ETH zürich

Multi-Genome Representations with MetaGraph

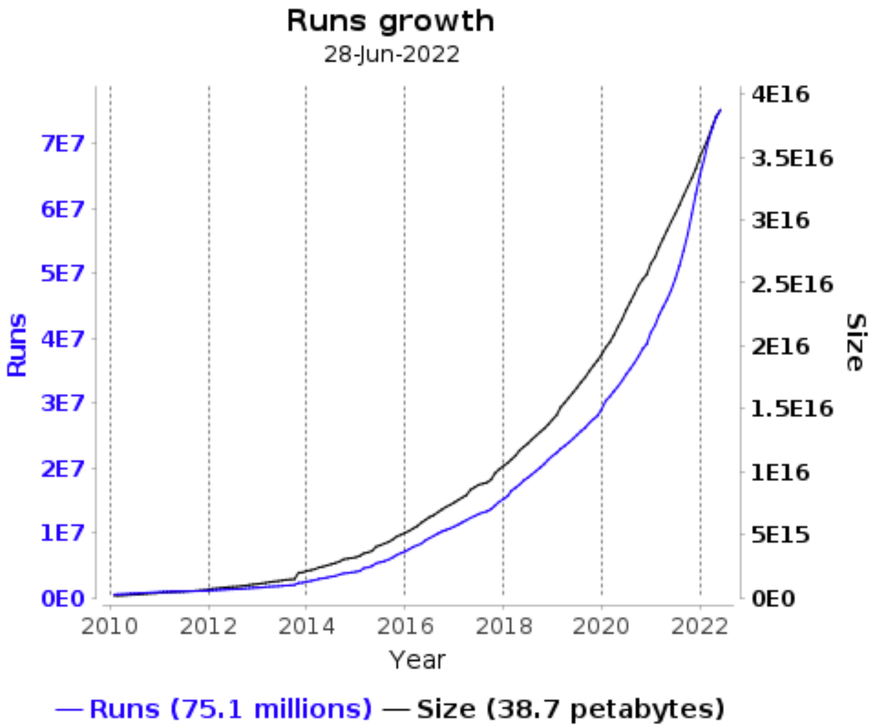
Mikhail Karasikov, Harun Mustafa, Gunnar Rätsch, André Kahles

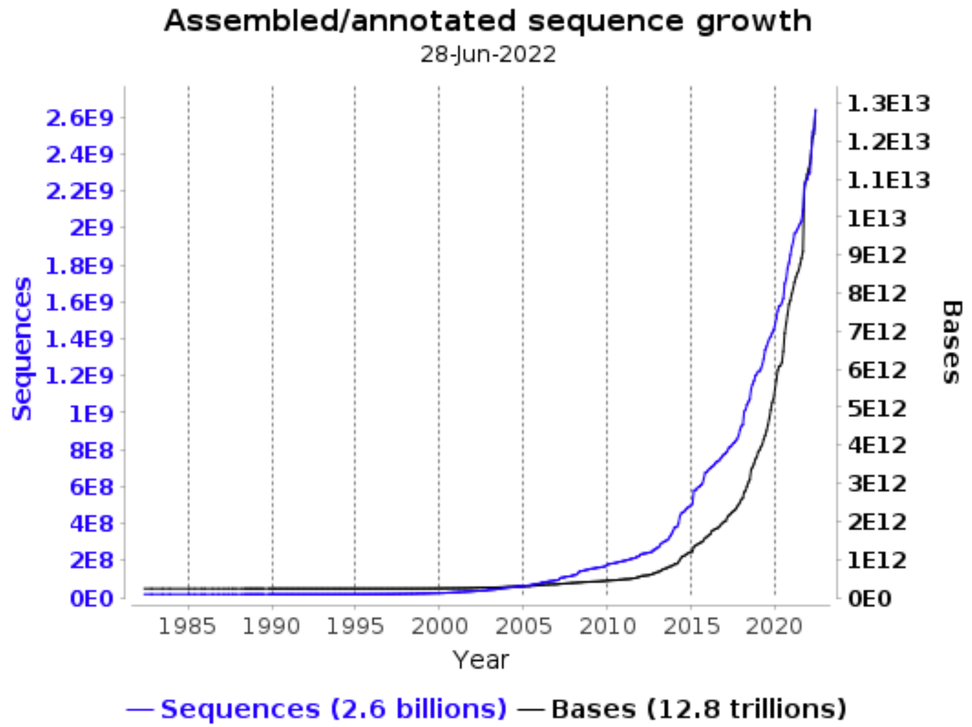



IGGSy 2022

4 July 2022

Growth of sequence archives

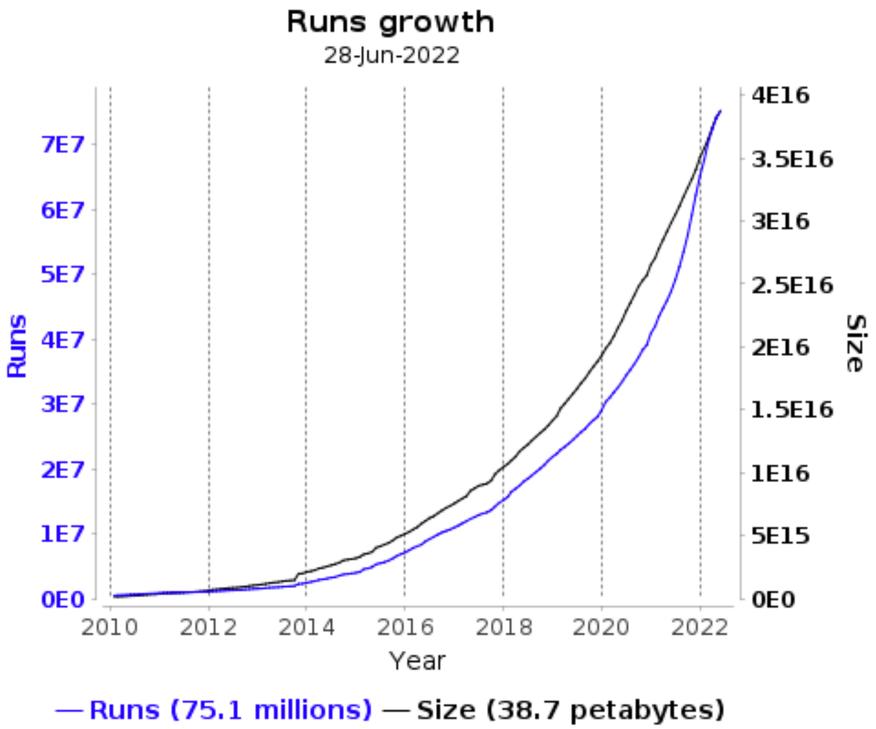


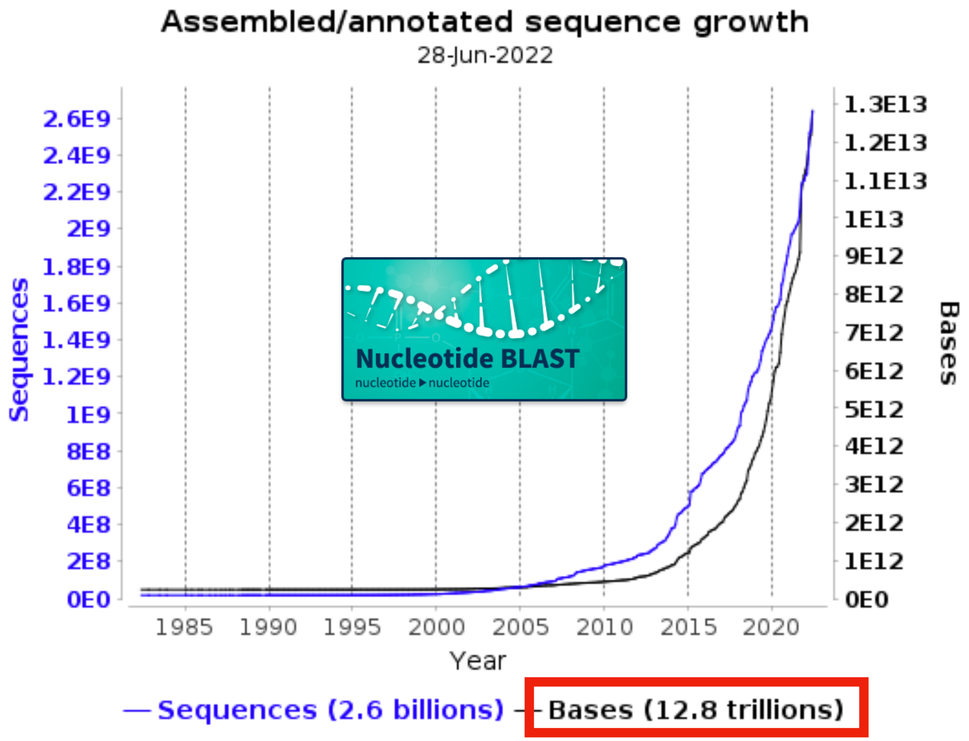


ENA
European Nucleotide Archive

Data source: https://www.ebi.ac.uk/ena/browser/about/statistics

Growth of sequence archives





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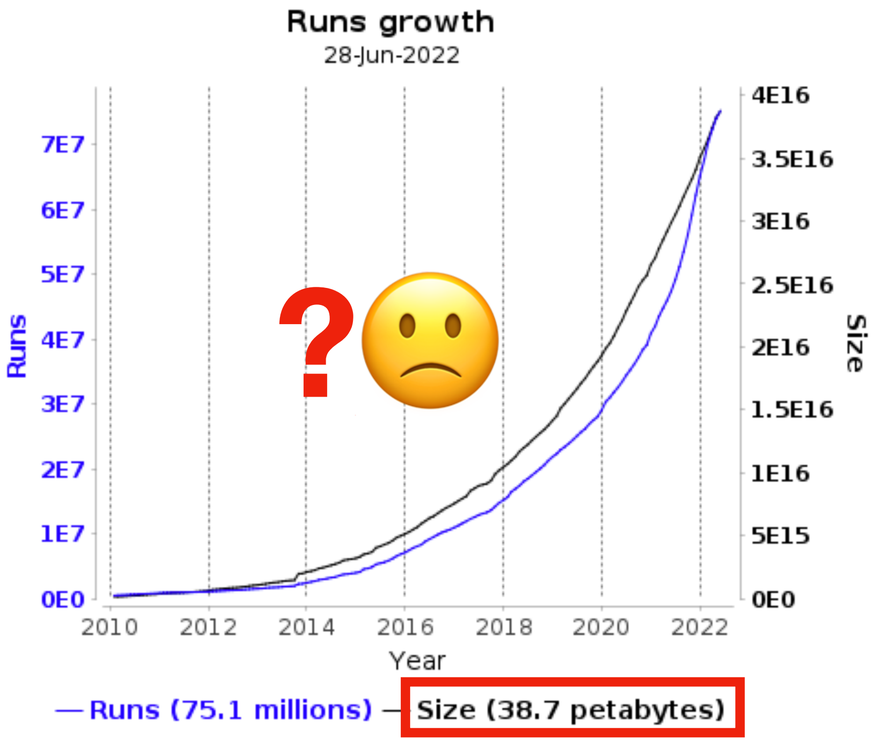

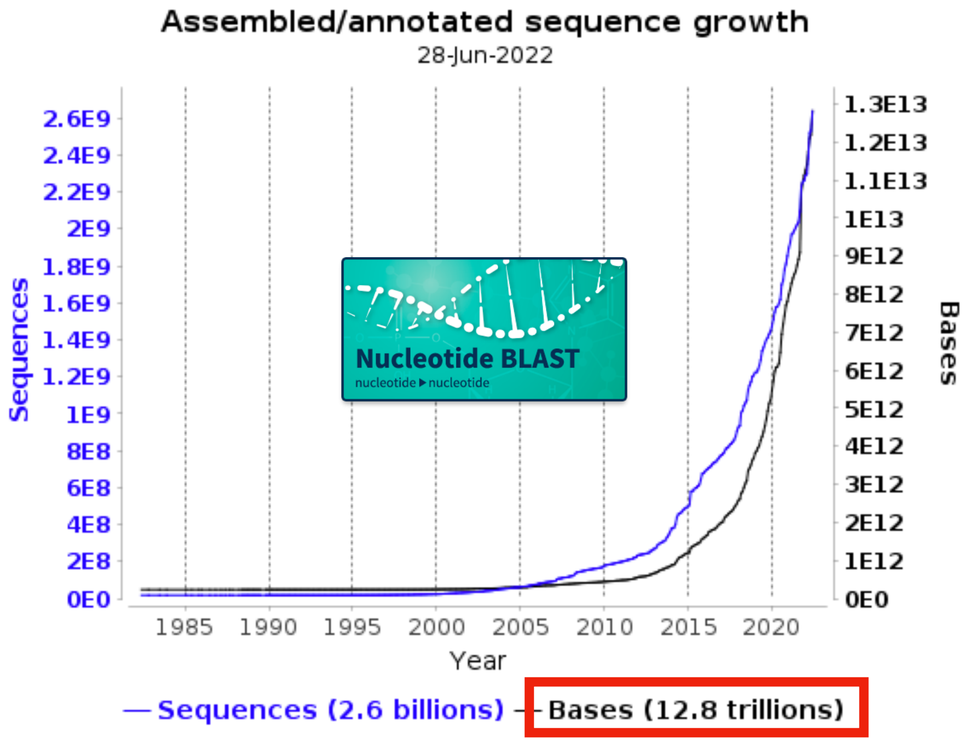

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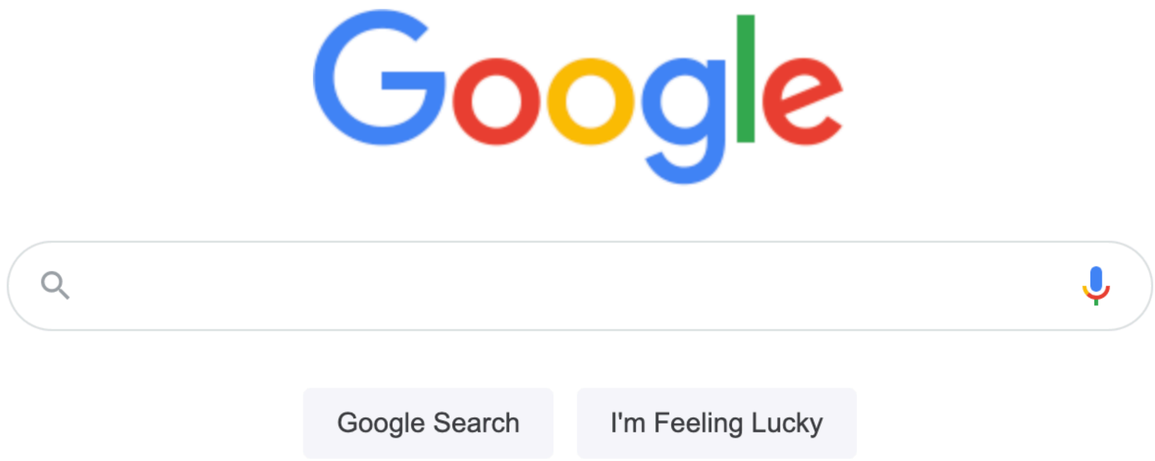
What we want



