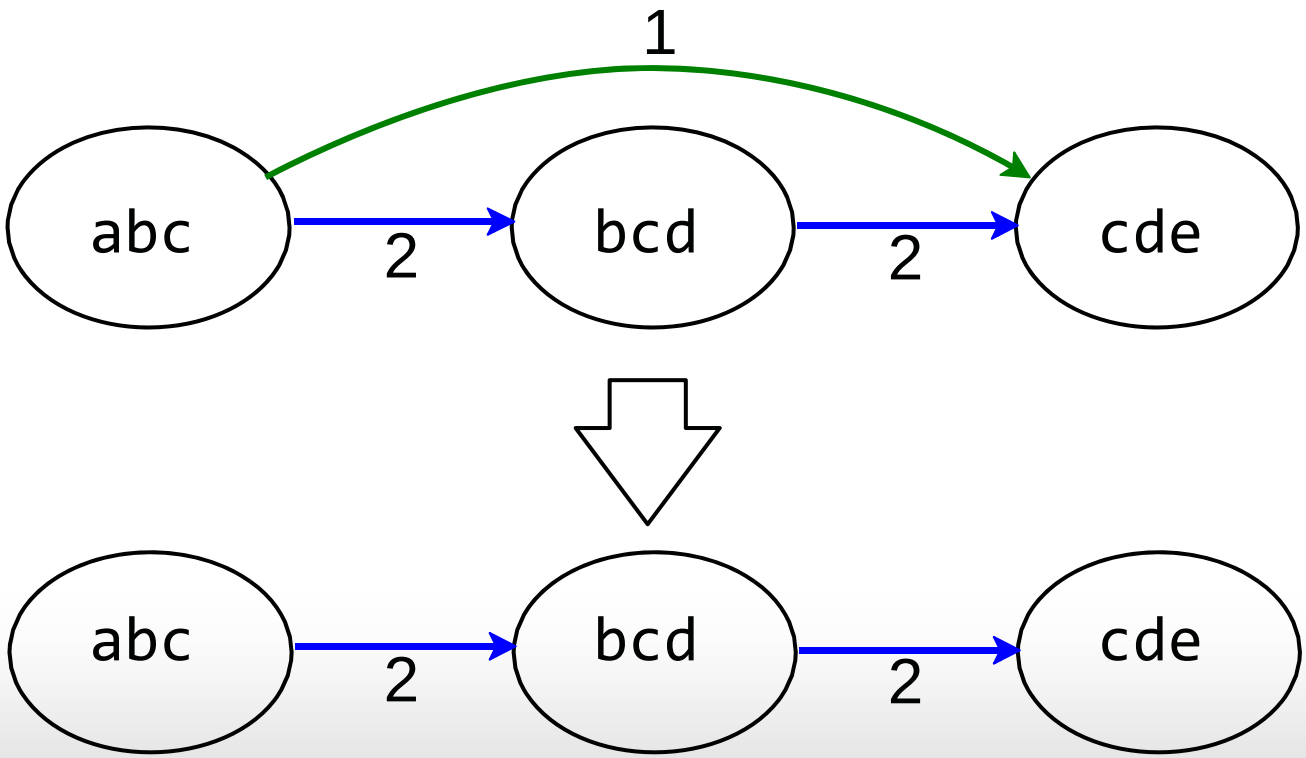
重叠图 to_every_thing_turn_turn_turn_there_is_a_season

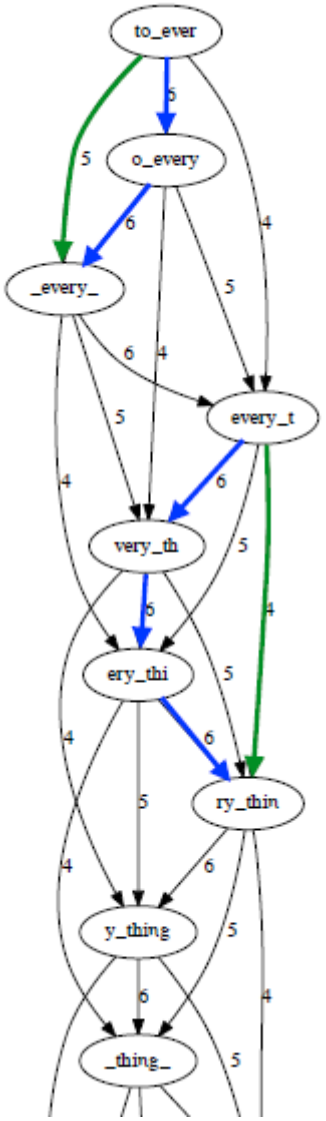
$l = 4, k = 7$



Layout

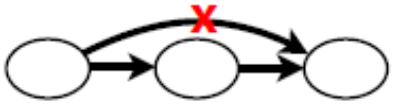
- 去掉可间接推断的（transitively-inferrible）边
- 例如绿色的连接可以由蓝色的间接获得