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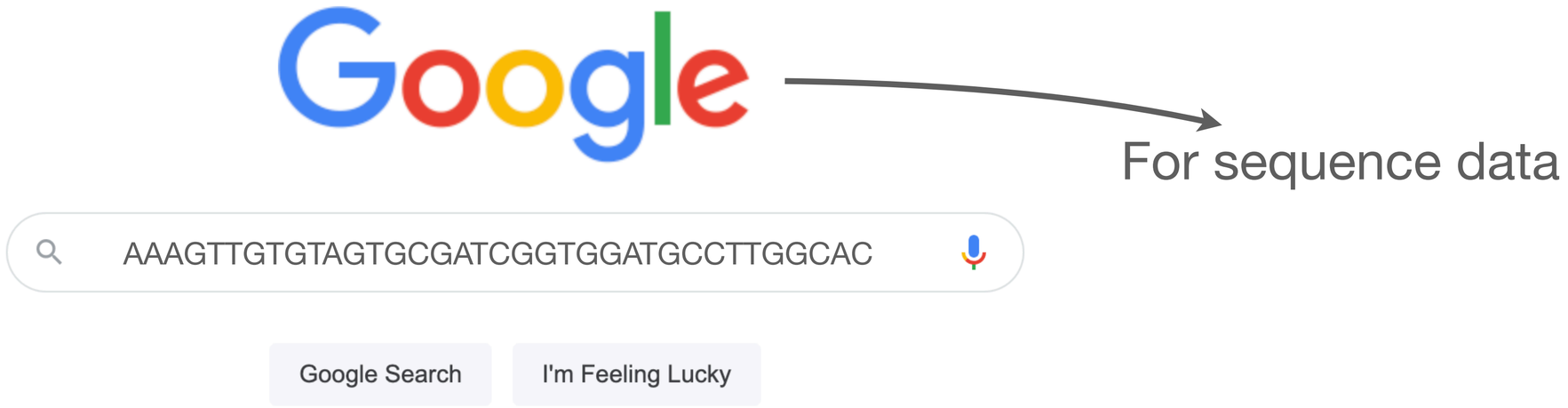
Google
For sequence data
AAAGTTGTGTAGTGCGATCGGTGGATGCCTTGGCAC
Google Search
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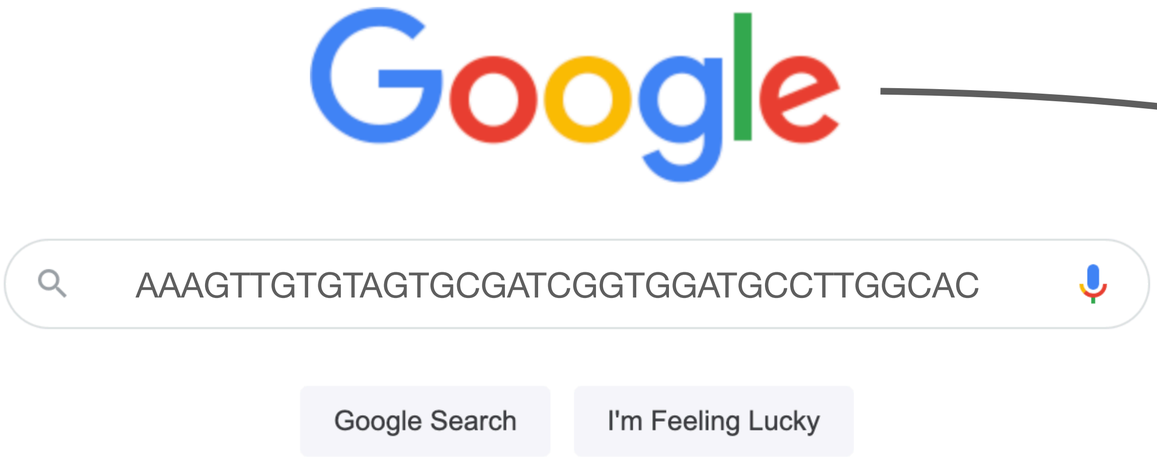


For sequence data

ENA European Nucleotide Archive

UK 10K

HMP

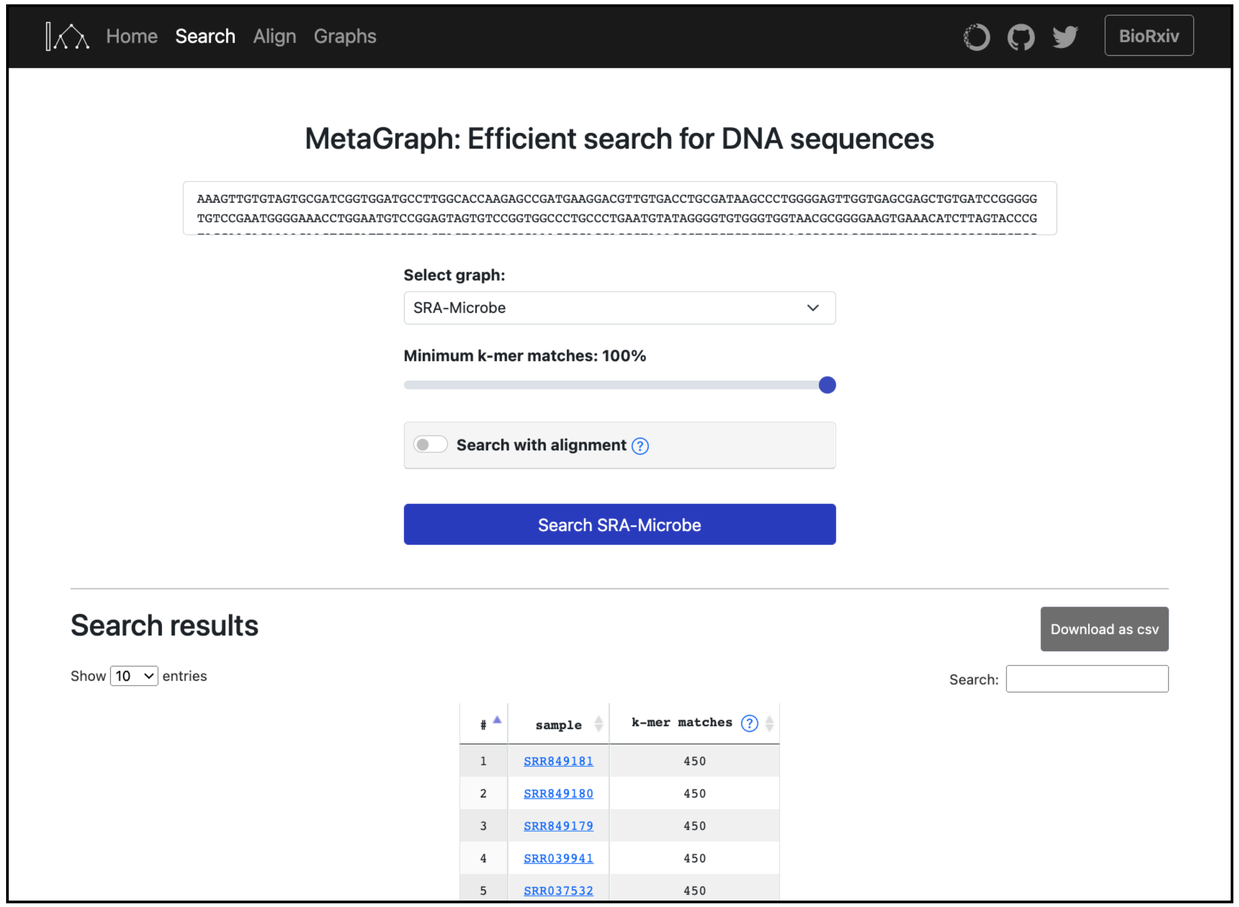
GENOME 10K

european genome-phenome archive

SRA

MetaSUB

• • •


Home
Search
Align
Graphs
BioRxiv
MetaGraph: Efficient search for DNA sequences
AAAGTTGTGTAGTGCGATCGGTGGATGCCTTGGCACCAAGAGCCGATGAAGGACGTTGTGACCTGCGATAAGCCCTGGGGAGTTGGTGAGCGAGCTGTGATCCGGGGG
TGTCCGAATGGGGAAACCTGGAATGTCCGGAGTAGTGTCCGGTGGCCCTGCCCTGAATGTATAGGGGTGTGGGTGGTAACGCGGGGAAGTGAAACATCTTAGTACCCG
Select graph:
SRA-Microbe
Minimum k-mer matches: 100%
Search with alignment
Search SRA-Microbe
Search results
Download as csv
Show 10 entries
Search:
sample k-mer matches
1 SRR849181 450
2 SRR849180 450
3 SRR849179 450
4 SRR039941 450
5 SRR037532 450

MetaGraph

Why MetaGraph

- MetaGraph is an open source **modular framework**
  - various (succinct) graph representations (Bowe *et al.*, 2012; Conway *et al.*, 2011)
  - different schemes for annotation representation (Almodaresi et al., 2017, Muggli et al., 2017, Karasikov et al., 2019, Danciu et al., 2021, Karasikov et al., 2022, …)
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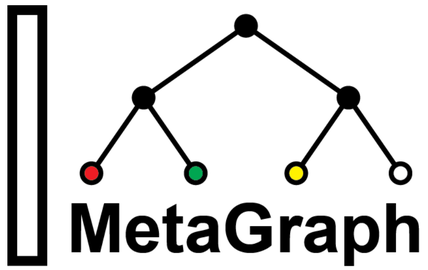

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  - scalable construction ⇒ works on Petabase size inputs
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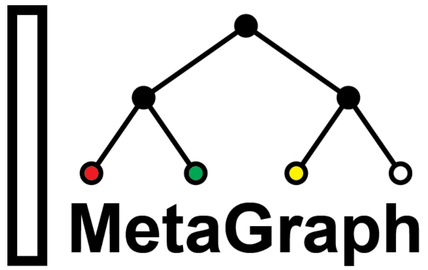

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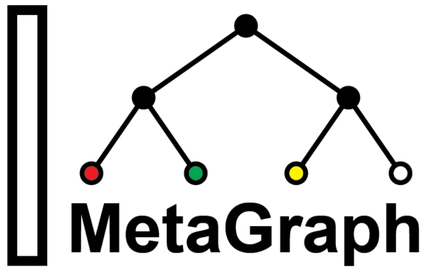

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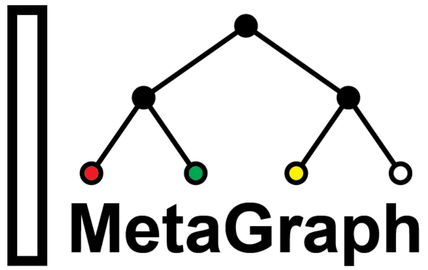

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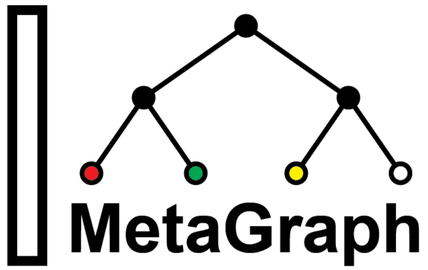
- Support for **integrative analysis**
  - novel concept of differential assembly



Indexing workflow

```
>smp_1
ACGTAC
ACGC
CGTAC
```

```
>smp_2
ACGAA
ACGTAC
ACG
```

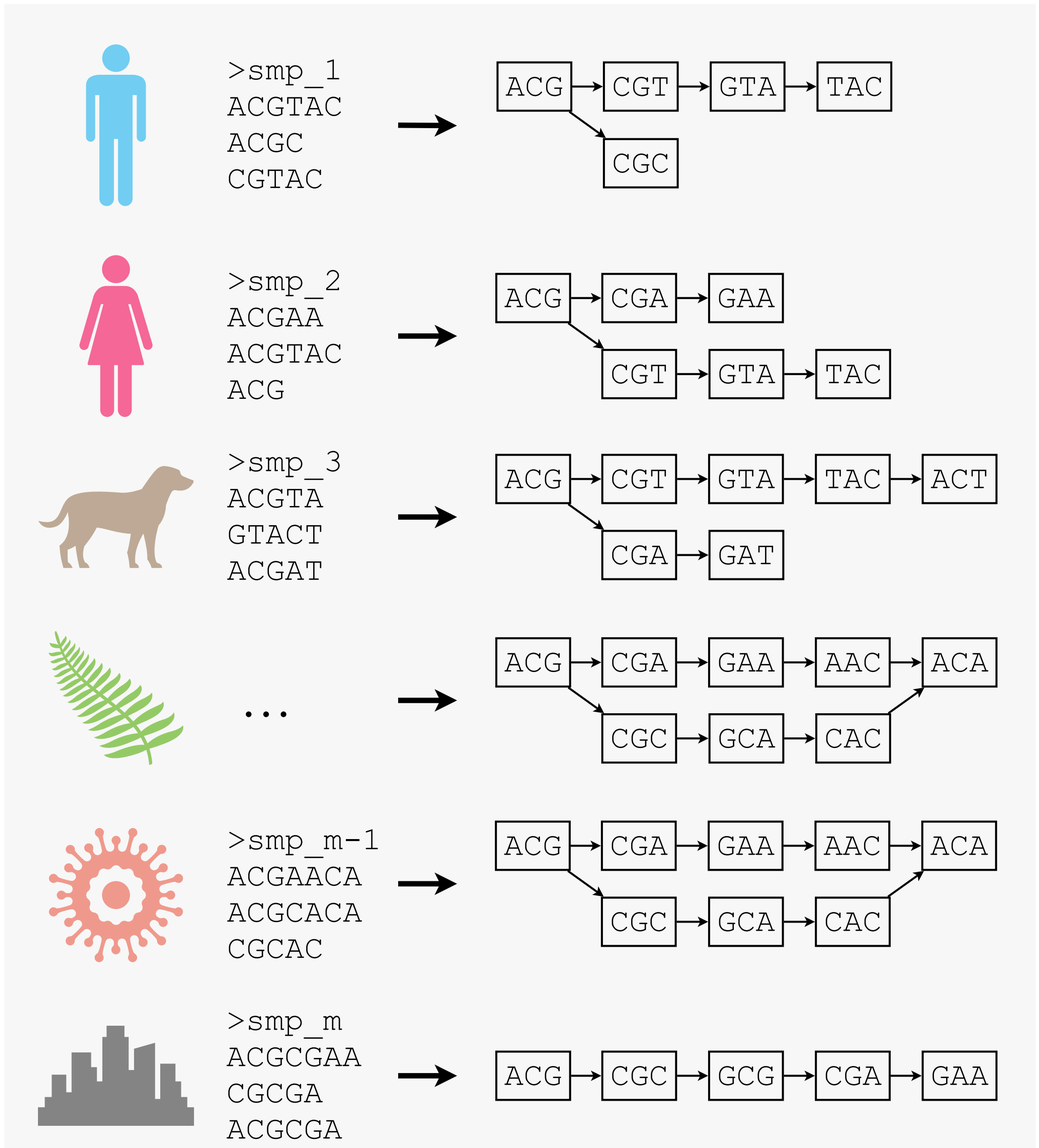
```
>smp_3
ACGTA
GTACT
ACGAT
```

...

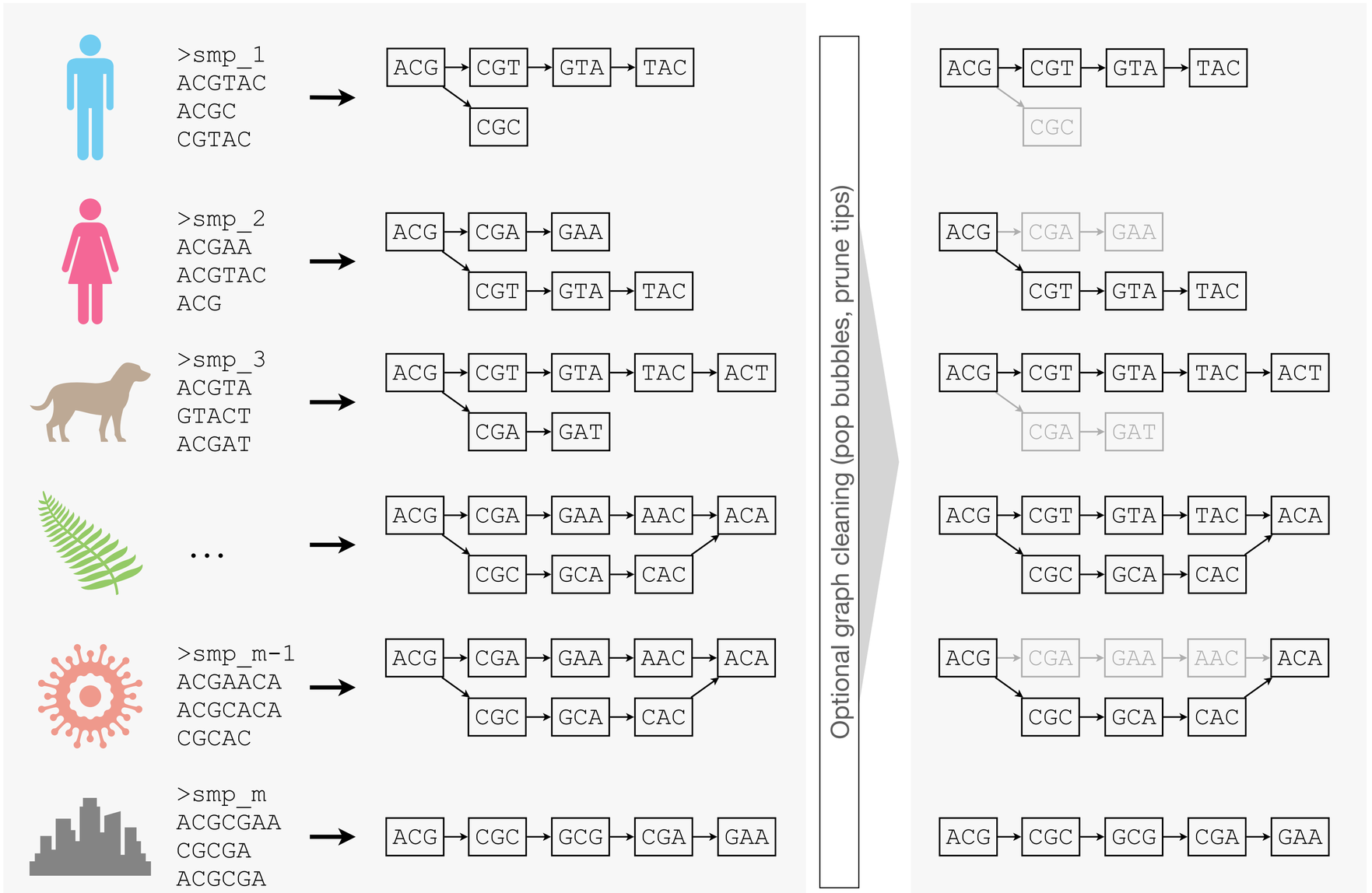
```
>smp_m-1
ACGAACA
ACGCACA
CGCAC
```

```
>smp_m
ACGCGAA
CGCGA
ACGCGA
```

Indexing workflow



Indexing workflow



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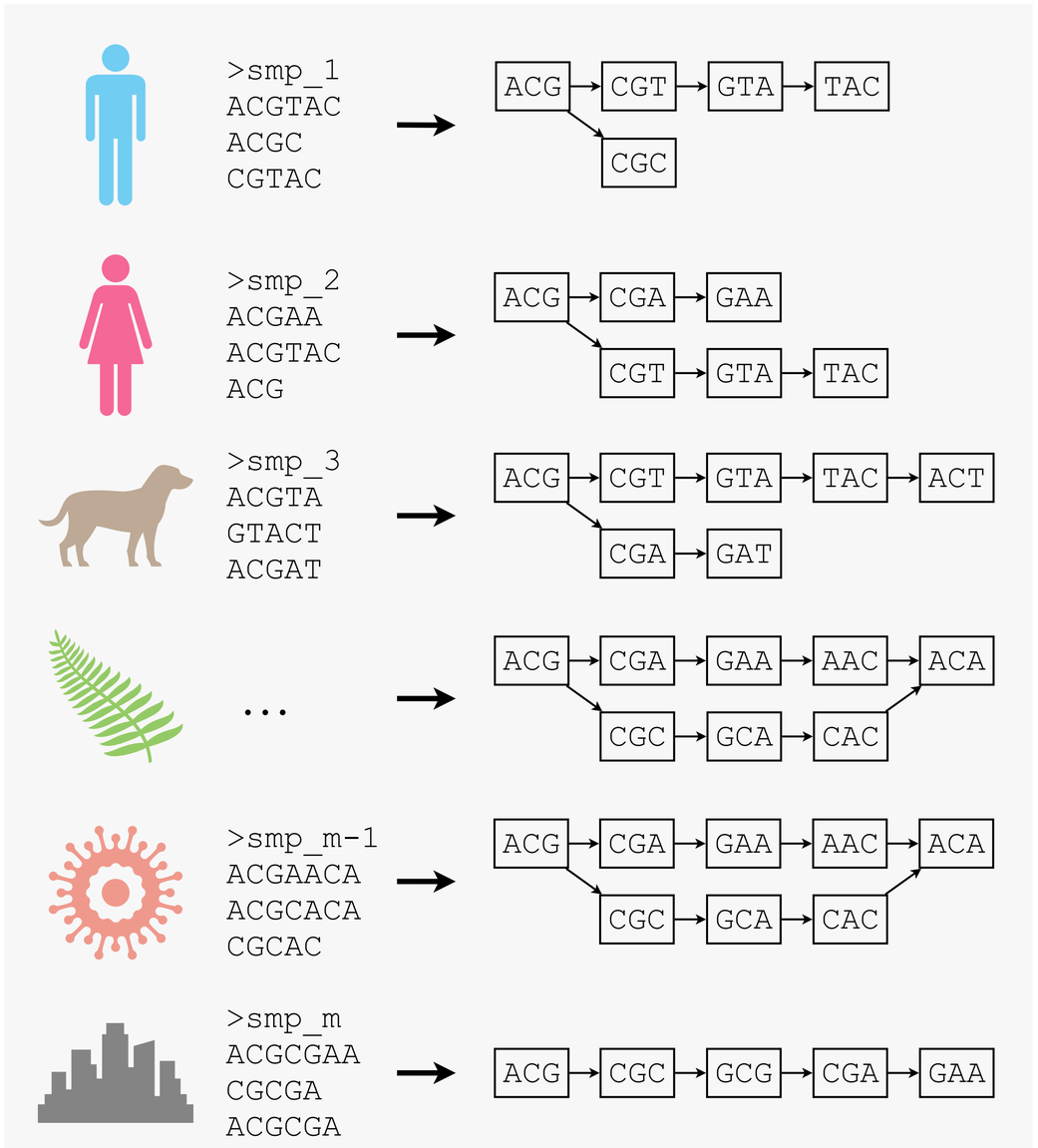
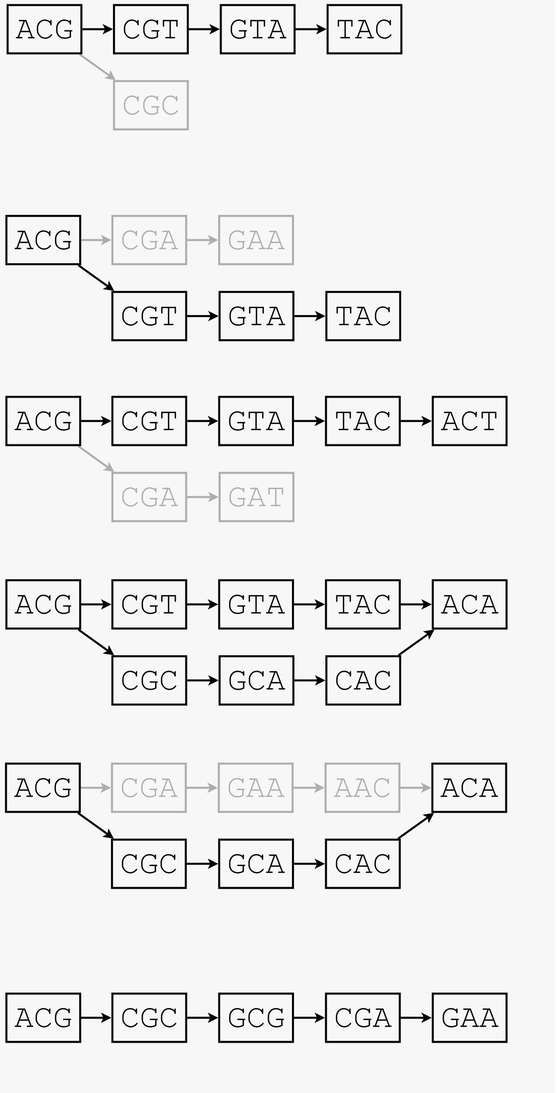
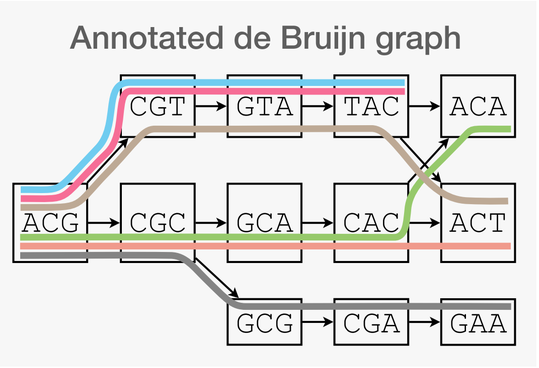


Optional graph cleaning (pop bubbles, prune tips)



Merge into a joint graph



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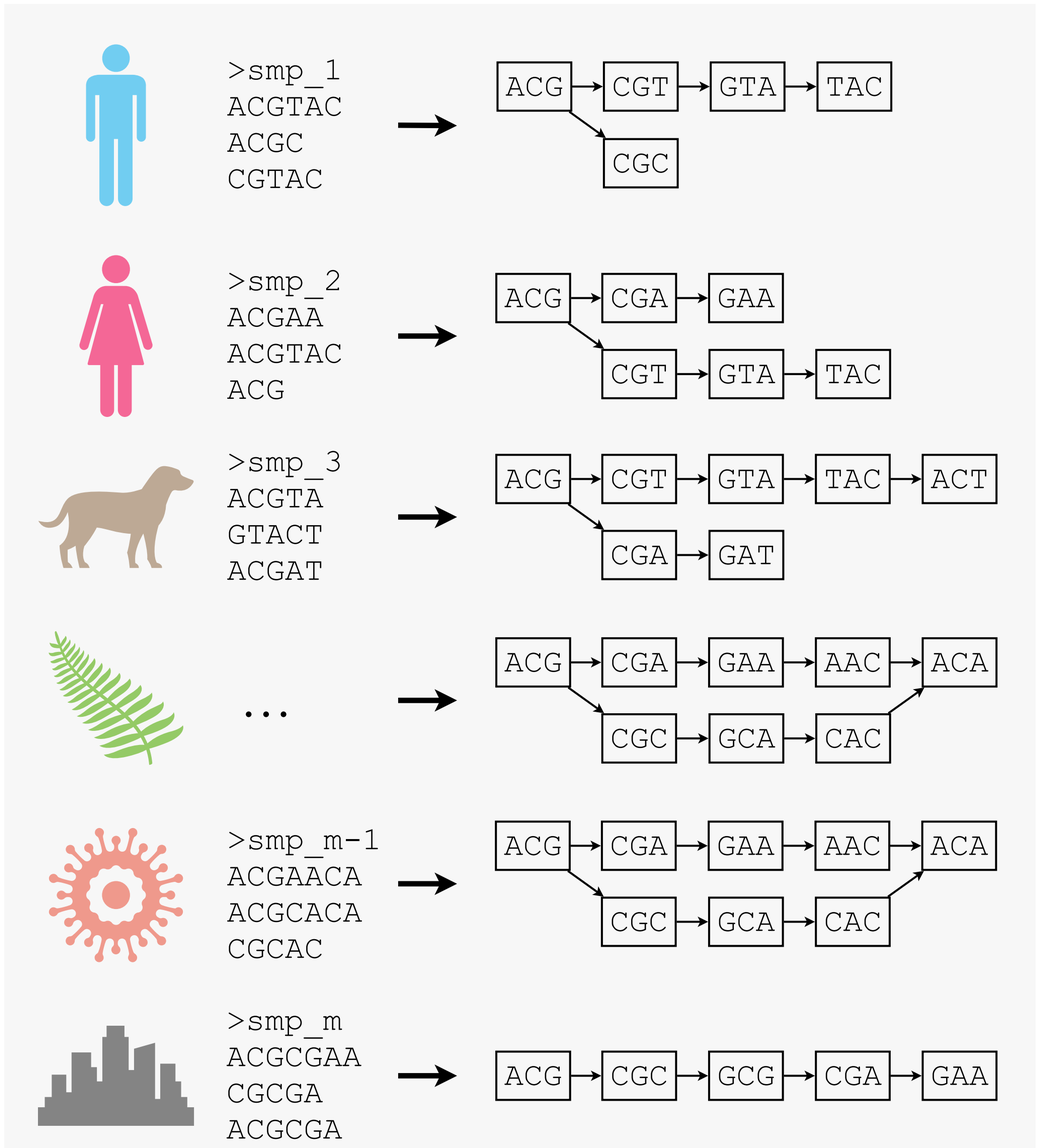

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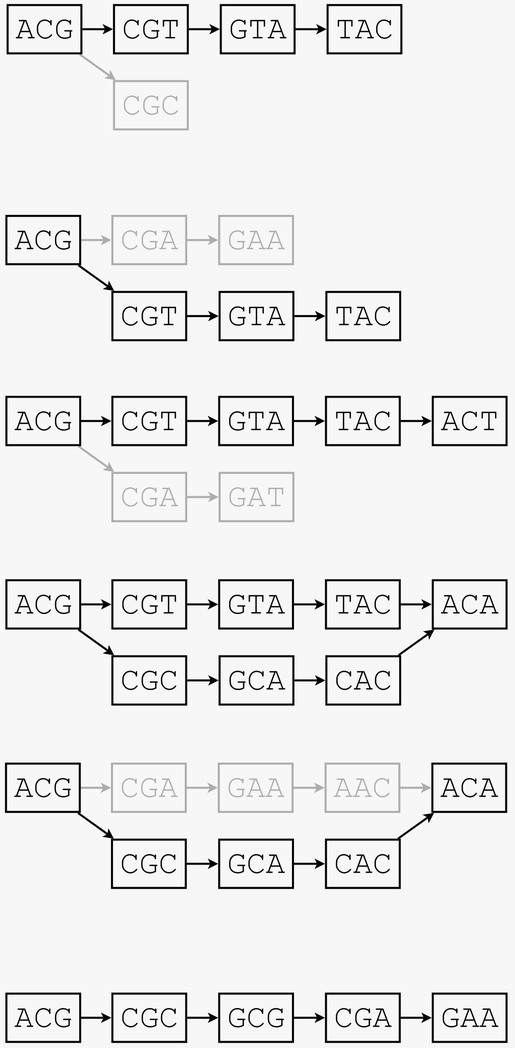

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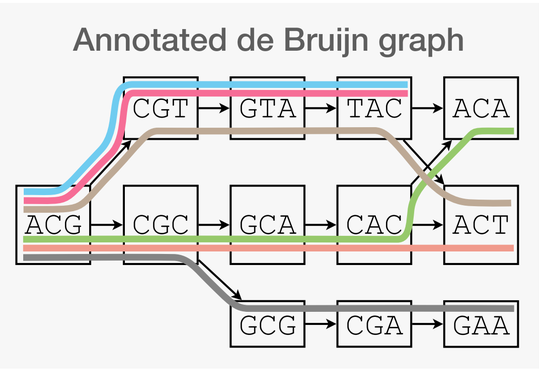