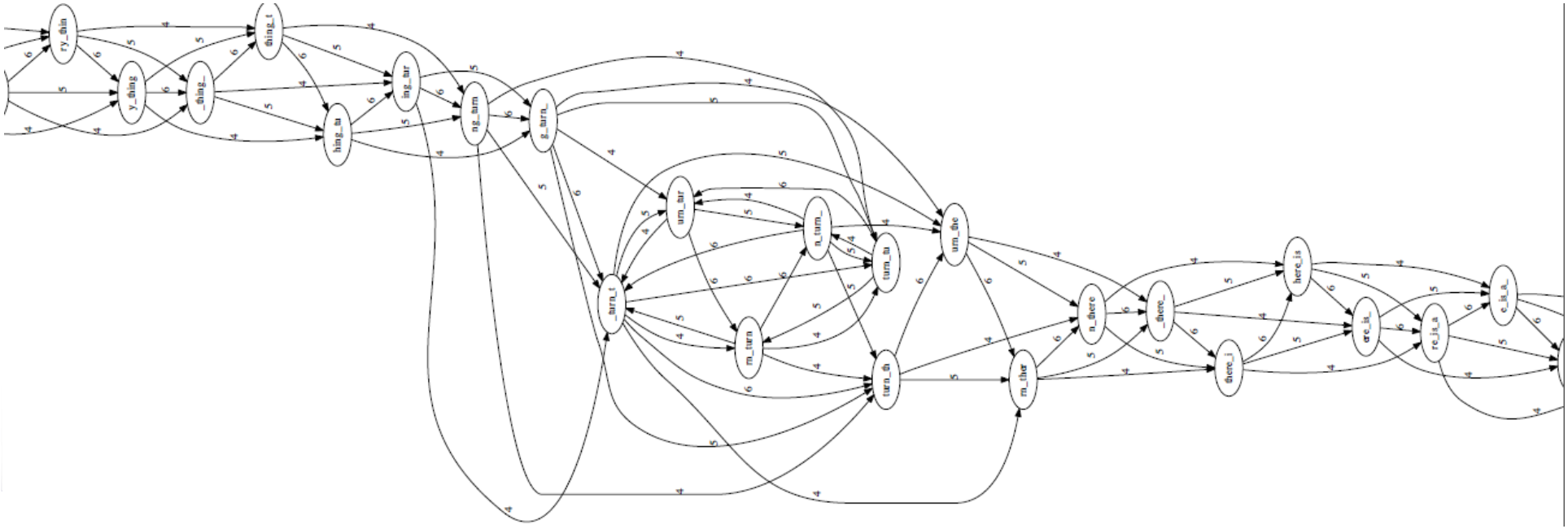


Layout

- 去掉可间接推断的 边



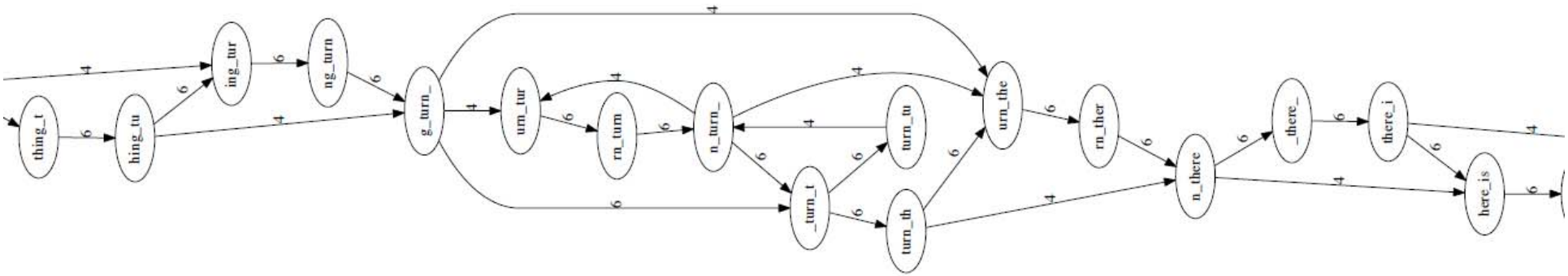
初始图



Layout

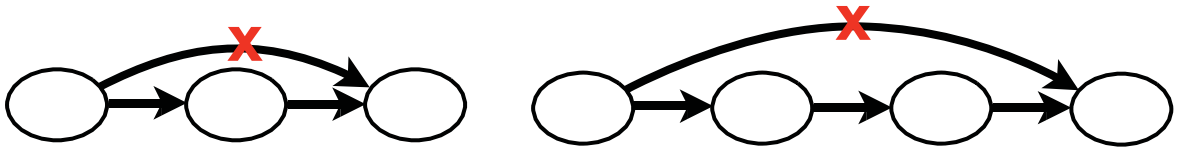
- 继续去掉可间接推断的 边

获得：

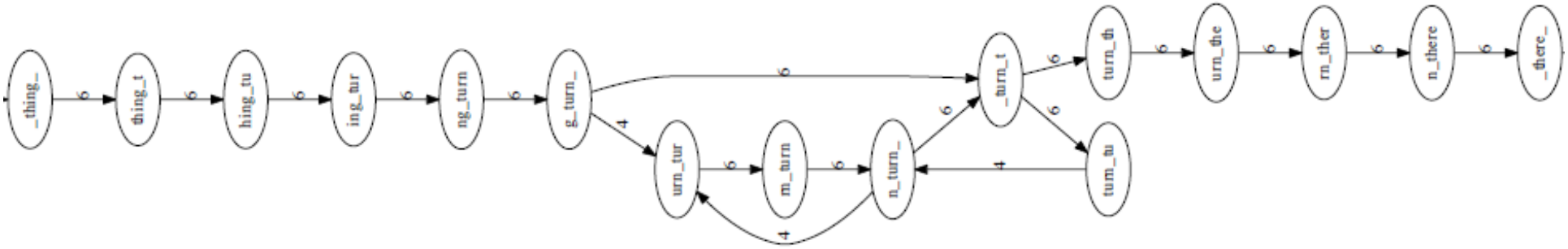


Layout

- 去掉所有可间接推断的 边

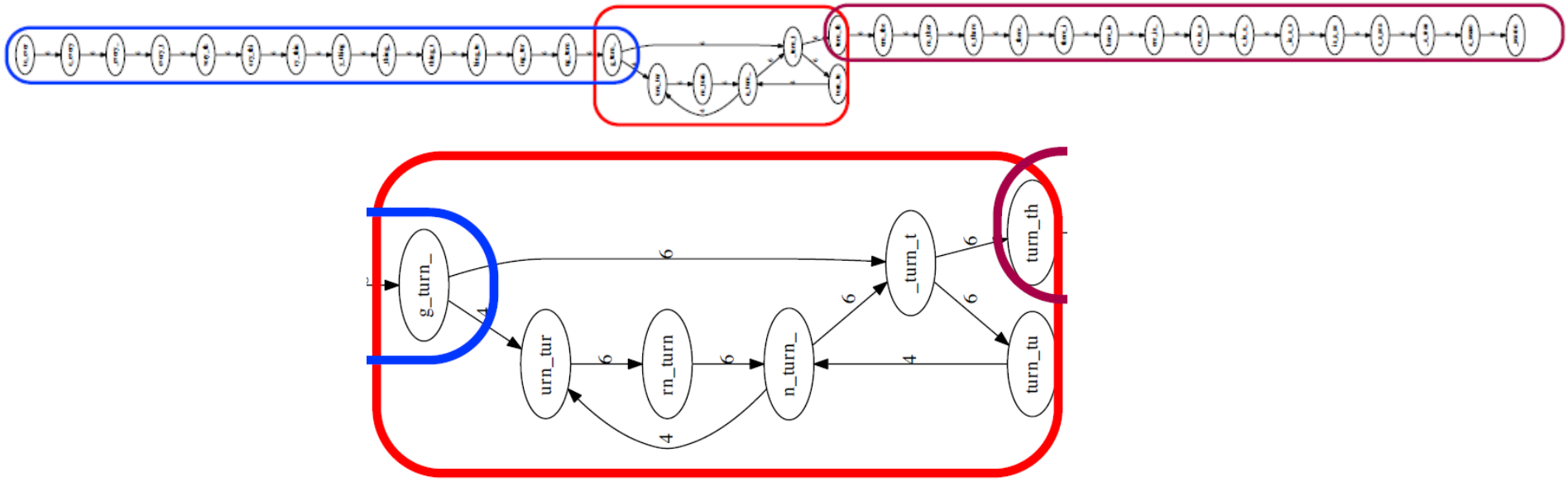


最终结果：



Layout

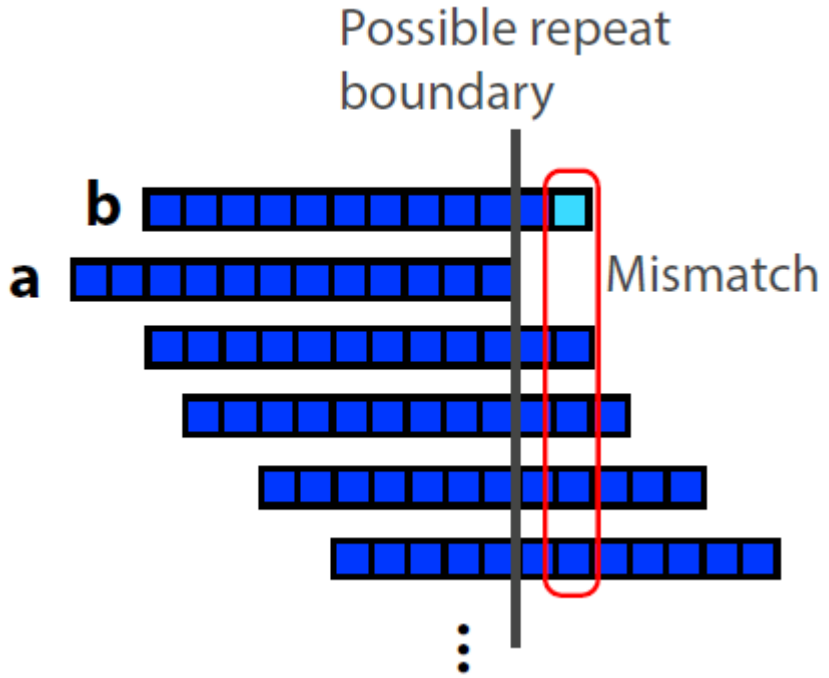
- **Contig: 没有分支**

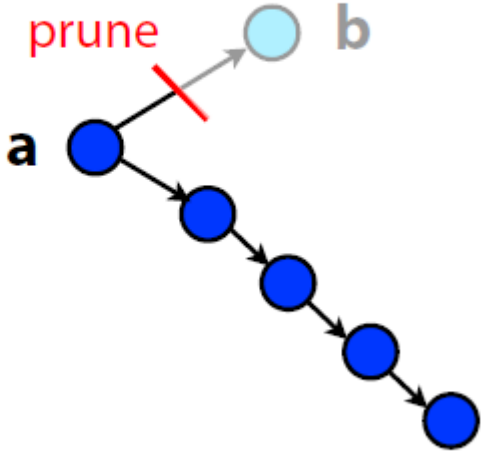


无法解决的重复序列

Layout

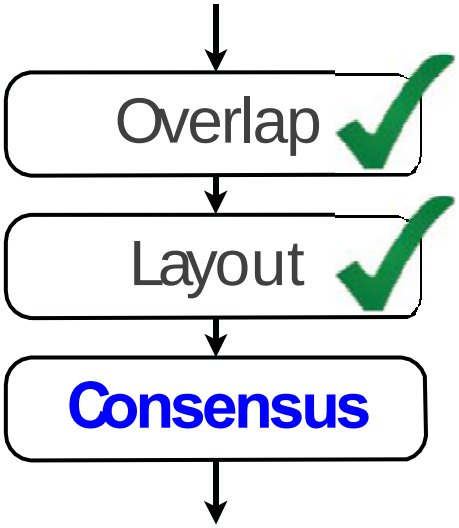
- 现实中，layout还需要处理有错误的子图，例如，测序错误





测序错误导致错配。通过b末端的路径引起错配，因此推断为测序错误，并删除相应路径

Overlap-Layout-Consensus



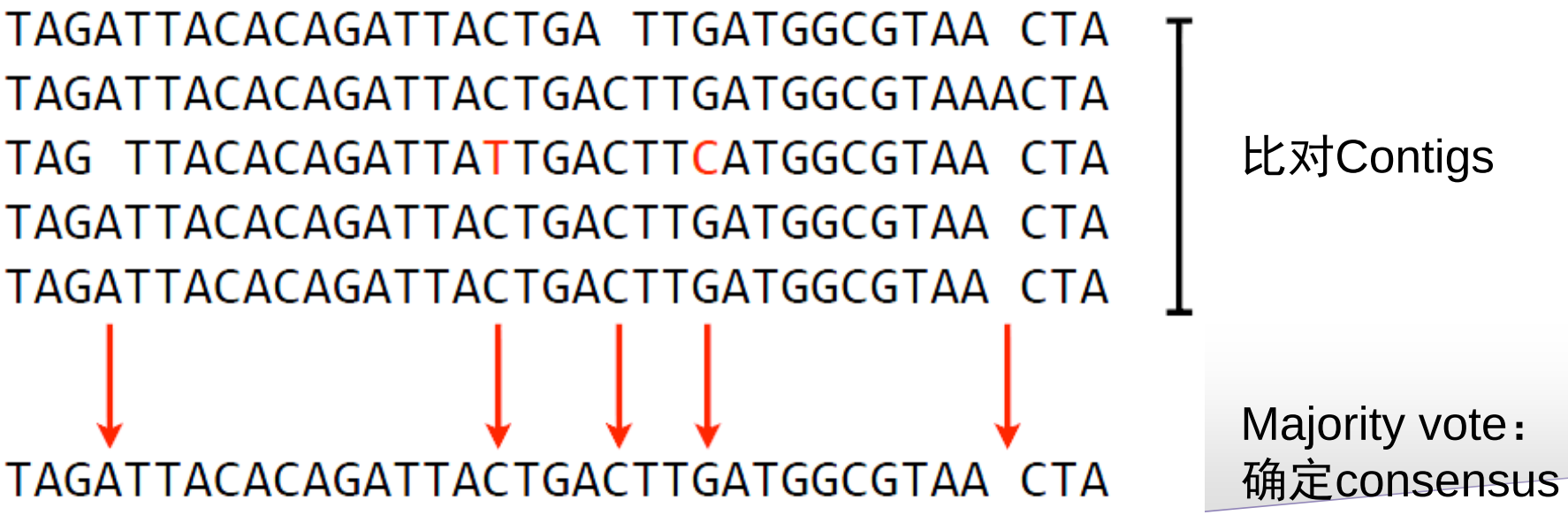
构建重叠图

将重叠图收束成contigs

每一个contig选择最有可能的核苷酸序列

Consensus

- 确定每个位置的碱基，需要考虑：
  - 测序错误？
  - 倍性 (ploidy)?
- 例如，若真实的genotype为AA
  - 测序错误高
  - 测序深度低：每个位置仅有6条读段

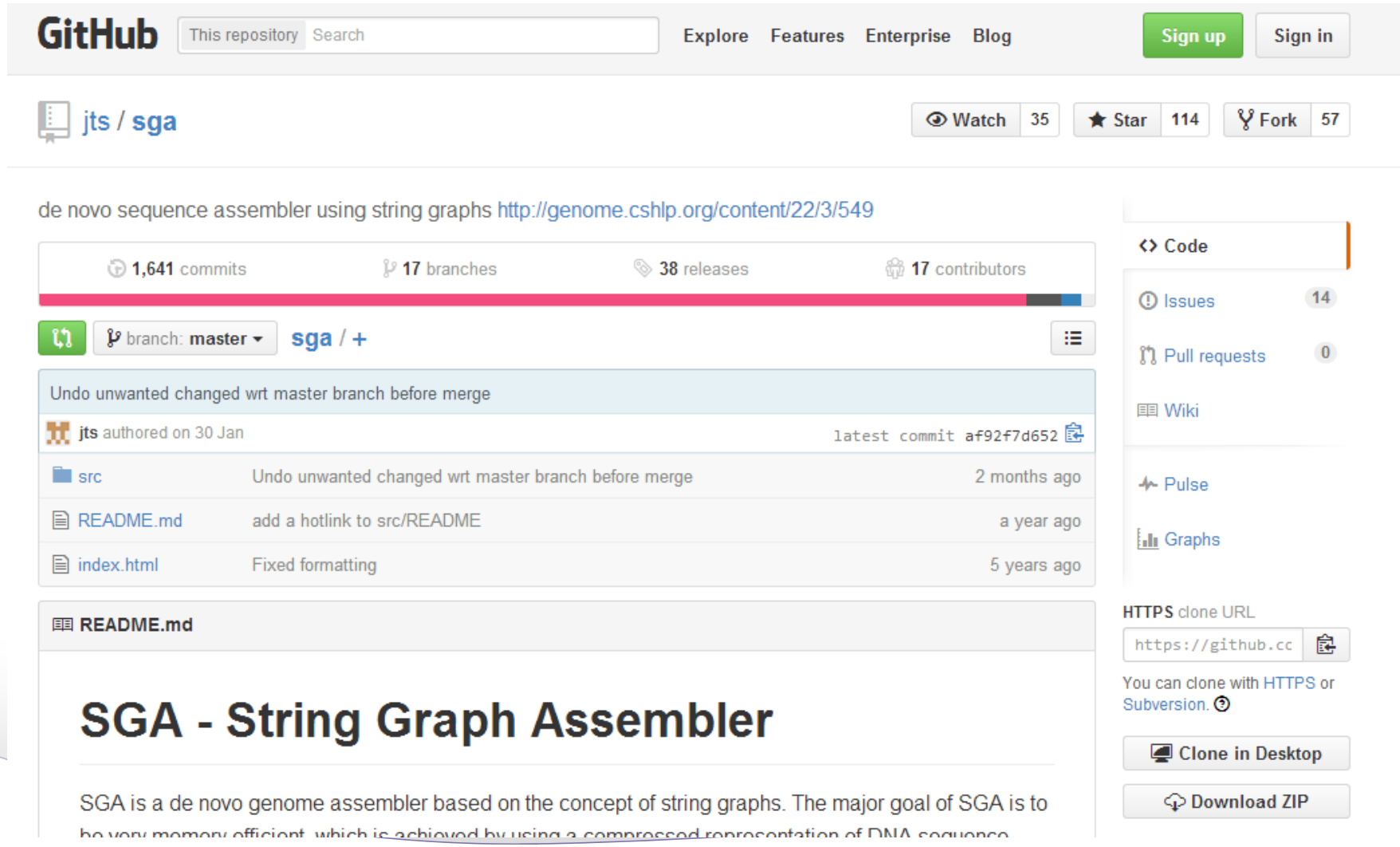


Overlap-Layout-Consensus

- **OLC算法的主要缺点：**
  - **重叠图构建的速度慢**
  - **NGS测序数据规模大：人类基因组30X，~$9*10^{10}$碱基**

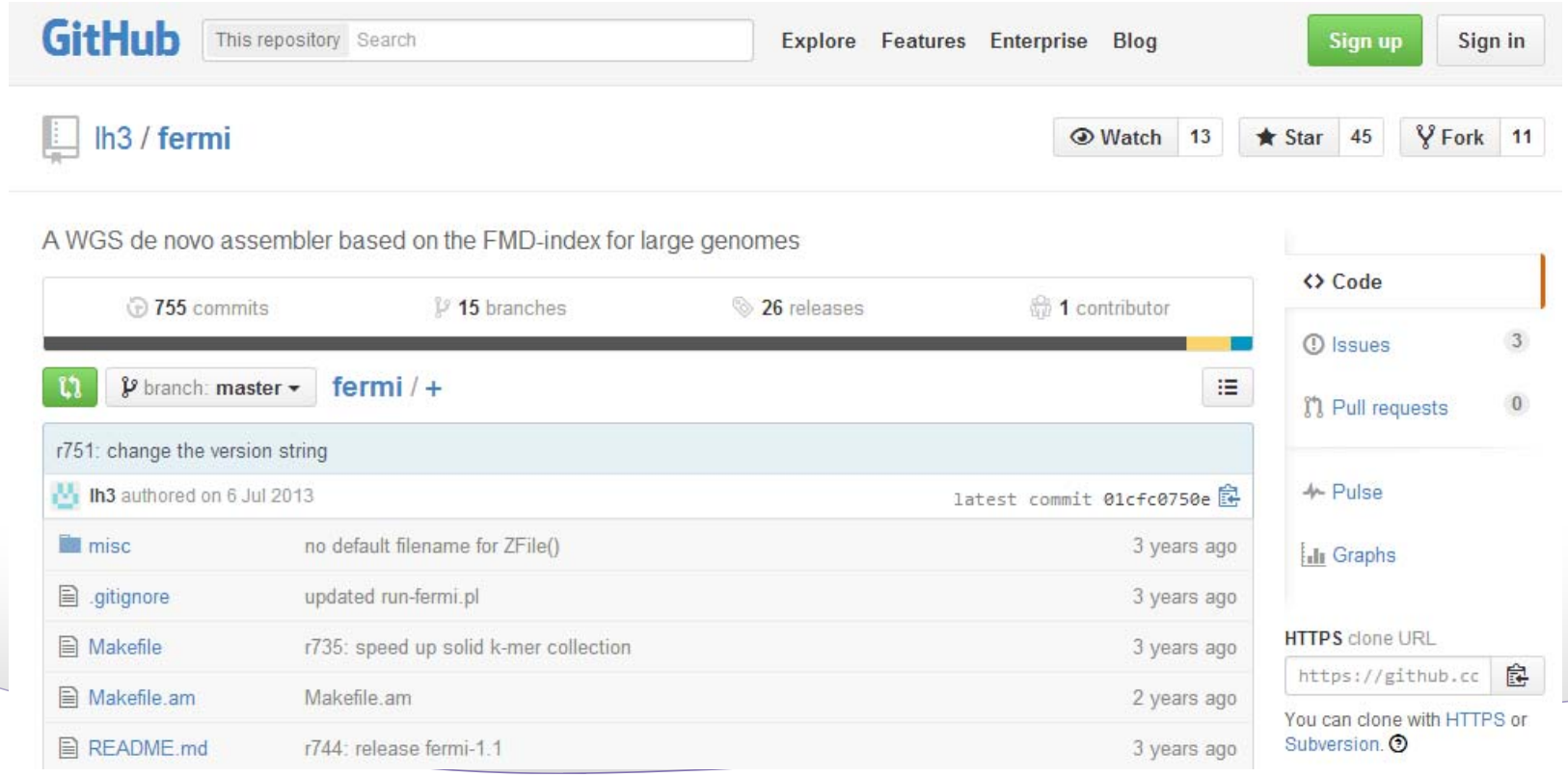
SGA - String Graph Assembler

- 2015年发布，https://github.com/jts/sga



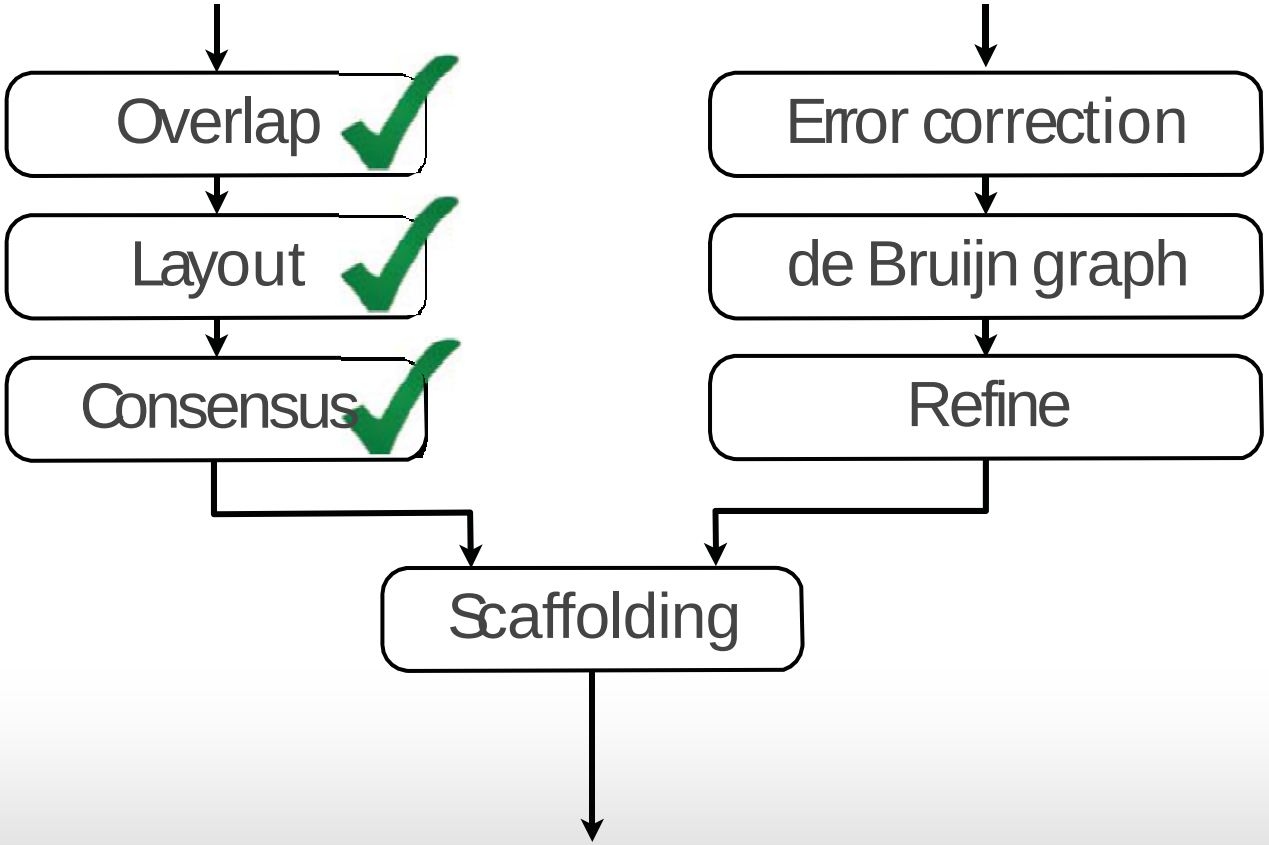
Fermi

- 李恒，2012年发布
- 全基因组的从头组装
- SNP和INDEL calling
- https://github.com/lh3/fermi



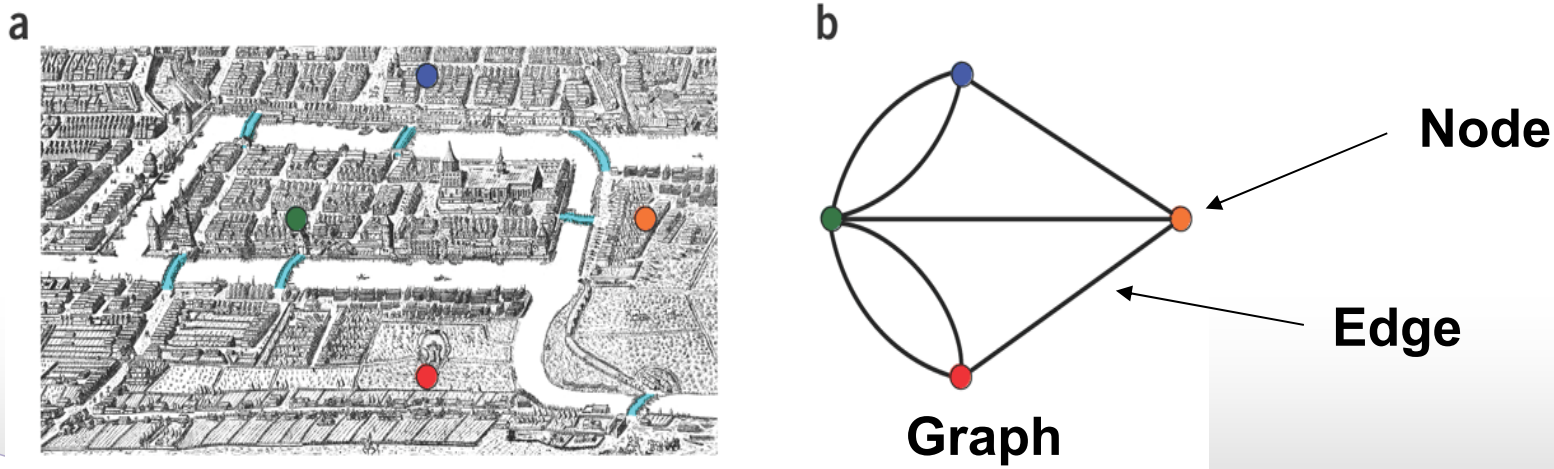
两大类组装算法

- OLC: Overlap-Layout-Consensus
- **DBG: De Bruijn graph**



De Bruijn graph

- “Seven Bridges of Königsberg”：哥尼斯堡七桥问题
  - Hamiltonian cycle：每个点遍历一次
  - Eulerian cycle：每条边遍历一次
- 点（Node）：读段或*k*-mer
- 边（Edge）：两点之间的关联



Velvet

- 第一个使用DBG算法的基因组组装工具
  - 小的或中等规模的基因组
- http://www.ebi.ac.uk/~zerbino/velvet/

EMBL-EBI

Velvet

Sequence assembler for very short reads

- Current version: 1.2.10
- Manual and extension for Columbus in pdf format
- Public Git URL: git clone git://github.com/dzerbino/velvet.git
- For up-to-date info, you can consult and/or subscribe to the mailing list.
- For transcriptomic assembly Velvet is extended by Oases.

ABySS

- 实现DBG的并行化：大基因组
- http://www.bcgsc.ca/platform/bioinfo/software/abyss

Platforms

- Bioinformatics
  - Bioinformatics Licenses
  - GSC Software Centre
    - PASsiT
    - Adapter Trimming for Small RNA Sequencing
    - Sealer
    - LINKS
    - Konnector