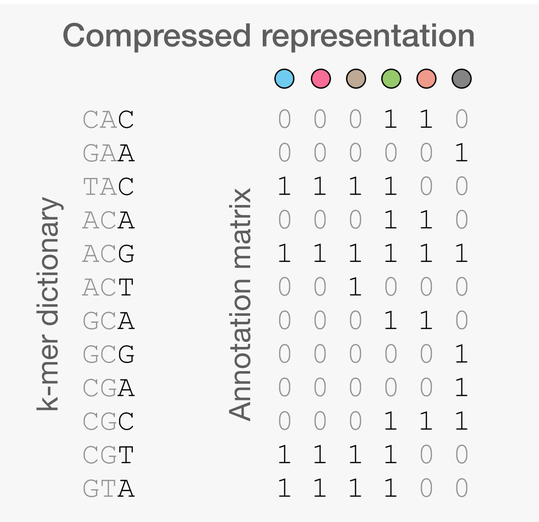

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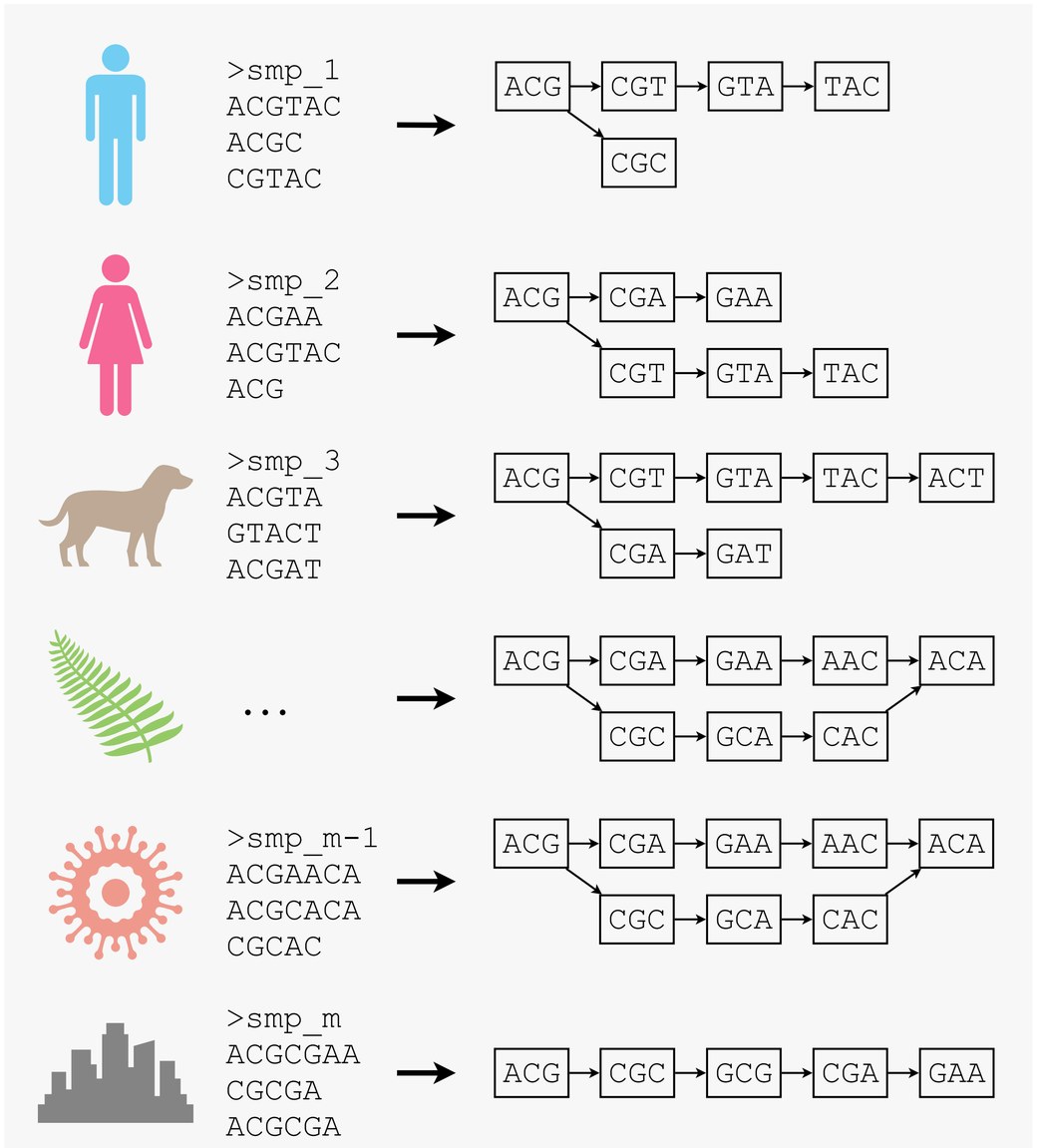

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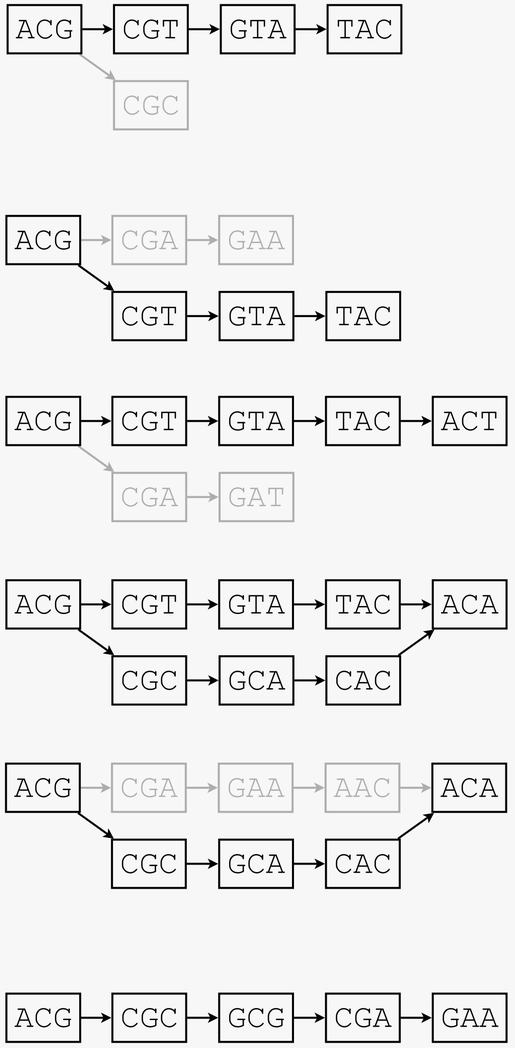

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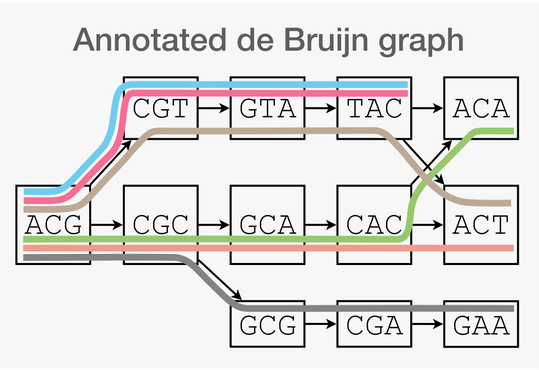

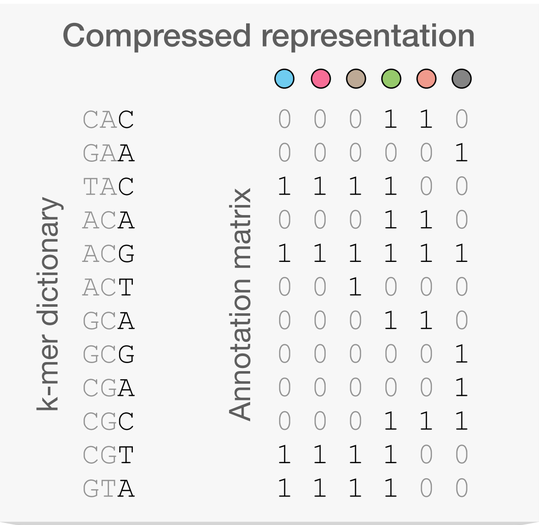

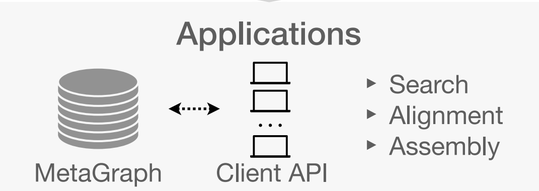

Indexing petabase-scale inputs

Dataset	Tbp	Input (gz)	k	# k-mers	# labels	Graph	Annot.	Index	Ratio
UHGG (catalog)	0.01	3.3 GB	31	$9.7 \cdot 10^9$	4,644	2.6 GB	0.6 GB	3.2 GB	1.0×
UHGG (all)	0.71	206.0 GB	31	$33.0 \cdot 10^9$	286,997	9.6 GB	17.7 GB	27.3 GB	7.6×
Tara Oceans (genomes)	0.06	17.9 GB	31	$26.5 \cdot 10^9$	6,414,647	7.3 GB	3.8 GB	11.1 GB	1.6×
Tara Oceans (assemblies)	0.36	106.8 GB	31	$119.4 \cdot 10^9$	318,205,057	34.4 GB	89.7 GB	124.1 GB	0.9×
RefSeq (85k taxID)	1.70	502.4 GB	31	$626.2 \cdot 10^9$	85,375	176.0 GB	87.5 GB	263.6 GB	1.9×
RefSeq (33M accessions)	1.70	502.5 GB	31	$626.2 \cdot 10^9$	32,881,348	176.0 GB	287.0 GB	463.1 GB	1.1×
Kingsford	8.0	2.9 TB	21	$3.9 \cdot 10^9$	2,652	1.8 GB	4.8 GB	6.6 GB	437×
GTEx	70.0	40.0 TB	41	$1.1 \cdot 10^9$	9,759	0.4 GB	8.0 GB	8.4 GB	4,742×
TCGA	81.2	65.0 TB	31	$1.1 \cdot 10^9$	11,095	0.4 GB	10.7 GB	11.1 GB	5,831×
MetaSUB	7.2	5.5 TB	19	$35.2 \cdot 10^9$	4,220	20.5 GB	185.9 GB	206.4 GB	27×
SRA-MetaGut	155.8	86.0 TB	31	$296.9 \cdot 10^9$	242,619	112.2 GB	999.0 GB	1,111.3 GB	77×
SRA-Microbe	221.1	170.0 TB	31	$39.5 \cdot 10^9$	446,506	15.4 GB	50.1 GB	65.5 GB	2,595×
SRA-Fungi	160.2	80.0 TB	31	$129.7 \cdot 10^9$	121,900	43.5 GB	64.7 GB	108.1 GB	740×
SRA-Plants	1,109.2	575.9 TB	31	$923.4 \cdot 10^9$	531,736	333.8 GB	1,510.3 GB	1,844.1 GB	312×
SRA-Human	725.4	345.7 TB	31	$343.9 \cdot 10^9$	436,502	127.6 GB	3,274.5 GB	3,402.1 GB	102×
SRA-Metazoa (Mouse)	146.6	61.3 TB	31	$50.2 \cdot 10^9$	57,938	21.1 GB	270.5 GB	291.6 GB	210×
SRA-Metazoa (10k)	33.4	16.5 TB	31	$293.3 \cdot 10^9$	10,000	94.0 GB	98.7 GB	192.7 GB	86×
SRA-Metazoa *	1,856.8	925.3 TB	31	$2749.8 \cdot 10^9$	797,883	960.4 GB	7,898.4 GB	8,858.8 GB	104×

Datasets: UHGG (Almeida *et al.*, 2020), Tara Oceans (Paoli, 2022), GTEx (Lonsdale *et al.*, 2013), TCGA (Kaiser, 2005), MetaSUB (Danko *et al.*, 2019), SRA-Microbe (Bradley *et al.*, 2019)

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Can we index k-mer positions as well?

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GTEx			41	$1.1 \cdot 10^9$	9,759	0.4 GB	8.0 GB	8.4 GB	4,742×
TCGA	81.2	65.0 TB	31	$1.1 \cdot 10^9$	11,095	0.4 GB	10.7 GB	11.1 GB	5,831×
MetaSUB	7.2	5.5 TB	19	$35.2 \cdot 10^9$	4,220	20.5 GB	185.9 GB	206.4 GB	27×
SRA-MetaGut	155.8	86.0 TB	31	$296.9 \cdot 10^9$	242,619	112.2 GB	999.0 GB	1,111.3 GB	77×
SRA-Microbe	221.1	170.0 TB	31	$39.5 \cdot 10^9$	446,506	15.4 GB	50.1 GB	65.5 GB	2,595×
SRA-Fungi	160.2	80.0 TB	31	$129.7 \cdot 10^9$	121,900	43.5 GB	64.7 GB	108.1 GB	740×
SRA-Plants	1,109.2	575.9 TB	31	$923.4 \cdot 10^9$	531,736	333.8 GB	1,510.3 GB	1,844.1 GB	312×
SRA-Human	725.4	345.7 TB	31	$343.9 \cdot 10^9$	436,502	127.6 GB	3,274.5 GB	3,402.1 GB	102×
SRA-Metazoa (Mouse)	146.6	61.3 TB	31	$50.2 \cdot 10^9$	57,938	21.1 GB	270.5 GB	291.6 GB	210×
SRA-Metazoa (10k)	33.4	16.5 TB	31	$293.3 \cdot 10^9$	10,000	94.0 GB	98.7 GB	192.7 GB	86×
SRA-Metazoa *	1,856.8	925.3 TB	31	$2749.8 \cdot 10^9$	797,883	960.4 GB	7,898.4 GB	8,858.8 GB	104×

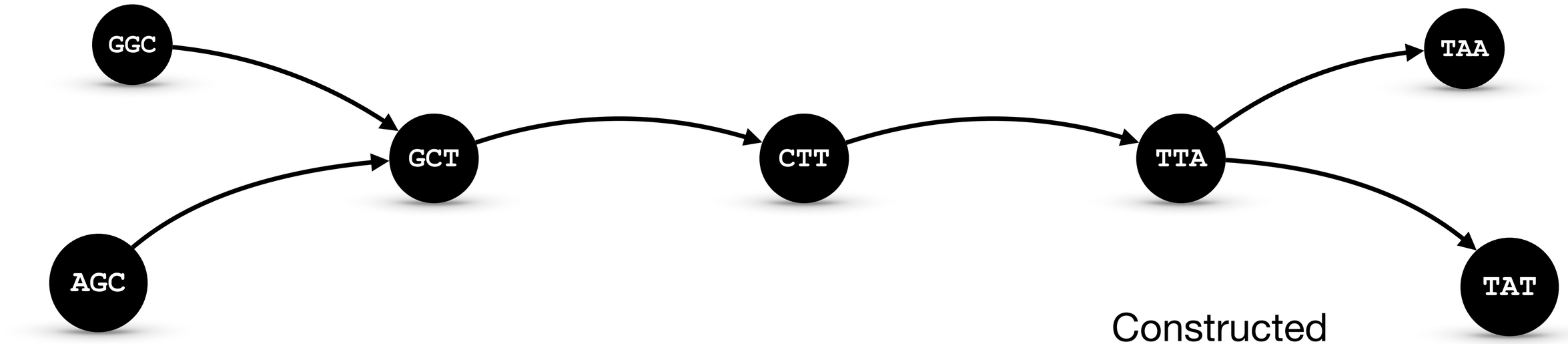
Can we index k-mer positions as well?

What about expression?

Datasets: UHGG (Almeida *et al.*, 2020), Tara Oceans (Paoli, 2022), GTEx (Lonsdale *et al.*, 2013), TCGA (Kaiser, 2005), MetaSUB (Danko *et al.*, 2019), SRA-Microbe (Bradley *et al.*, 2019)

Background

Annotated de Bruijn Graphs



Constructed
from sequences

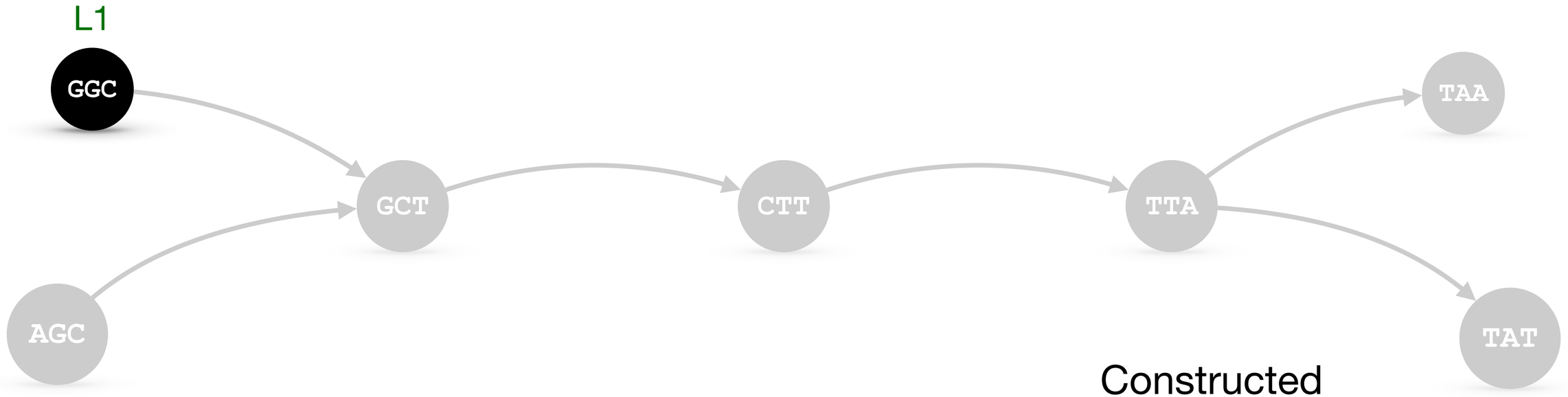
L1: GGCTTAT

L2: AGCTTAA

L3: TTAA

Background

Annotated de Bruijn Graphs



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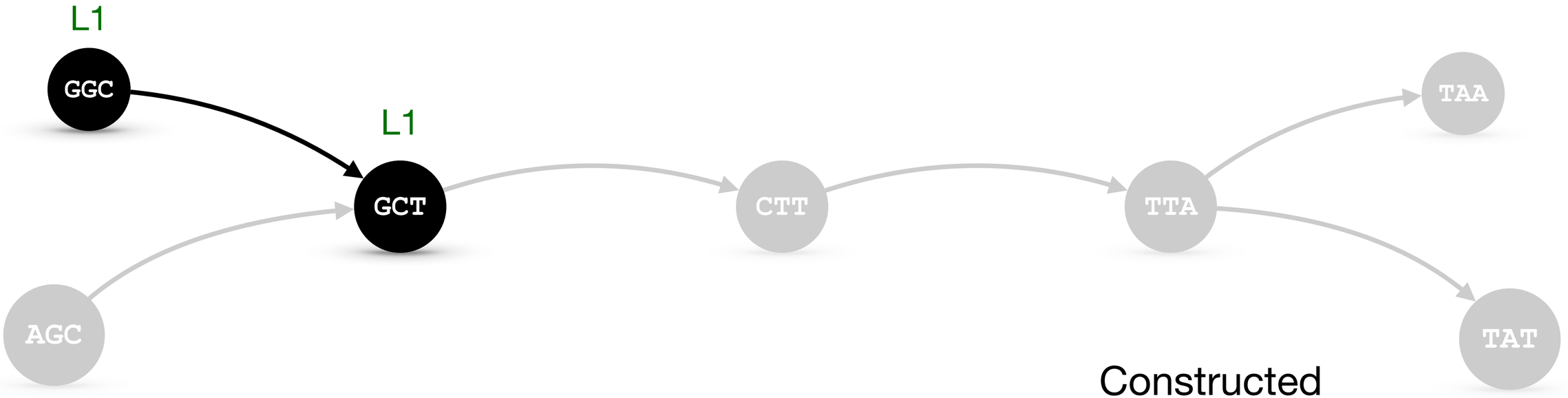