    - Spark
    - TASR
    - XpressAlign: FPGA Short Read Aligner
    - Barnacle
    - Satellog

ABySS

Assembly By Short Sequences - a de novo, parallel, paired-end sequence assembler

Project Description

ABySS is a *de novo*, parallel, paired-end sequence assembler that is designed for short reads. The single-processor version is useful for assembling genomes up to 100 Mbases in size. The parallel version is implemented using MPI and is capable of assembling larger genomes.

To assemble transcriptome data, see Trans-ABySS.

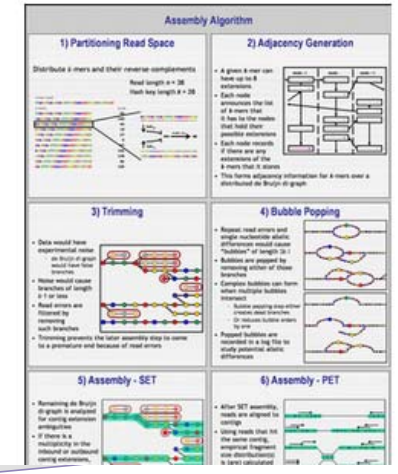
Publications

- ABySS: A parallel assembler for short read sequence data. Simpson JT, Wong K, Jackman SD, Schein JE, Jones SJ, Birol I. Genome Research, 2009-June. (Genome Research, PubMed)
- De novo Transcriptome Assembly with ABySS. İnanç Birol, Shaun D Jackman, Cydney Nielsen, Jenny Q Qian, Richard Varhol, Greg Stazyk, Ryan D Morin, Yongjun Zhao, Martin Hirst, Jacqueline E Schein, Doug E Horsman, Joseph M

Project Resources

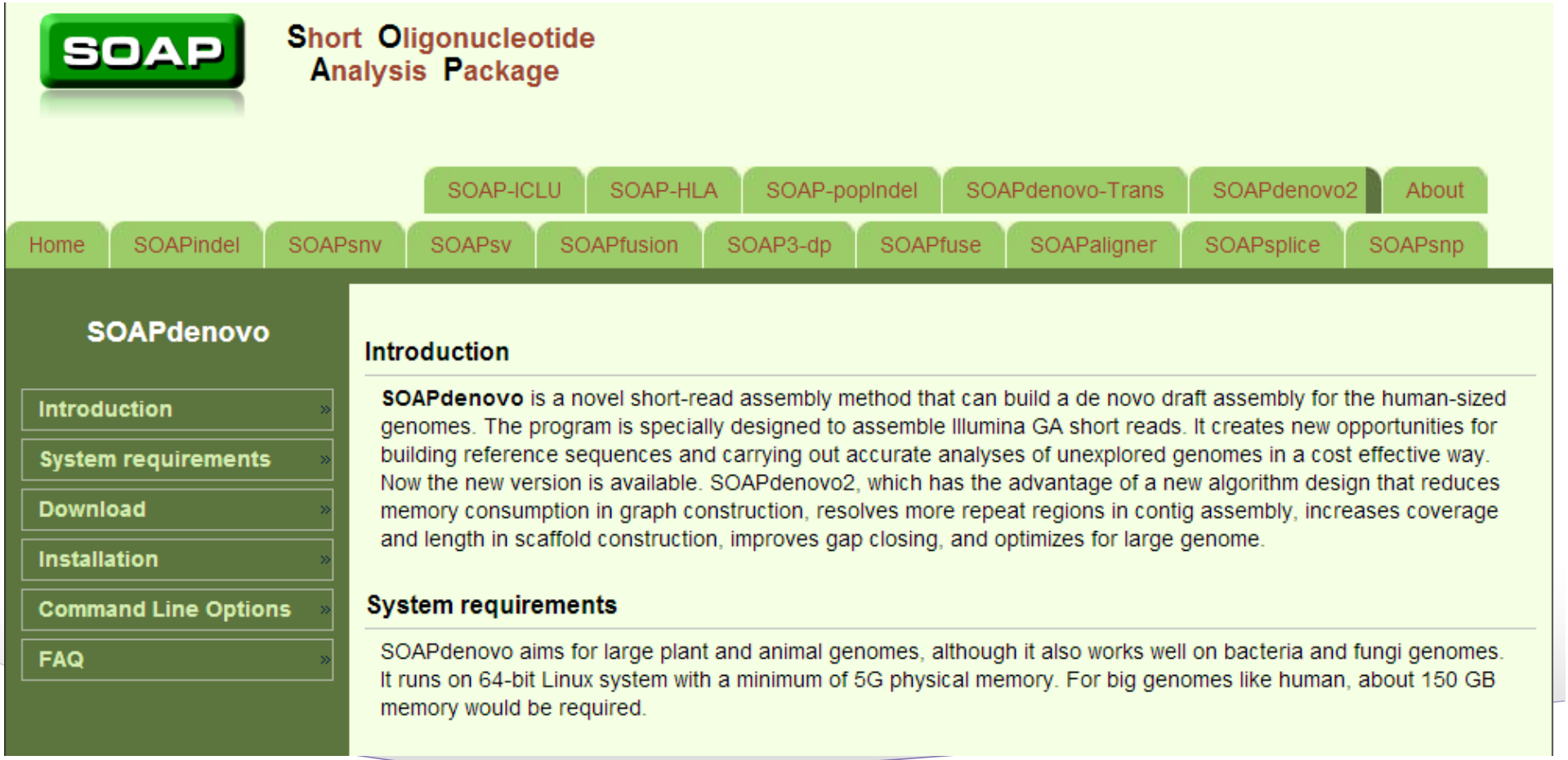
- Releases
- Documentation
- Issue tracker
- Support
- Contact address

Project owner: Anthony Raymond



SOAPdenovo & SOAPdenovo2

- 华大基因：大基因组
- http://soap.genomics.org.cn/soapdenovo.html



De Bruijn graph

- 设计理念类似SCS，各有优缺点
- ***k*-mer**

读段S: GGCGATTCATCG

S的一个4-mer: ATTC

S的所有3-mer:

GGC
GCG
CGA
GAT
ATT
TTC
TCA
CAT
ATC
TCG

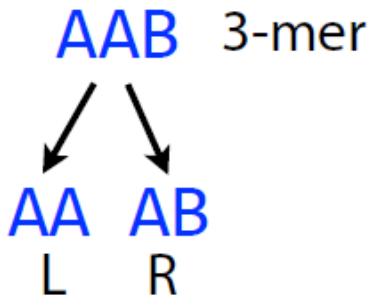
- ***k*-1-mer：长度为*k*-1的子串**

De Bruijn graph

- 给定一系列来源于参考基因组的读段，获得*k*-mer，*k*=3

AAA, AAB, ABB, BBB, BBA

- AAB是一个*k*-mer (*k*=3)
  - AA是左*k*-1-mer
  - AB是右*k*-1-mer



AAB's left 2-mer　　AAB's right 2-mer

De Bruijn graph

- 将每一个长度为3的字串切分成长度为2的、两个字串重叠的子串

读段S: AAABBBA

S的所有3-mer: AAA, AAB, ABB, BBB, BBA

所有左/右2-mer: AA, AA, AA, AB, AB, BB, BB, BB, BB, BA

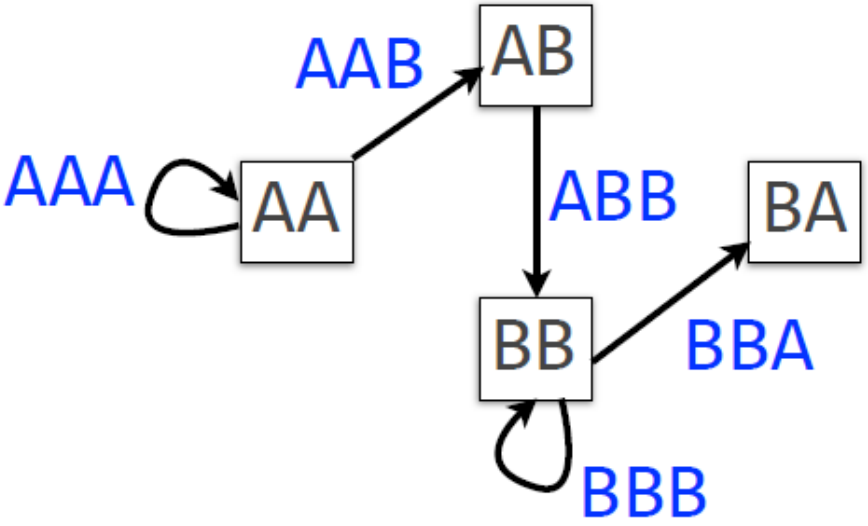
L R L R L R L R L R

- 令2-mer为新图的结点
- 根据左2-mer ->右2-mer的重叠方向确定有向边

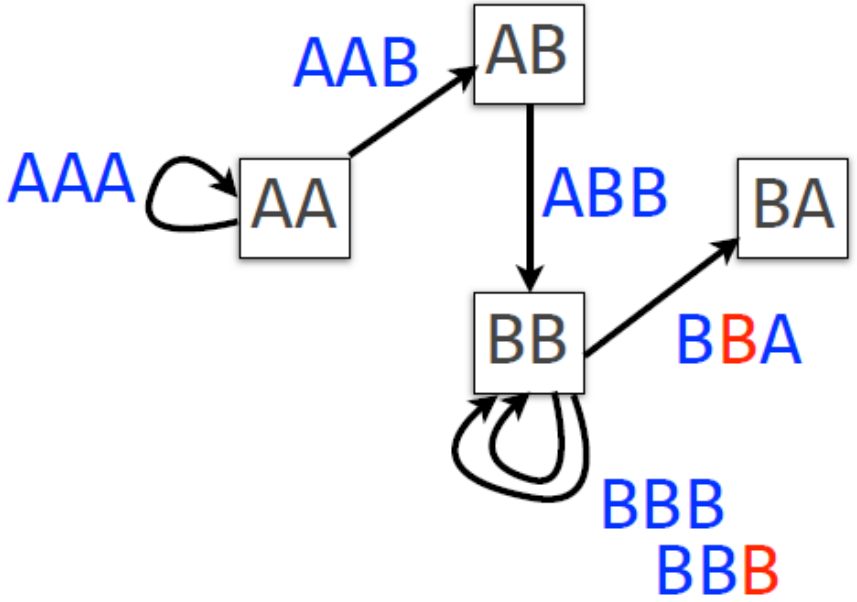
De Bruijn graph

- 图中每一条边代表长度为3的字串，等于*k*-mer
- 若在读段中再加一个B: **AAABBBBA**
- 重建De Bruijn graph：多边（Multiedge）

AAABBBA

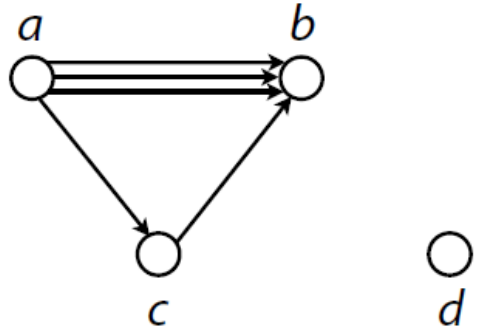


AAABBBBA



Eulerian walk

- De Bruijn graph：有向多重图（Directed multigraph）
  - 一系列顶点/结点V，多重有向边E
  - 结点入度 (indegree) = 进入的边
  - 结点出度 (outdegree) = 出去的边
  - 平衡 (balanced) 结点：入度=出度
  - 半平衡 (semi-balanced) 结点：入度与出度差1
  - 连接图：所有结点都可通过其他结点访问
- 欧拉行走
  - 遍历每条边仅一次
- 欧拉图
  - 仅有两个半平衡结点
  - 其余都是平衡结点



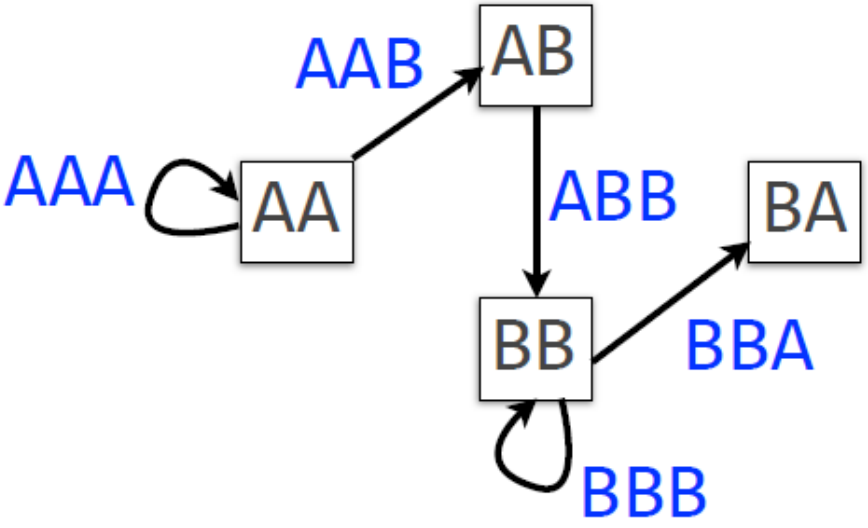
$V = \{a, b, c, d\}$

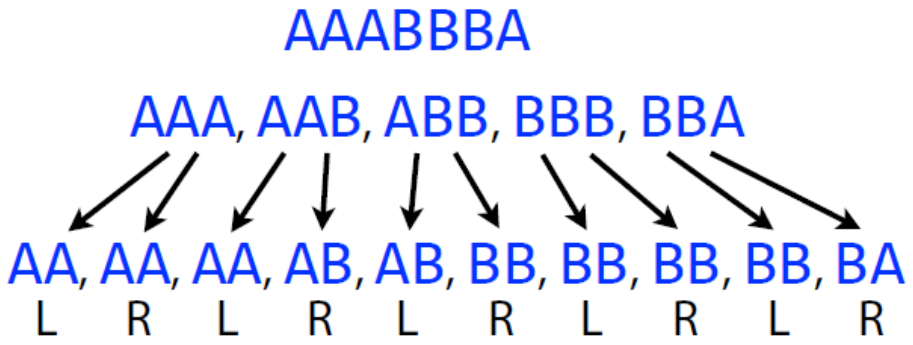
$E = \{(a, b), (a, b), (a, b), (a, c), (c, b)\}$

Repeated

De Bruijn graph

- 欧拉图：读段**AAABBBA**生成的De Bruijn graph
  - 所有结点都可访问：**AA→ AA→ AB→ BB→ BB→ BA**
  - **AA**和**AB**为半平衡结点，**AB**和**BB**为平衡结点





De Bruijn graph

- 基因组De Bruijn graph的构建流程
- 假设没有测序错误

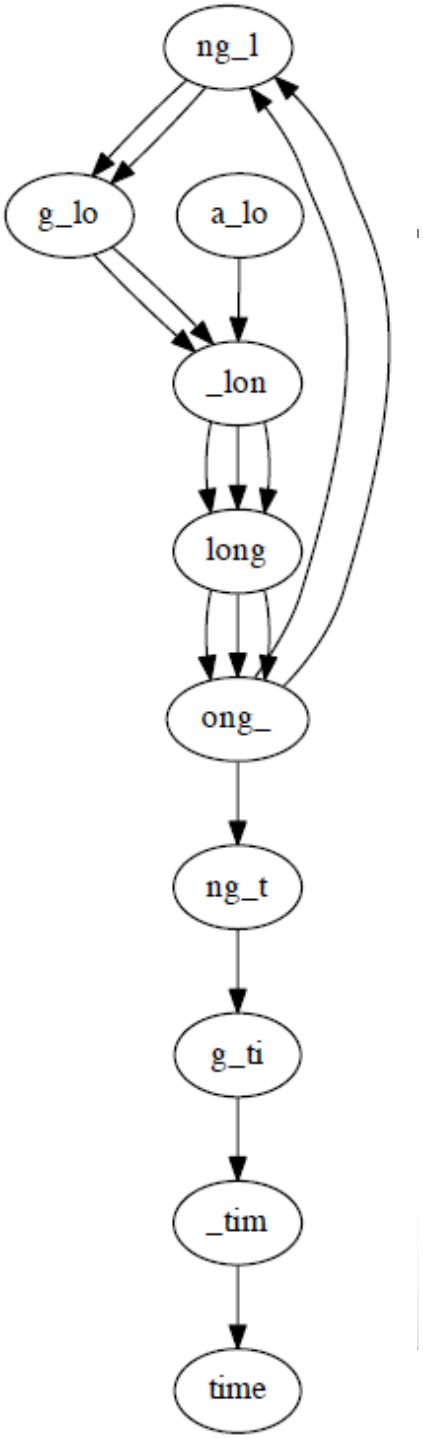
读段长度*k*=5: 5

参考序列: a_long_long_long_time

将*k*-mer切分成左/右*k*-1-mer:

long_

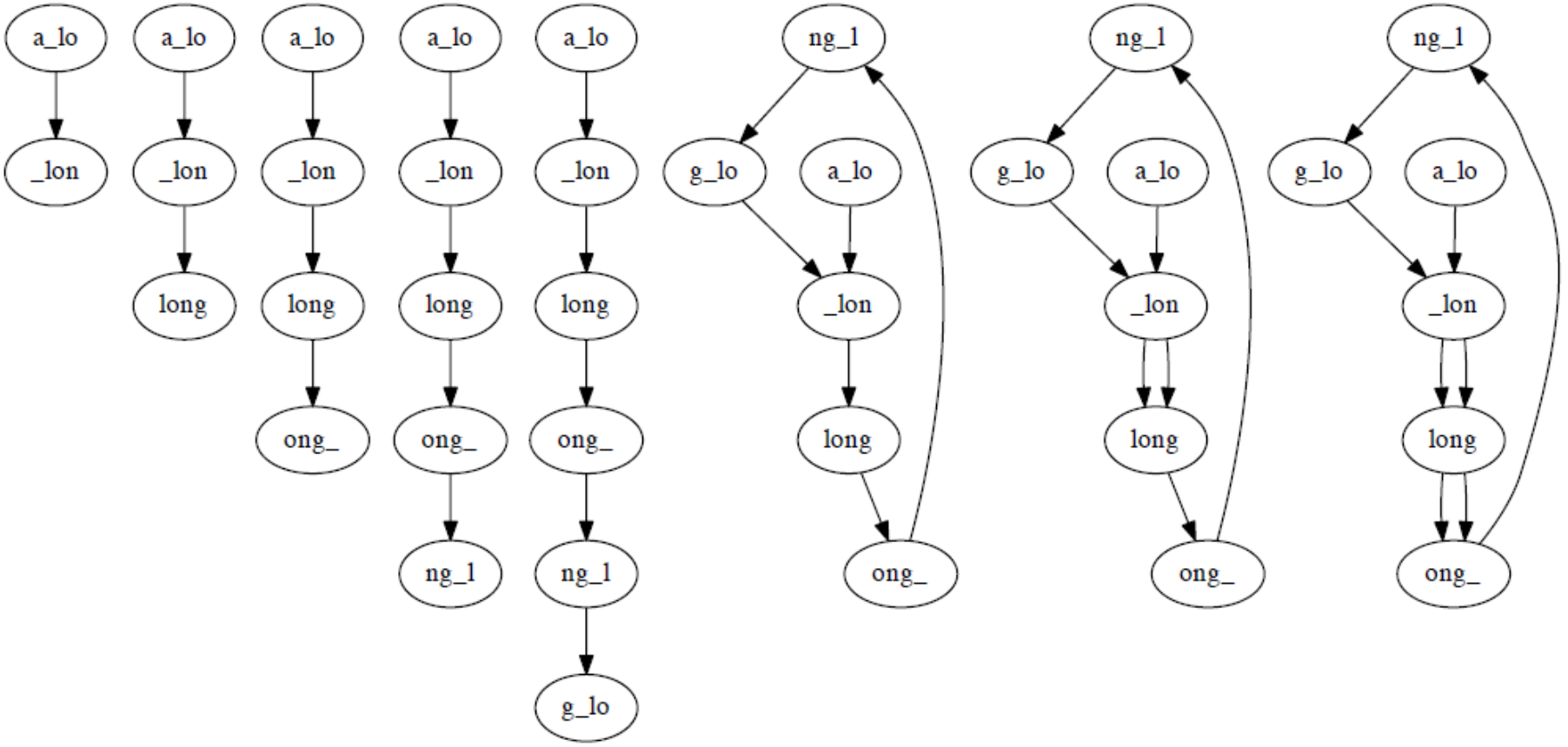
long ong_



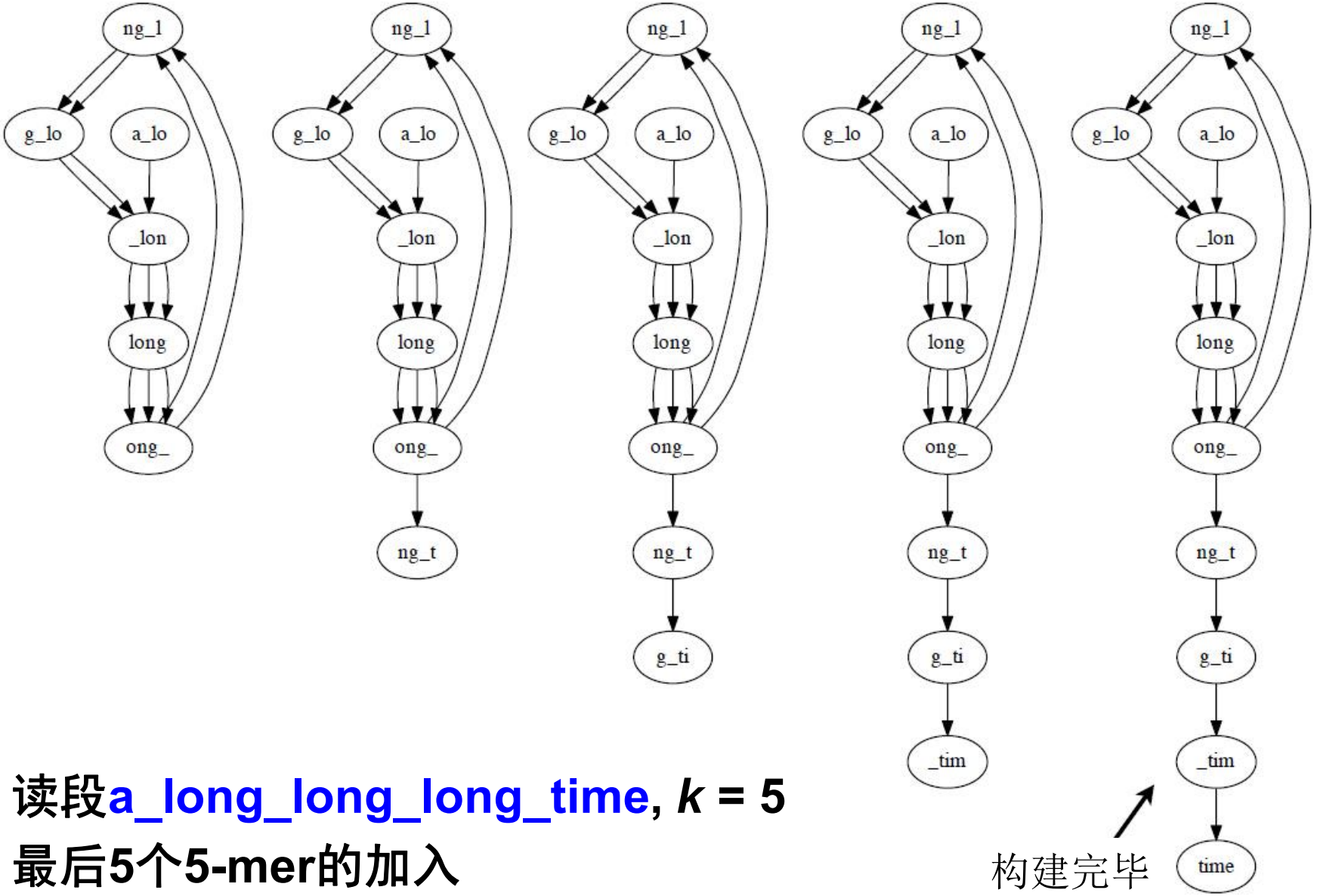
- 将新的*k*-1-mer作为结点加入图中
- 根据左*k*-1-mer -> 右*k*-1-mer重叠加边

De Bruijn graph

- 读段a_long_long_long_time, $k = 5$
- 8个5-mer的加入



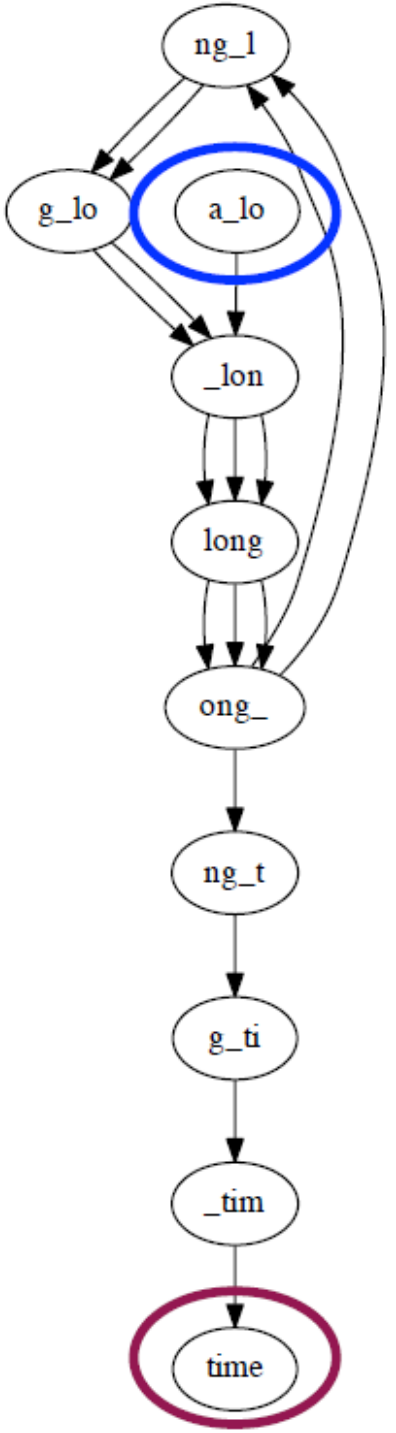
De Bruijn graph



- 读段a_long_long_long_time, $k = 5$
- 最后5个5-mer的加入

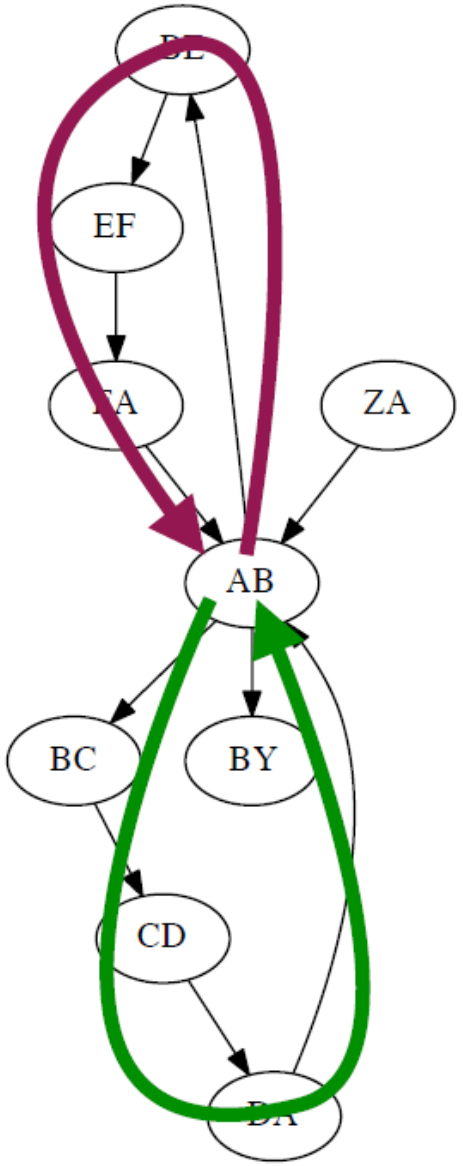
De Bruijn graph

- 若是完美测序，该流程产生欧拉图
- 半平衡结点
  - 左端*k*-1-mer结点，出度比入度多1
  - 右端*k*-1-mer结点，入度比出度多1
- 其他结点为平衡结点
- 因此，欧拉行走可以实现
- 问题：是否总是如此？