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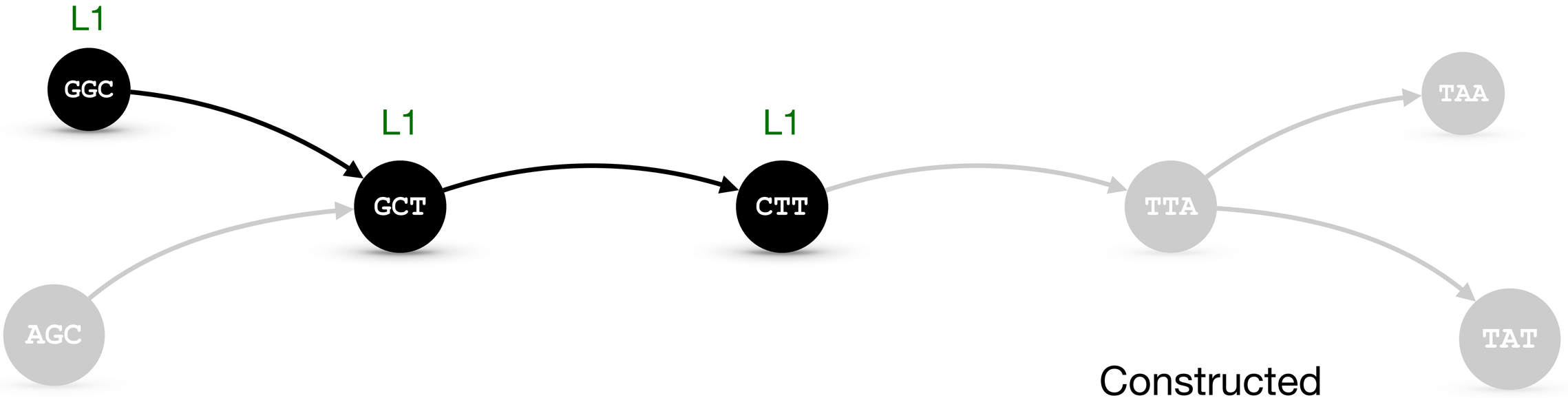

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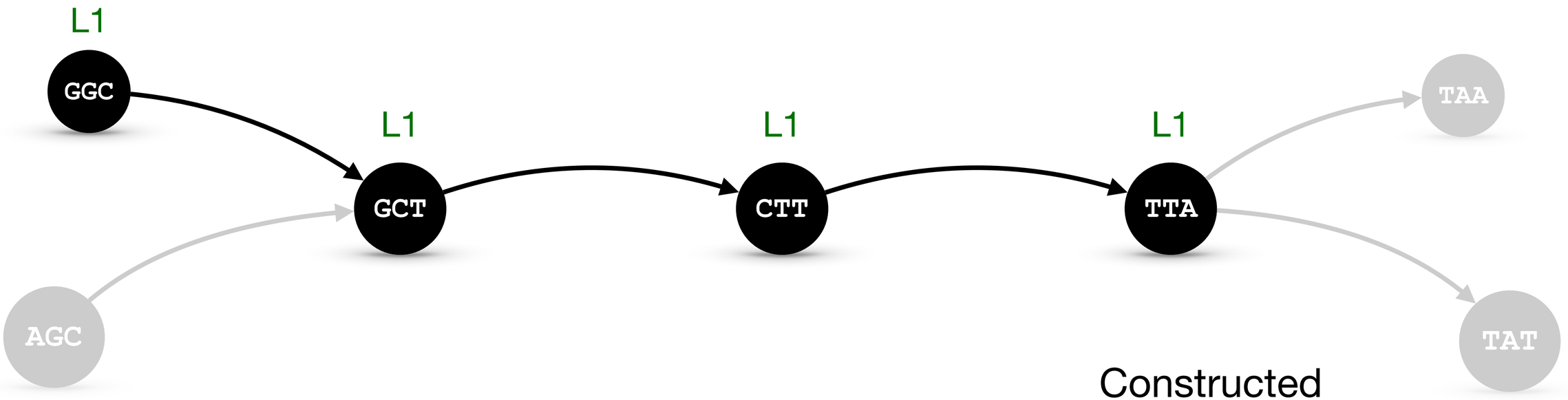

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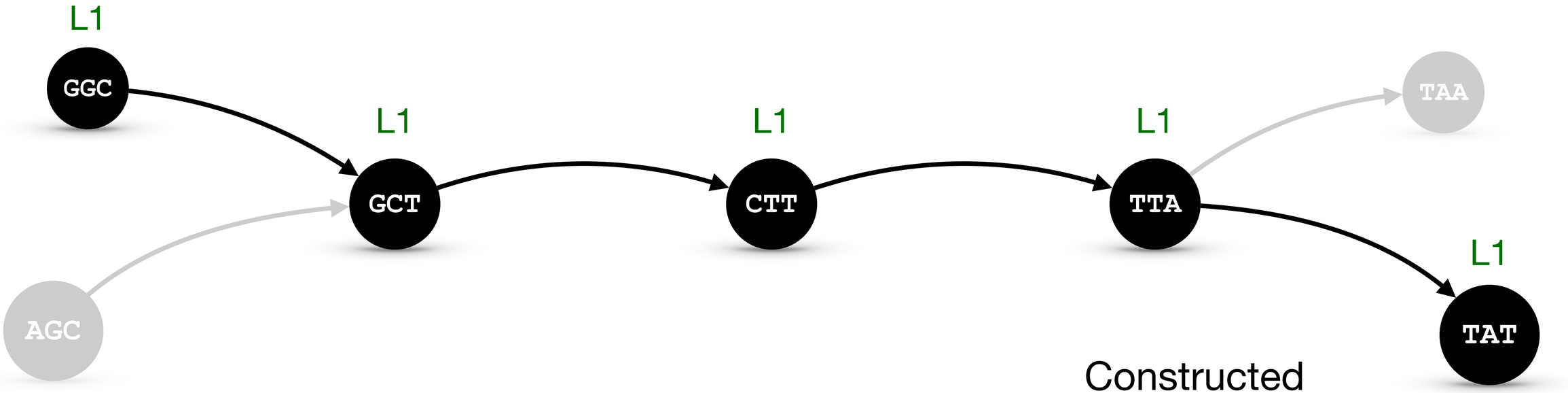

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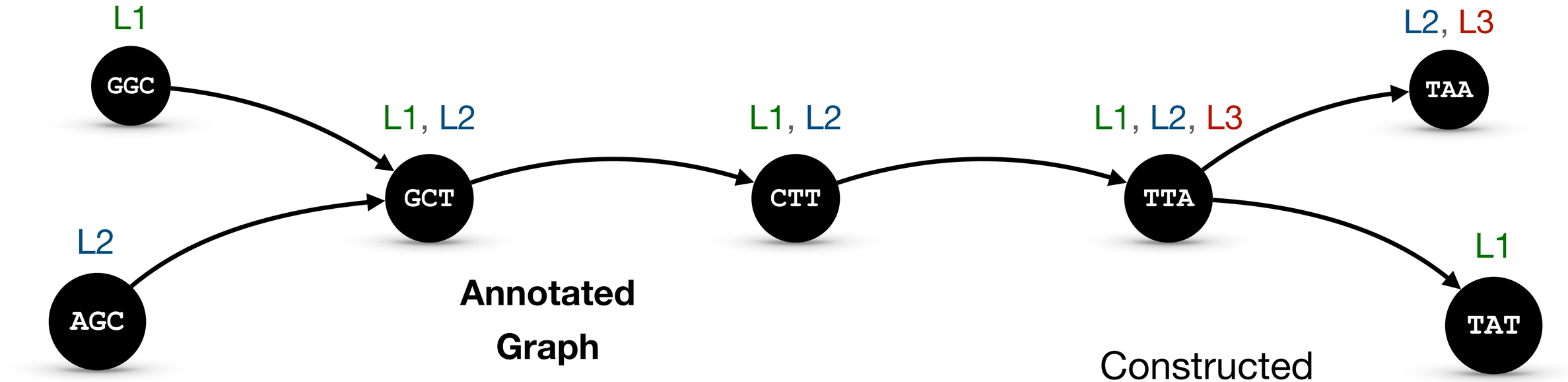

Annotated Graph

Constructed from sequences

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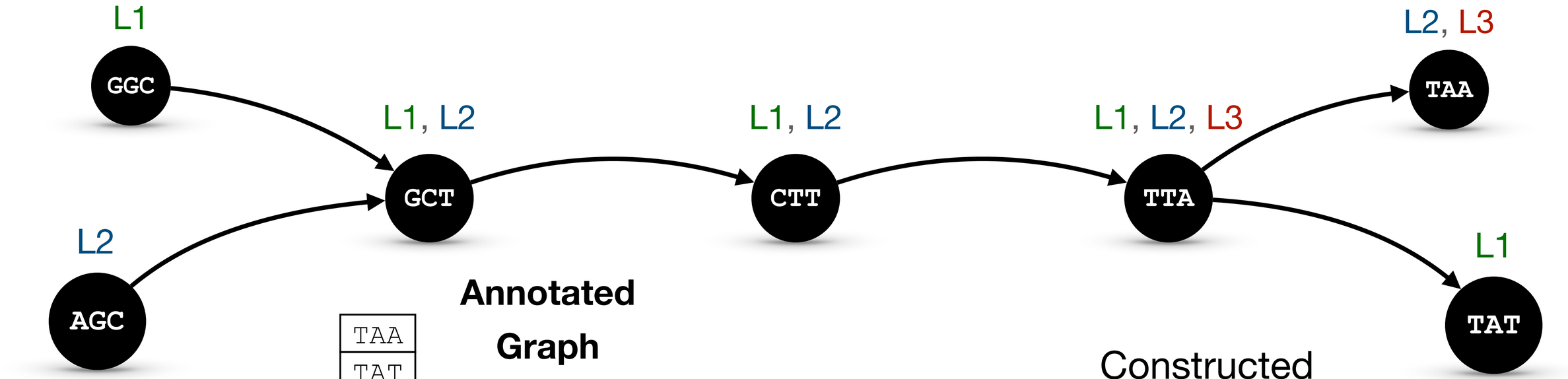
Background

Annotated de Bruijn Graphs



Annotated Graph

TAA
TAT
GCT
AGC
GGC
CTT
TTA

k-mer dictionary
(de Bruijn Graph)

Constructed from sequences

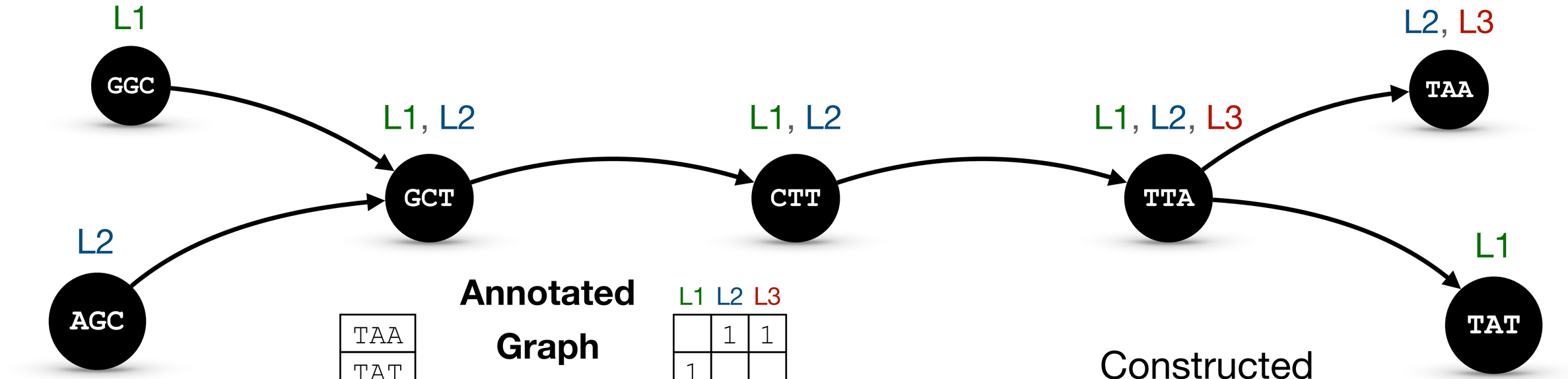
L1: GGCTTAT

L2: AGCTTAA

L3: TTAA

Background

Annotated de Bruijn Graphs



Annotated Graph

TAA
TAT
GCT
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CTT
TTA

k-mer dictionary
(de Bruijn Graph)

L1	L2	L3
	1	1
1		
1	1	
	1	
1		
1	1	
1	1	1

Graph annotation
(node labeling)

Constructed from sequences

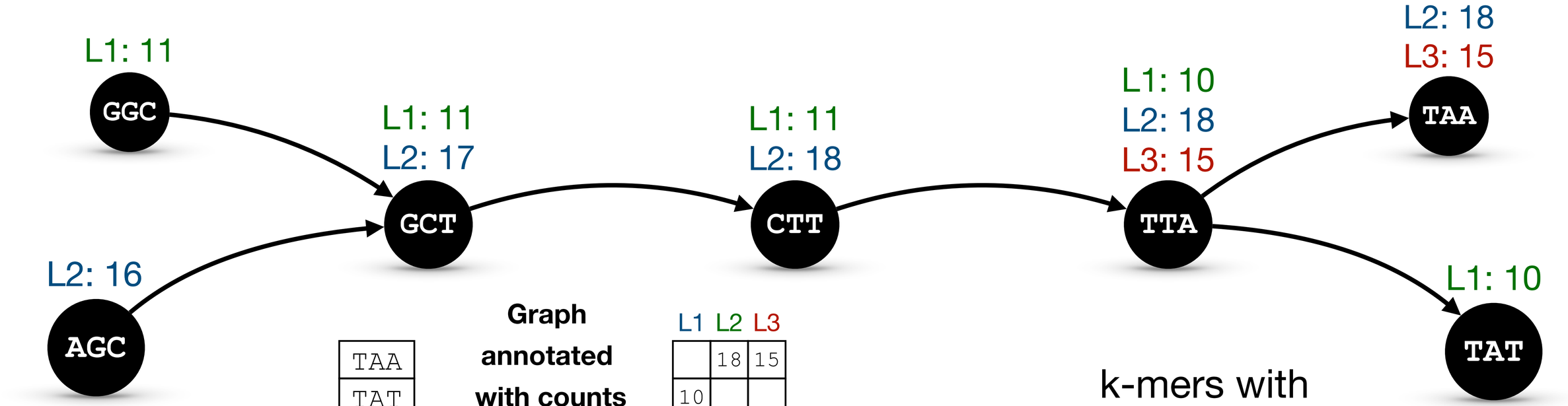
L1: GGCTTAT

L2: AGCTTAA

L3: TTAA

Motivation

1. Representing **k-mer abundances**



Graph annotated with counts

TAA
TAT
GCT
AGC
GGC
CTT
TTA

k-mer dictionary
(de Bruijn Graph)