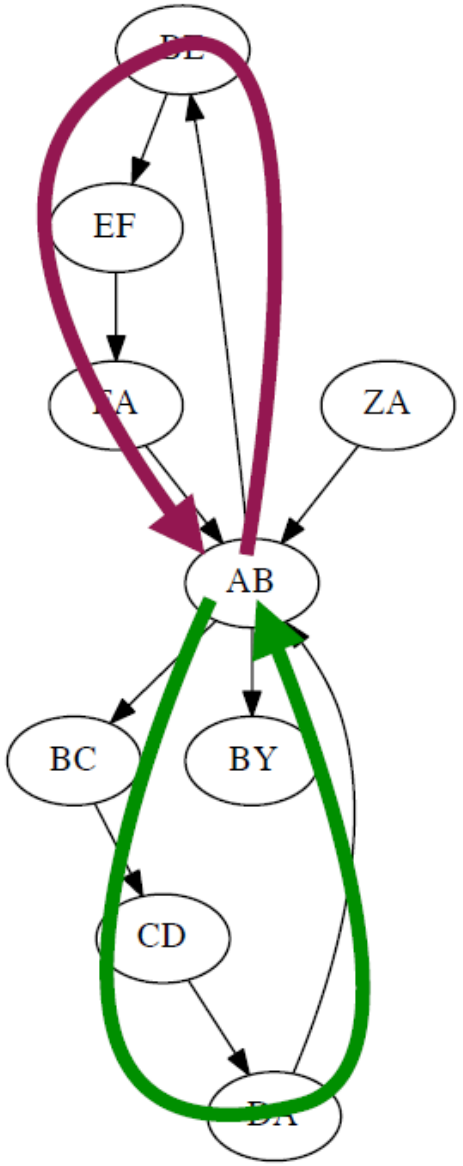
De Bruijn graph

- 可能有多个欧拉行走的路线，仅有一条符合原始的参考序列
- 例如，DBG图：ZABCDABEFABY, $k = 3$
- 可选的欧拉行走路线
  - ZA→AB→BE→EF→FA→AB→BC→CD→DA→AB→BY
  - ZA→AB→BC→CD→DA→AB→BE→EF→FA→AB→BY
- 结点AB
  - 两条不连接的有向环
  - AB是重复序列: ZABCDABEFABY



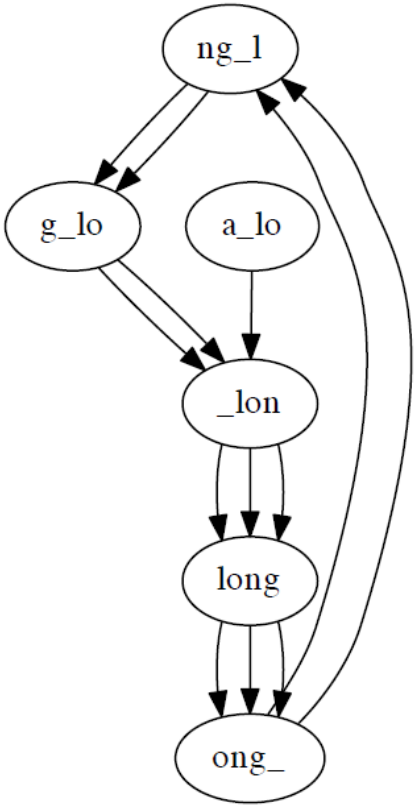
重复序列的影响

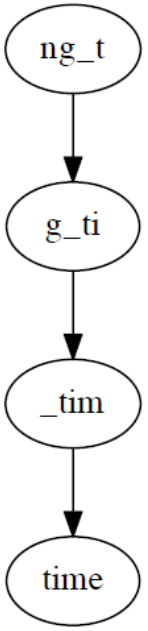
- 可能有多个欧拉行走的路线，仅有一条符合原始的参考序列
- 例如，DBG图：ZABCDABEFABY, $k = 3$
- 可选的欧拉行走路线
  - ZA→AB→BE→EF→FA→AB→BC→CD→DA→AB→BY
  - ZA→AB→BC→CD→DA→AB→BE→EF→FA→AB→BY
- 结点AB
  - 两条不连接的有向环
  - AB是重复序列: ZABCDABEFABY
- DBG不能解决所有问题
  - 存在重复序列

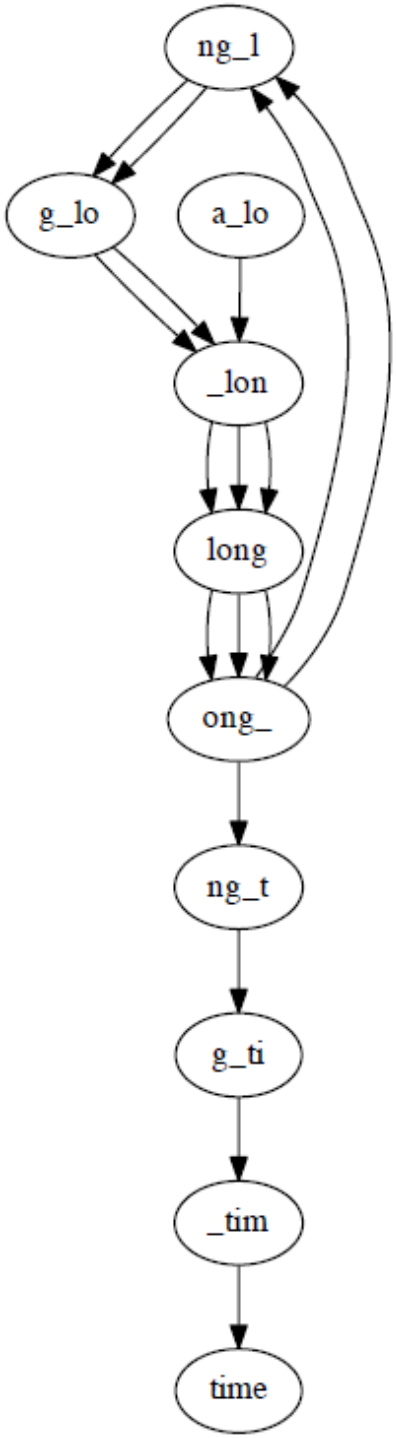


测序深度的影响

- 读段a_long_long_long_time, $k = 5$
- 若ong_t没有测到
  - 两个欧拉图
  - 每个图都可以欧拉遍历
  - 但整张图不是欧拉图