L1	L2	L3
	18	15
10		
11	17	
	16	
11		
11	18	
10	18	15

Graph annotation
(node labeling)

k-mers with multiplicities

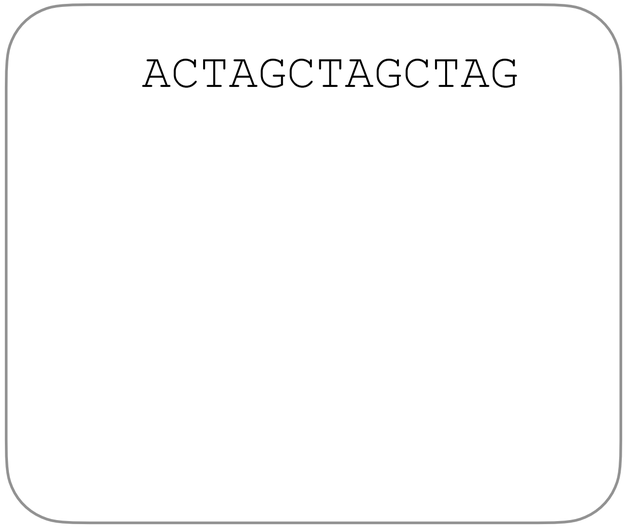
L1: GGC: 11, …

L2: AGC: 16, …

L3: TTA: 15, …

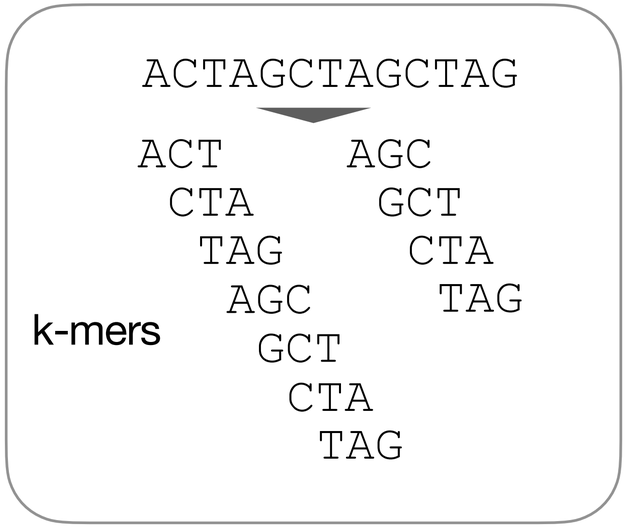
Motivation

2. Representing **k-mer coordinates**



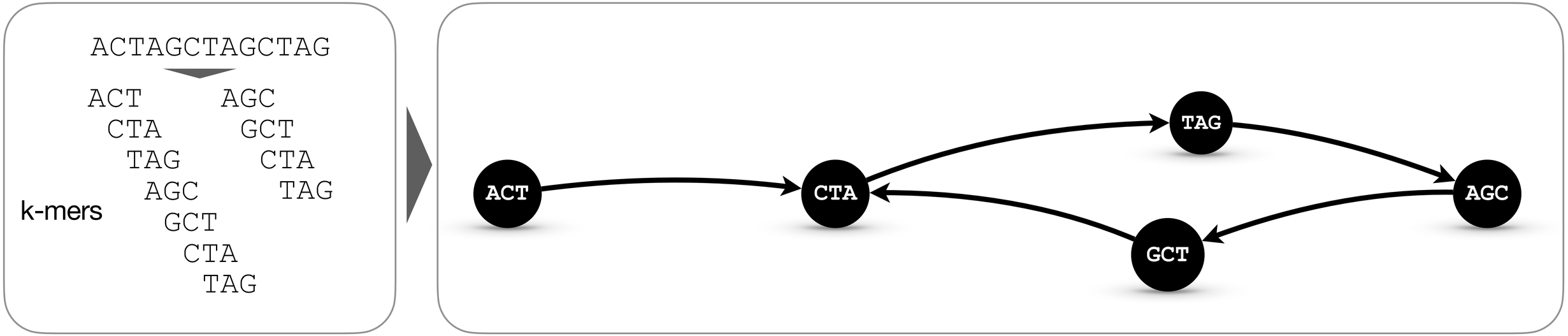
Motivation

2. Representing **k-mer coordinates**



Motivation

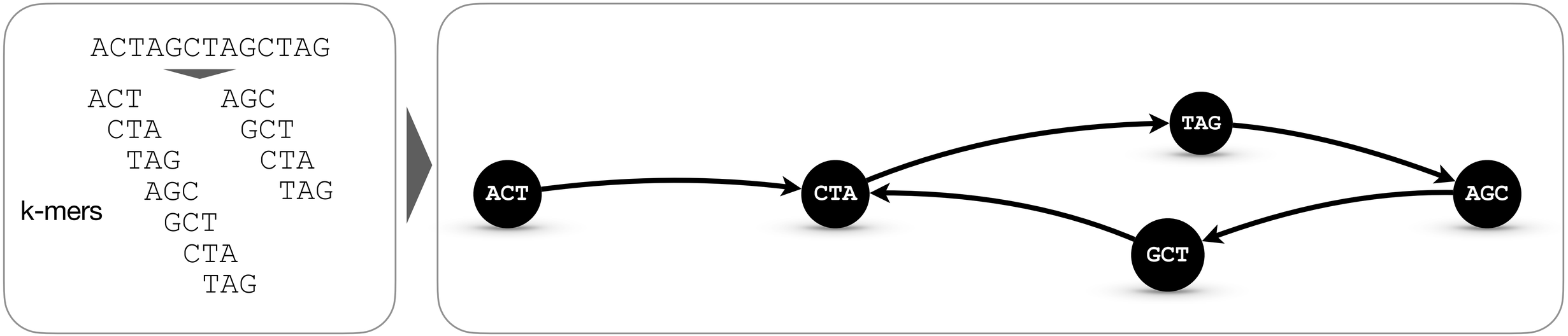
2. Representing **k-mer coordinates**



de Bruijn graph

Motivation

2. Representing **k-mer coordinates**

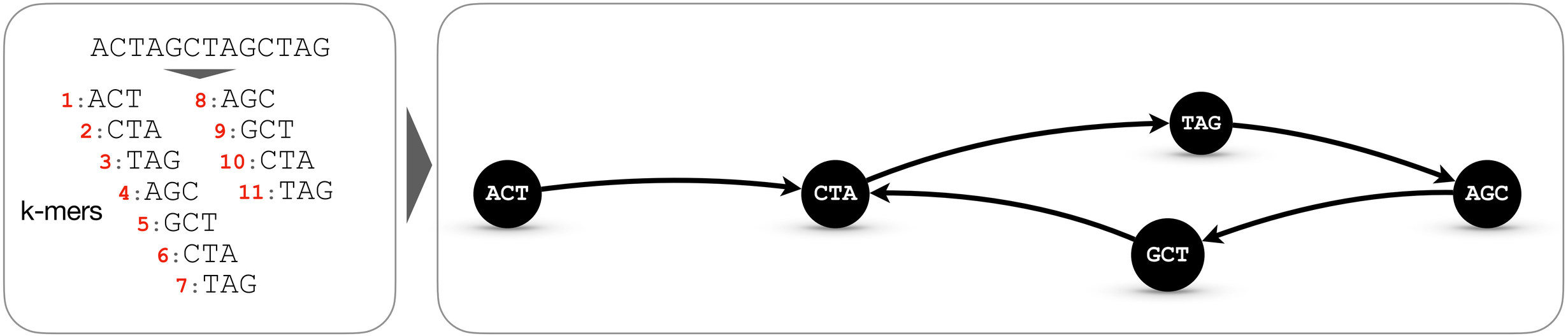


Not invertible representation 😕

de Bruijn graph

Motivation

2. Representing **k-mer coordinates**



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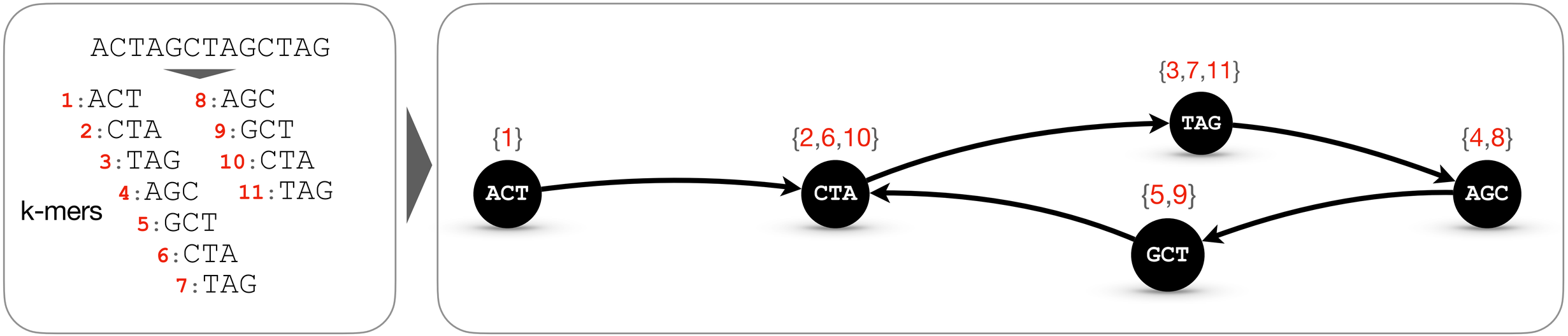
de Bruijn graph

Motivation

2. Representing **k-mer coordinates**



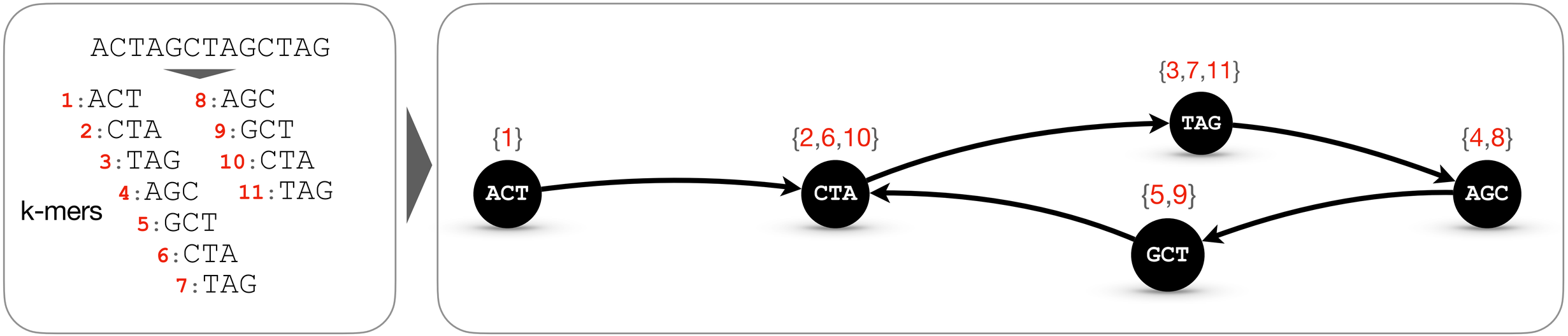
Invertible 🙂

de Bruijn graph

with k-mer coordinates

Motivation

2. Representing **k-mer coordinates**



Encoding ***sequence traces*** allows

- reconstructing indexed sequences

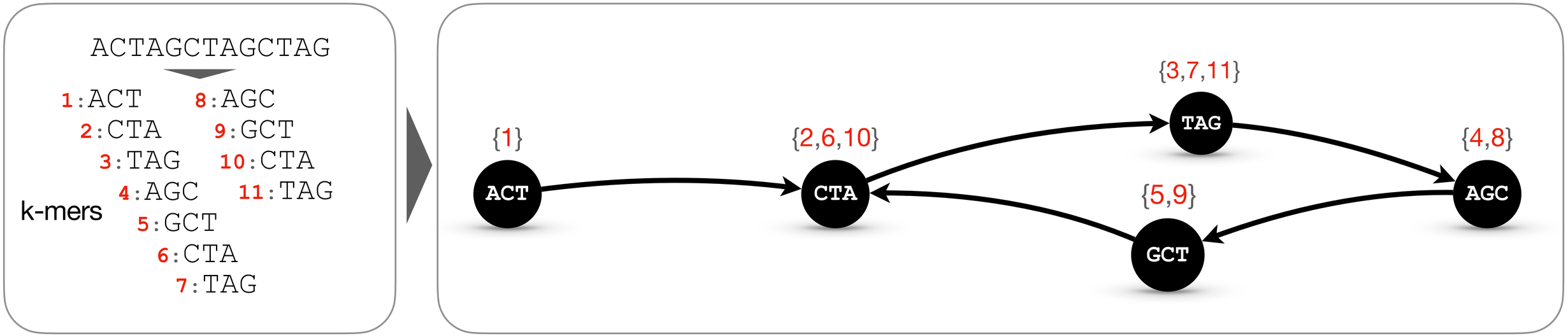
  (hence, **lossless sequence representation)**

de Bruijn graph

with k-mer coordinates

Motivation

2. Representing **k-mer coordinates**



Encoding ***sequence traces*** allows

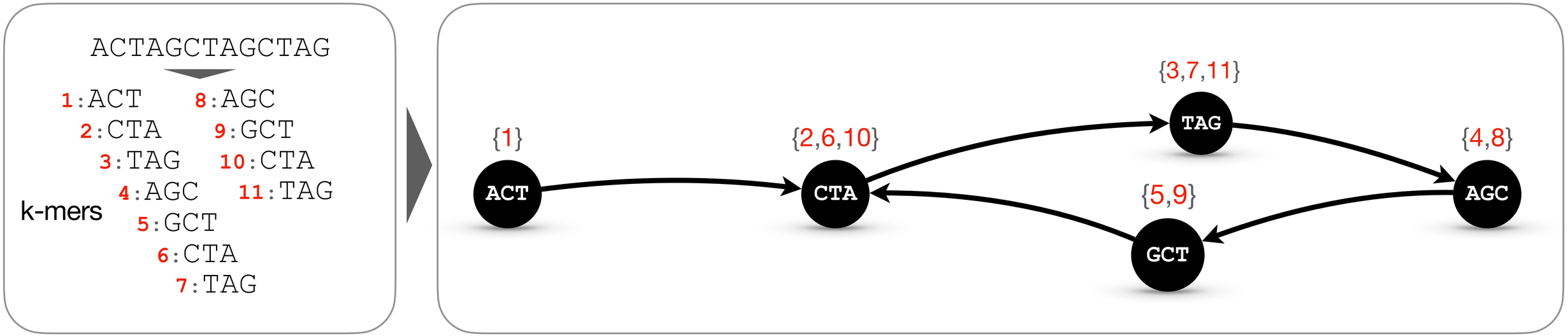
- reconstructing indexed sequences
  (hence, **lossless sequence representation)**
- performing exact sequence alignment

de Bruijn graph

with k-mer coordinates

Motivation

2. Representing **k-mer coordinates**



Encoding ***sequence traces*** allows

- reconstructing indexed sequences
  (hence, **lossless sequence representation)**
- performing exact sequence alignment
- retrieving all **traces** crossing a node

de Bruijn graph

with k-mer coordinates

Questions to address

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1. How to **efficiently represent** a huge sparse **non-binary matrix**?