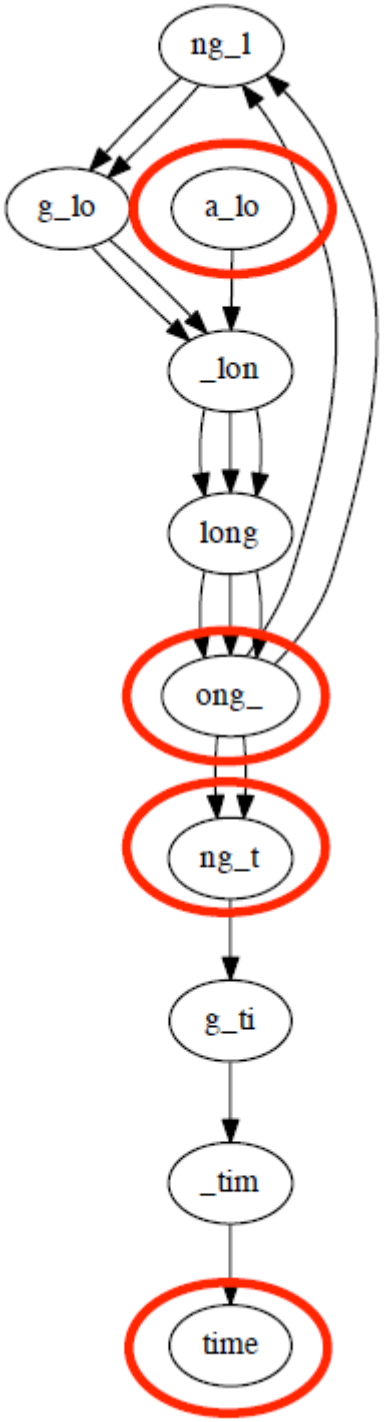






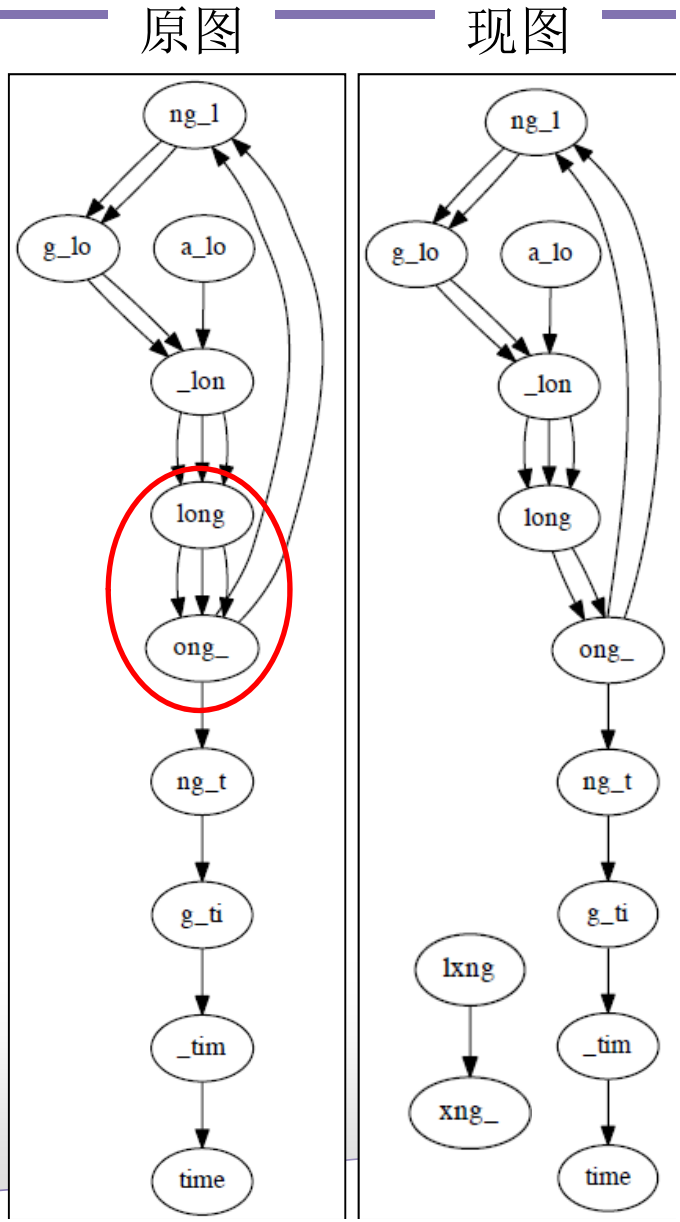
测序深度的影响

- 读段a_long_long_long_time, $k = 5$
- 若ong_t测到2次
  - 全图有4个半平衡结点
  - 非欧拉图，不能作欧拉行走



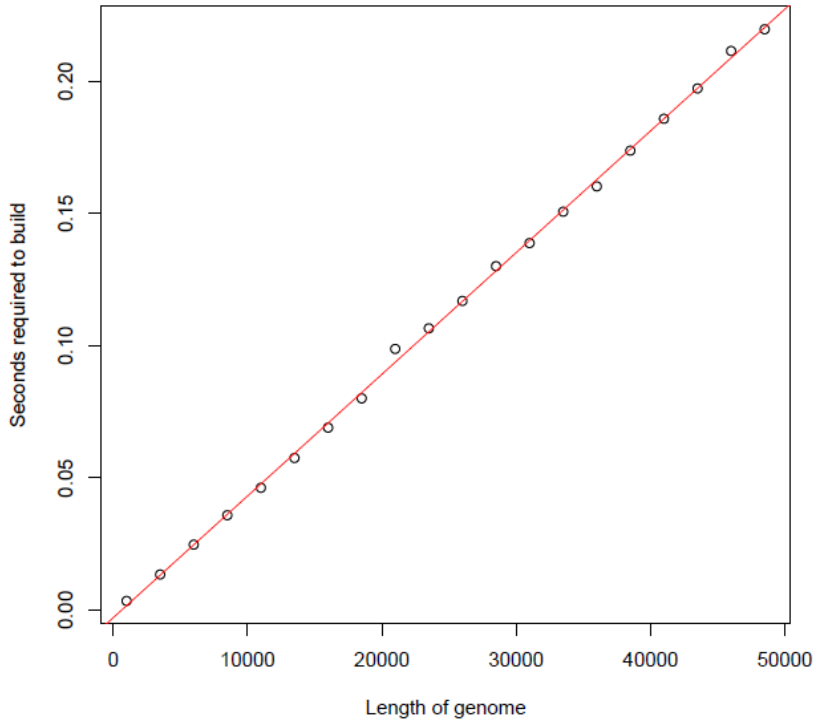
测序错误的影响

- 测序错误和染色体之间的差异有影响
- 读段a_long_long_long_time, $k = 5$
- 若其中一个long_测为lxng_
  - 现图非欧拉图
  - 主要部分有四个半平衡结点



De Bruijn graph

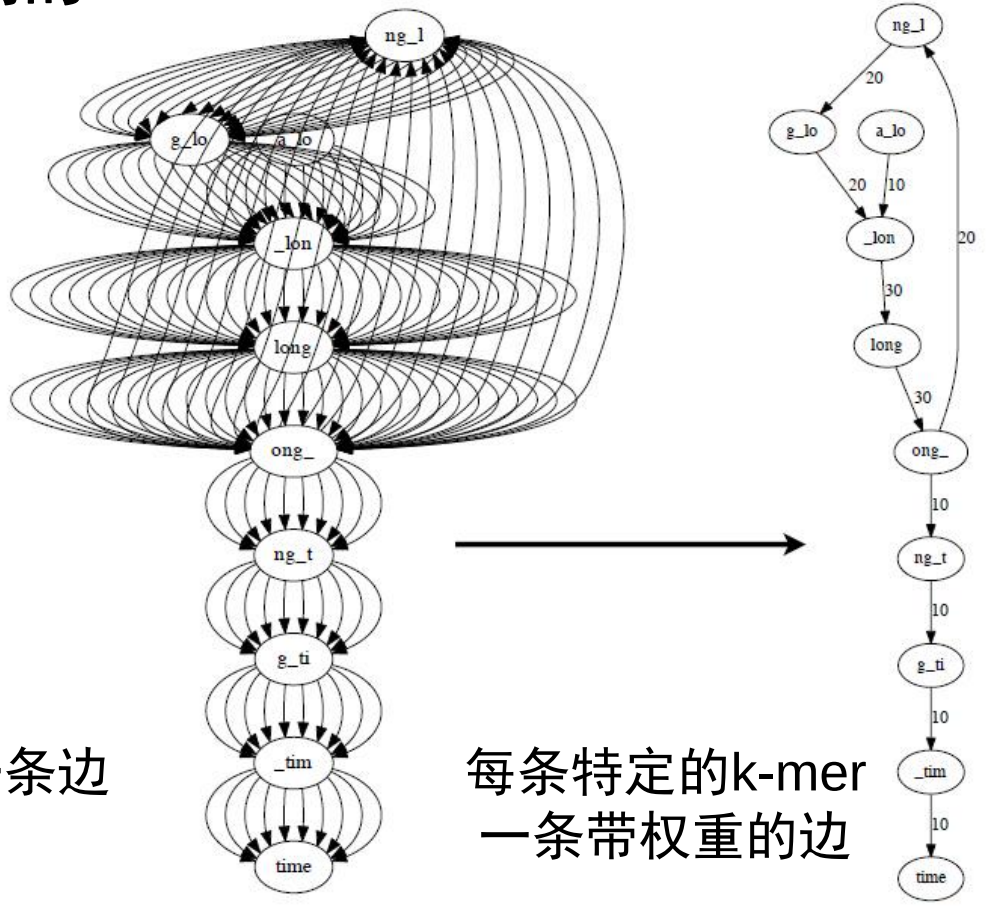
- DBG构建的时间复杂度
- 单个*k*-mer
  - 加上1条边和最多2个结点
  - 时间复杂度O(1)
- 利用哈希表编码结点和边
  - 建立结点O(1)
  - 搜索/加入键值=O(1)
- *N*个*k*-mer
  - 时间复杂度O(*N*)



- 噬菌体基因组的DBG构建，~50,000bp, *k*=14

De Bruijn graph

- 现实中一般测序深度为~ 30 - 50X
- 相同边出现多次：边的权重
- 利用边的权重代表每条不同的*k*-mer

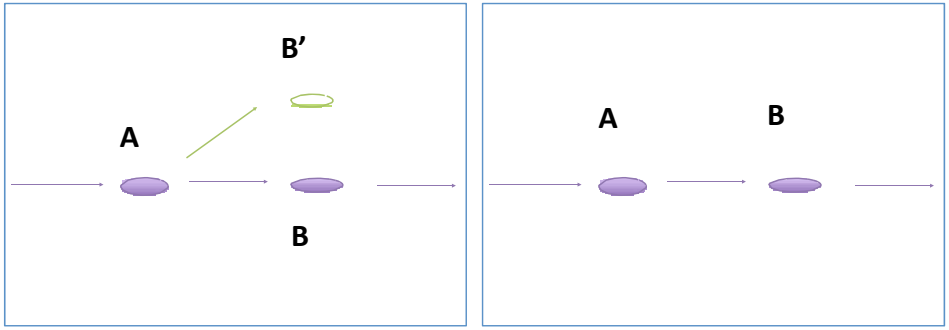


一条k-mer一条边

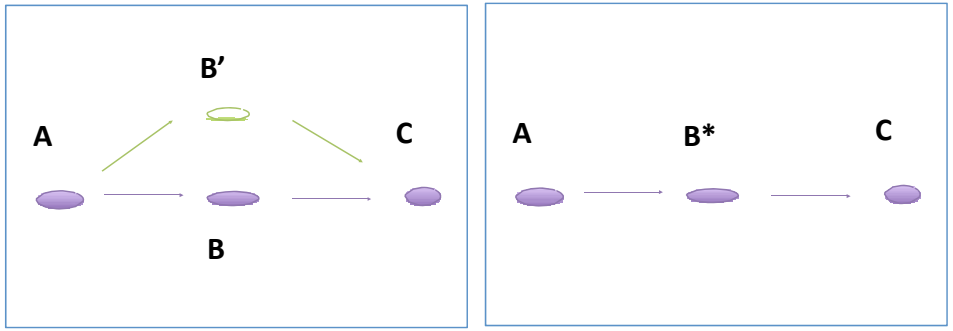
每条特定的k-mer
一条带权重的边

Error correction

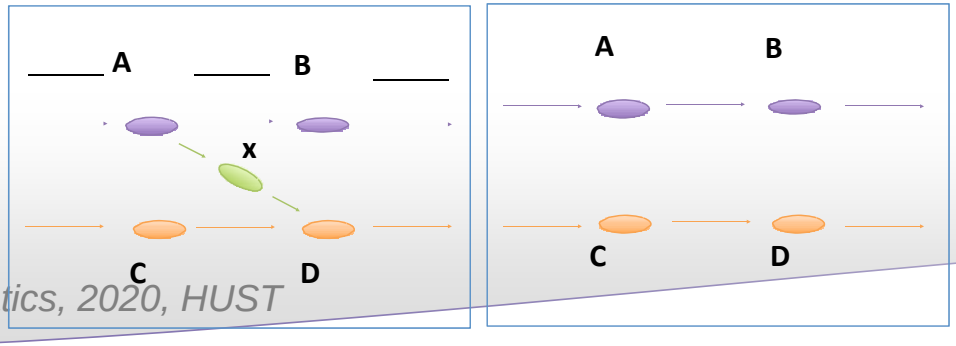
- 基于图的拓扑结构
- 读段尾端
  - 去掉不能延伸的结点



- 读段中间
  - 序列比对，合并



- 嵌合边
  - 去掉覆盖率低的边



DBG算法的缺点

- 读段需要被切分成更短的*k*-mer
- 不能解决重复序列的问题
- 存在测序错误时很难解决
- 丢失序列一致性：有些路径与输入读段不一致
- 各有优缺点：OLC → DBG

OLC *vs.* DBG

- **N50：将Contig从长至短排序，加和长度达到总长度一半时，最后一个Contig长度即为 N50**
- **DBG更快，OLC需要内存小**

	t=75	*k*=61	*k*=67	*k*=59

Table 1. Assembly statistics for *C. elegans* data set

	SGA	Velvet	ABySS	SOAPdenovo
Scaffold N50 size	26.3 kbp	31.3 kbp	23.8 kbp	31.1 kbp
Aligned contig N50 size	16.8 kbp	13.6 kbp	18.4 kbp	16.0 kbp
Mean aligned contig size	4.9 kbp	5.3 kbp	6.0 kbp	5.6 kbp
Sum aligned contig size	96.8 Mbp	95.2 Mbp	98.3 Mbp	95.4 Mbp
Reference bases covered	96.2 Mbp	94.8 Mbp	95.9 Mbp	95.1 Mbp
Reference bases covered by contigs ≥1 kb	93.0 Mbp	92.1 Mbp	93.9 Mbp	92.3 Mbp
Mismatch rate at all assembled bases	1 per 21,545 bp	1 per 8786 bp	1 per 5577 bp	1 per 26,585 bp
Mismatch rate at bases covered by all assemblies	1 per 82,573 bp	1 per 18,012 bp	1 per 8209 bp	1 per 81,025 bp
Contigs with split/bad alignment (sum size)	458 (4.4 Mbp)	787 (7.2 Mbp)	638 (9.1 Mbp)	483 (4.4 Mbp)
Total CPU time	41 h	2 h	5 h	13 h
Max memory usage	4.5 GB	23.0 GB	14.1 GB	38.8 GB

100 MBase genome, 33.8M read pairs, 100bp reads each end, 250bp insert size

性能比较

- 性能大致相当
- 参考序列：50 bp ~ 5000 bp, 10,000条读段