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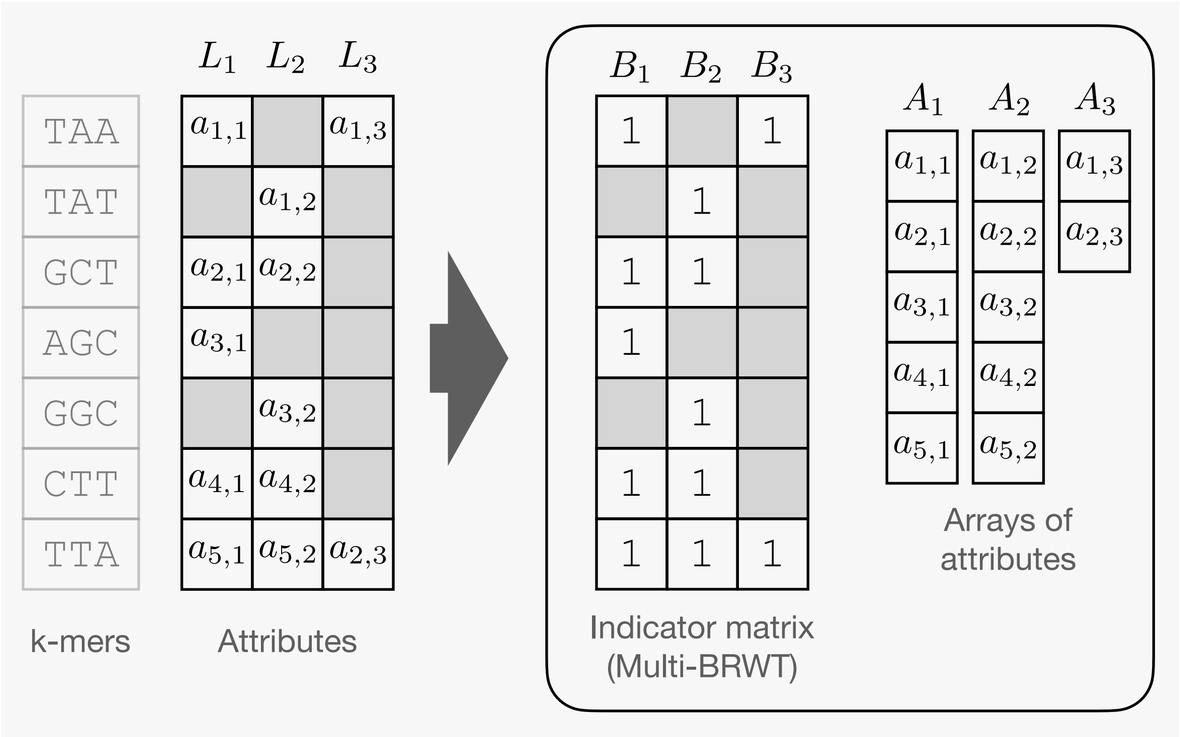
2. Can we **employ existing repr. schemes** for binary matrices?
3. How to **exploit regularities in graph** annotations?

Method

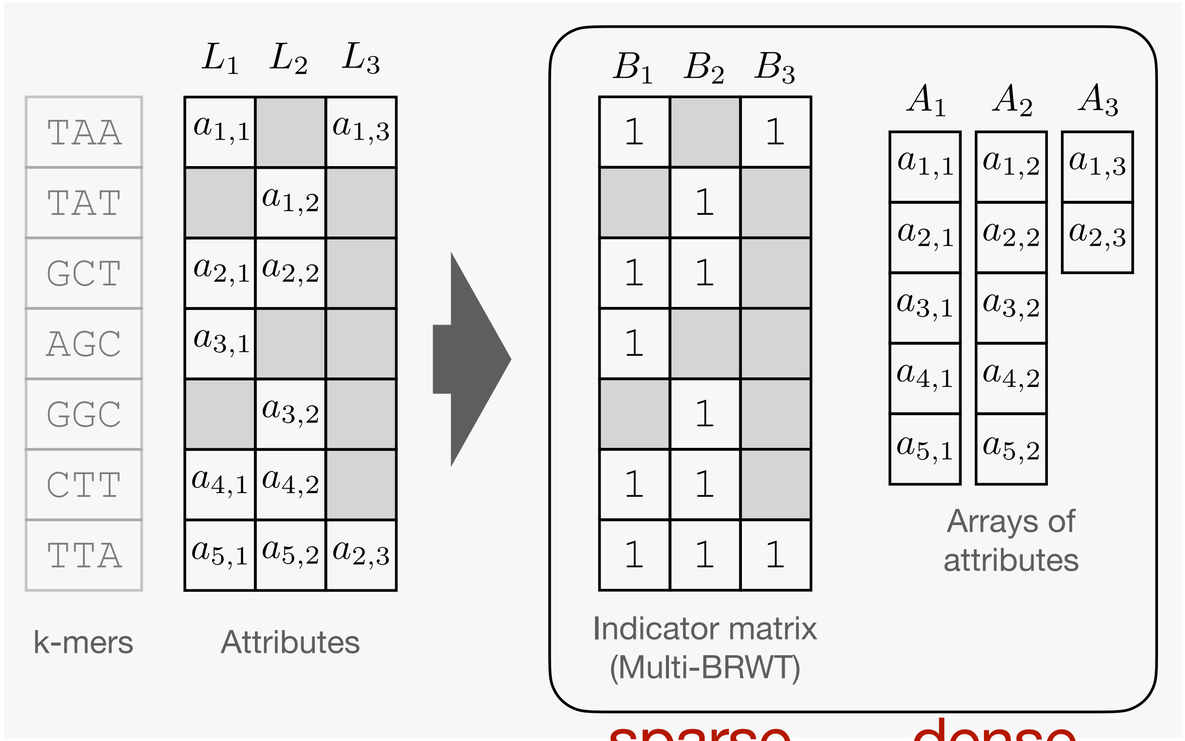
Method

General scheme for sparse matrices



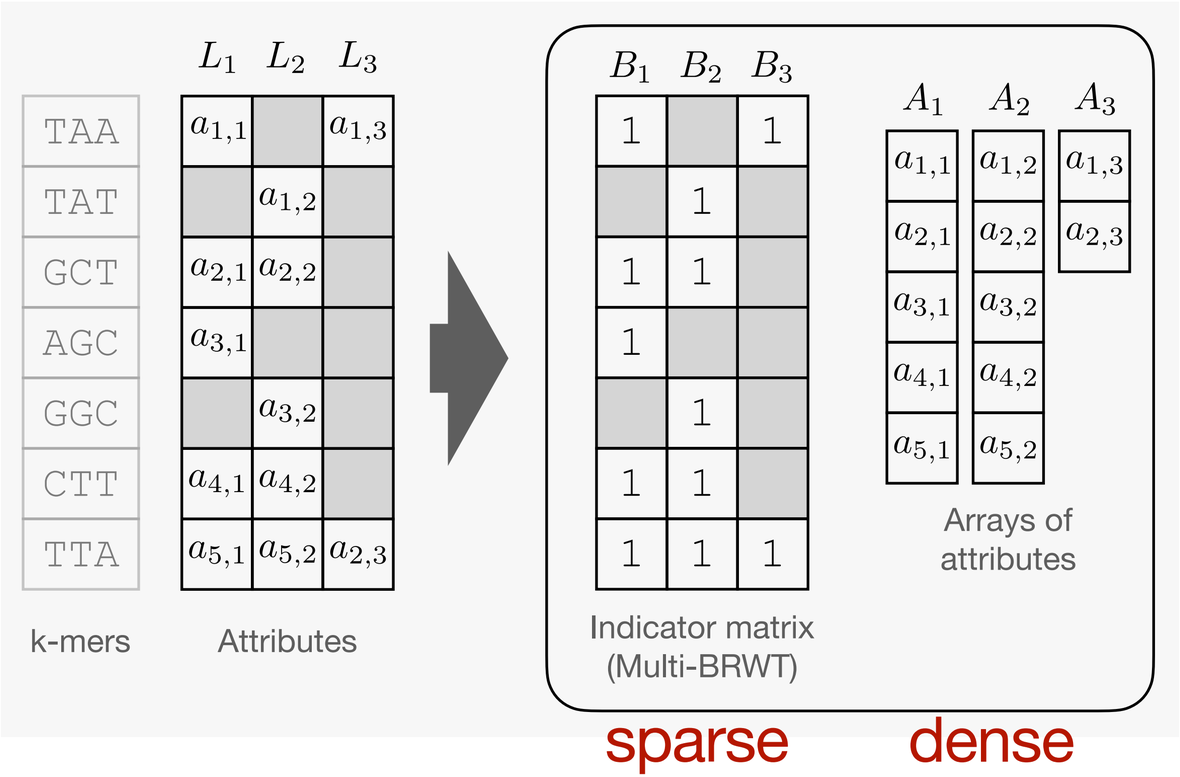
Method

General scheme for sparse matrices



Method

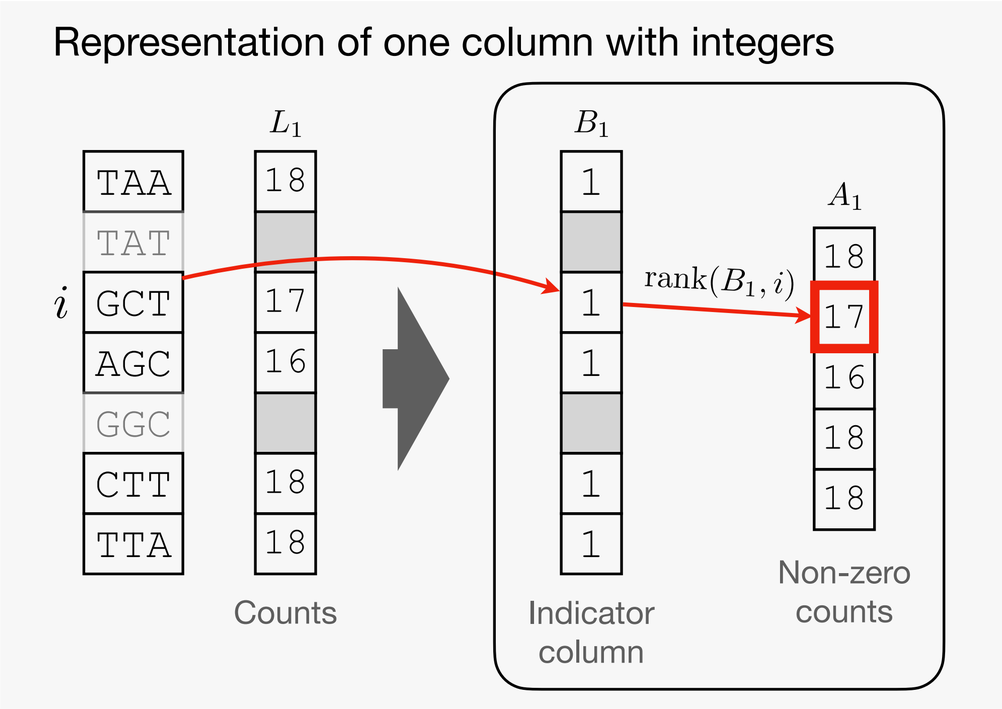
General scheme for sparse matrices

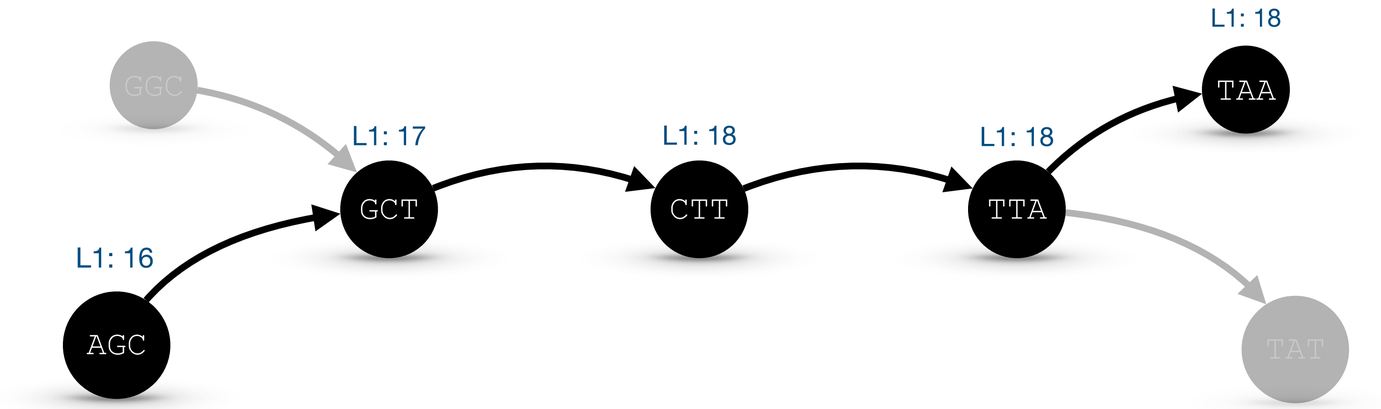


Theorem 1. *If both the indicator matrix and the arrays of attributes are represented succinctly, the proposed scheme also is a succinct representation of the matrix. That is, there is no other data structure that could represent any such matrix with asymptotically fewer bits.*

Method

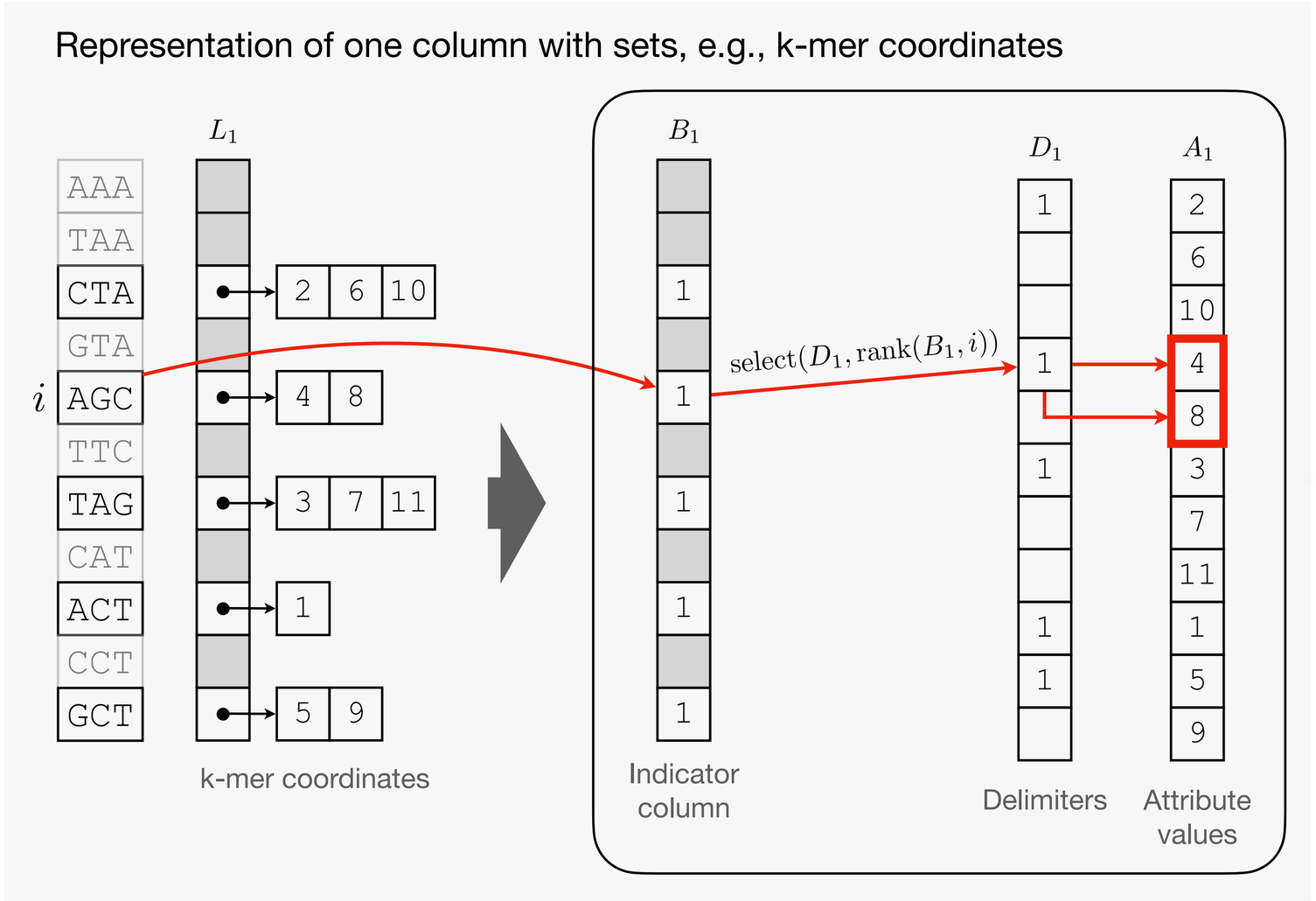
1. One column with **integers** (k-mer abundances)

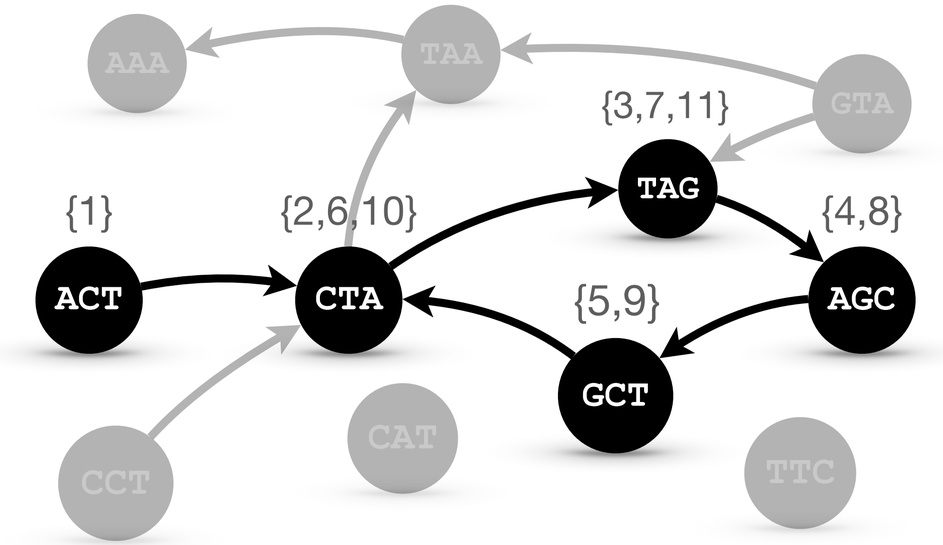




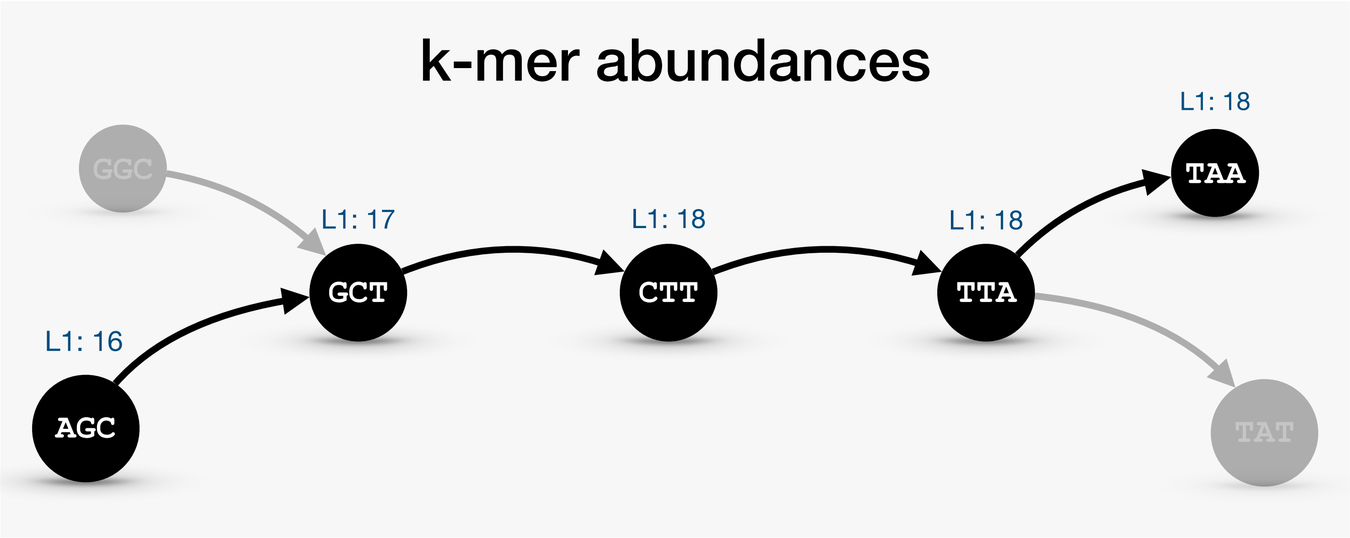
Method

2. One column with integer **tuples** (k-mer coordinates)





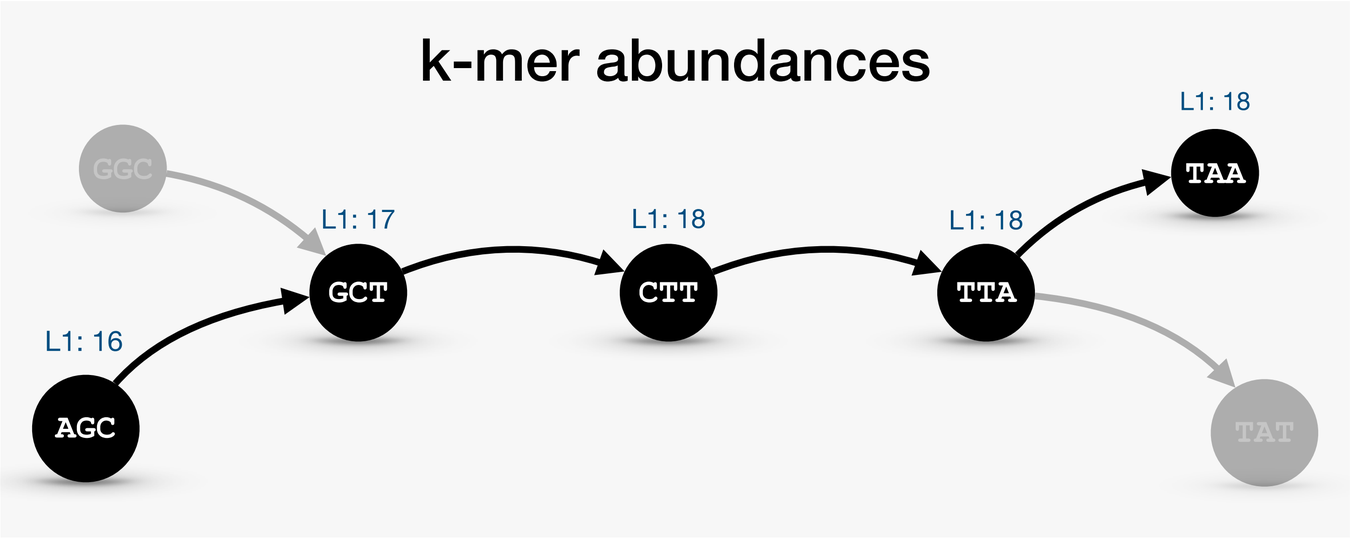
Exploiting regularities

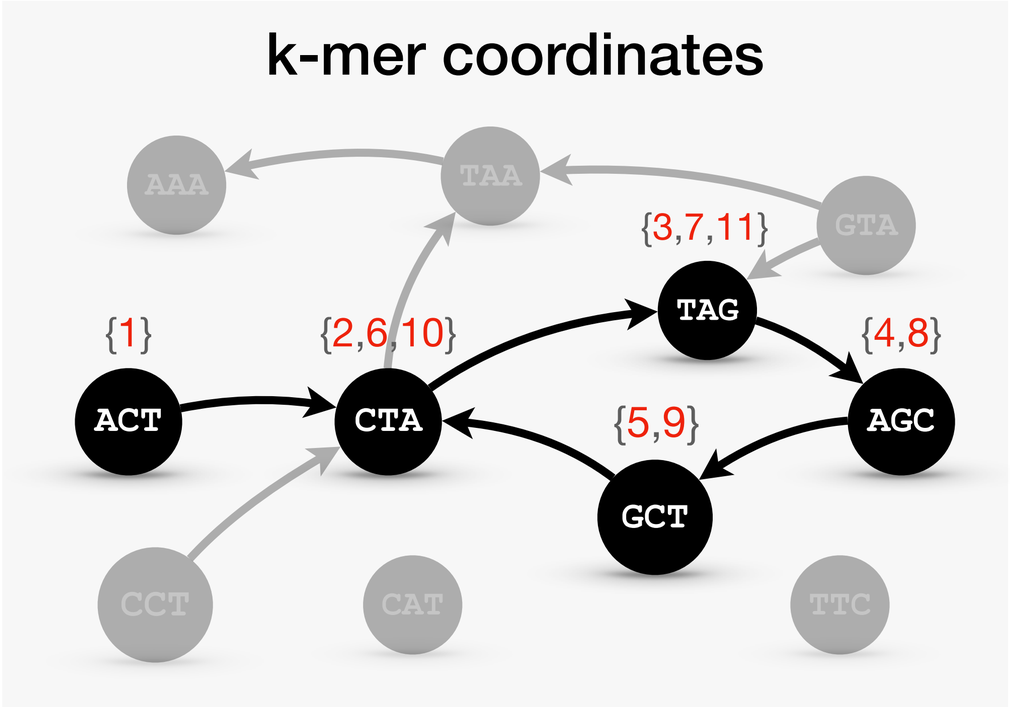


Observe regularities:

- Abundances of neighboring k-mers are often similar

Exploiting regularities

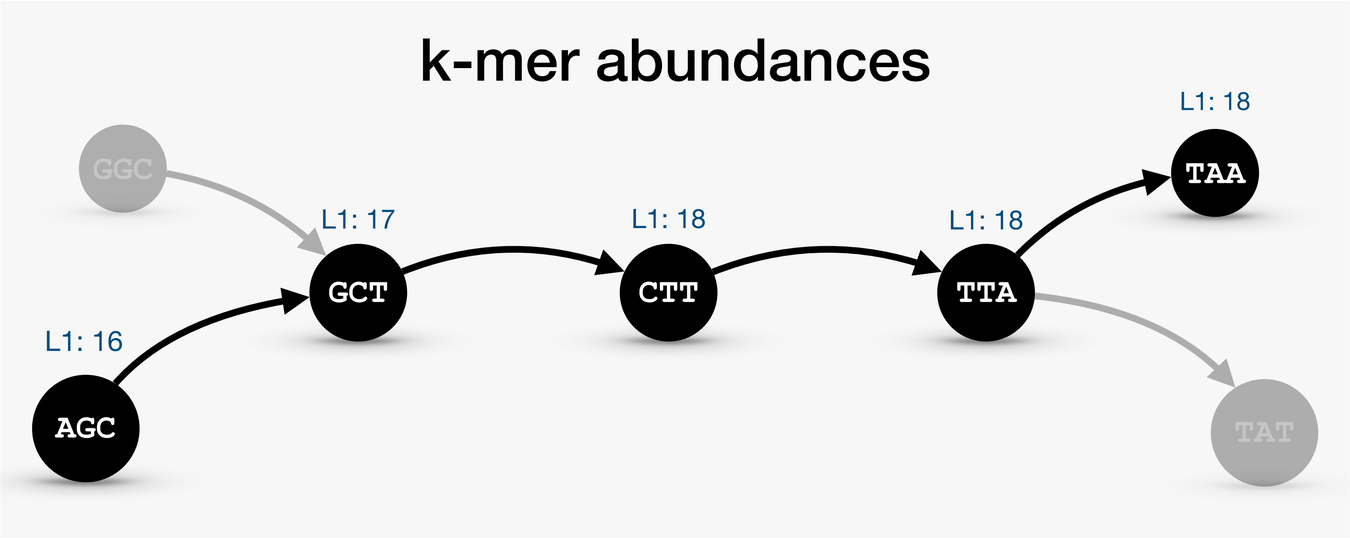


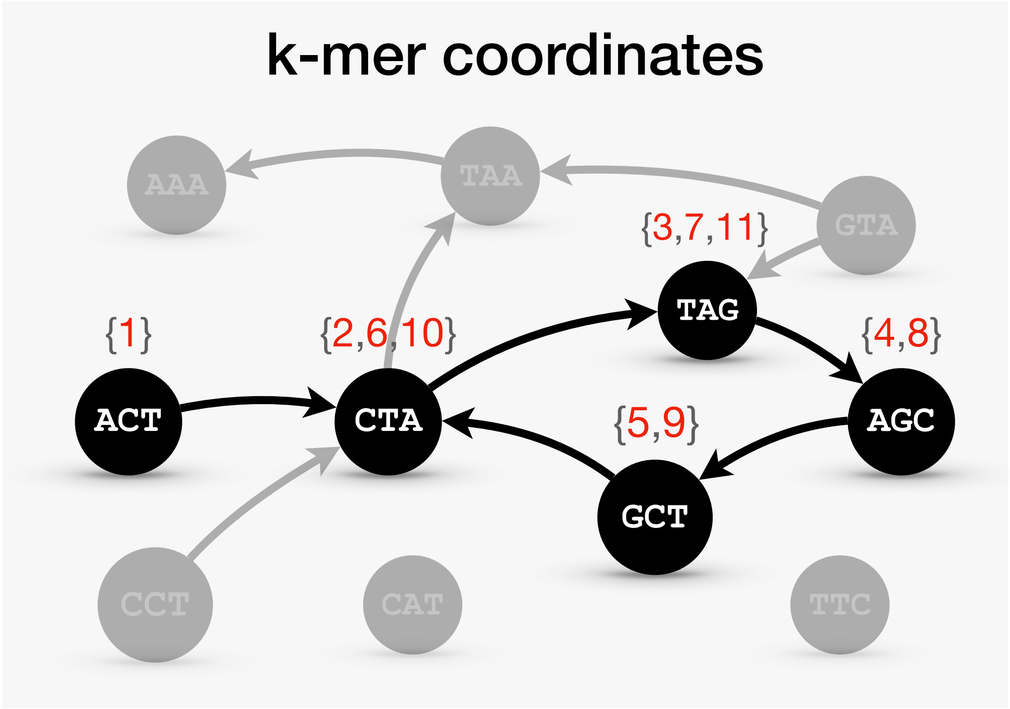


Observe regularities:

- Abundances of neighboring k-mers are often similar
- Coordinates for adjacent k-mers always differ by +1

Exploiting regularities





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Idea

Generalize the RowDiff scheme


Bioinformatics, 37, 2021, i169–i176
doi: 10.1093/bioinformatics/btab330
ISMB/ECCB 2021
OXFORD

Topology-based sparsification of graph annotations

Daniel Danciu[1,2,†], Mikhail Karasikov[1,2,3,†], Harun Mustafa[1,2,3], André Kahles[1,2,3,*] and Gunnar Rätsch[1,2,3,4,*]

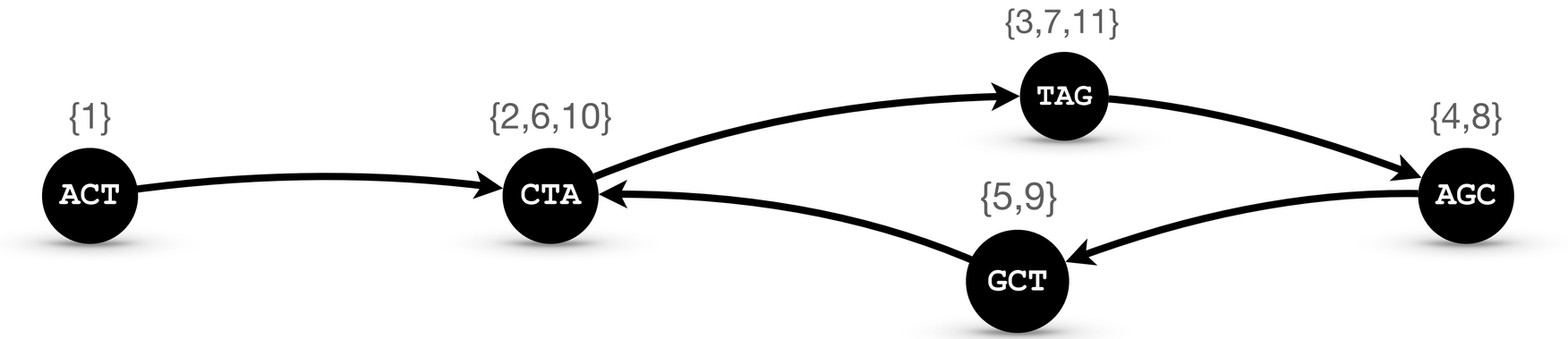
Delta coding for k-mer coordinates

A. Enumeration of k-mers

ACTAGCTAGCTAG

1:ACT
2:CTA
3:TAG
4:AGC
5:GCT
6:CTA
7:TAG
8:AGC
9:GCT
10:CTA
11:TAG

B. Delta-coding of coordinate annotations (sets)



Delta coding for k-mer coordinates

A. Enumeration of k-mers

```
ACTAGCTAGCTAG

1:ACT    8:AGC
 2:CTA    9:GCT
  3:TAG   10:CTA
   4:AGC  11:TAG
    5:GCT
     6:CTA
      7:TAG
```

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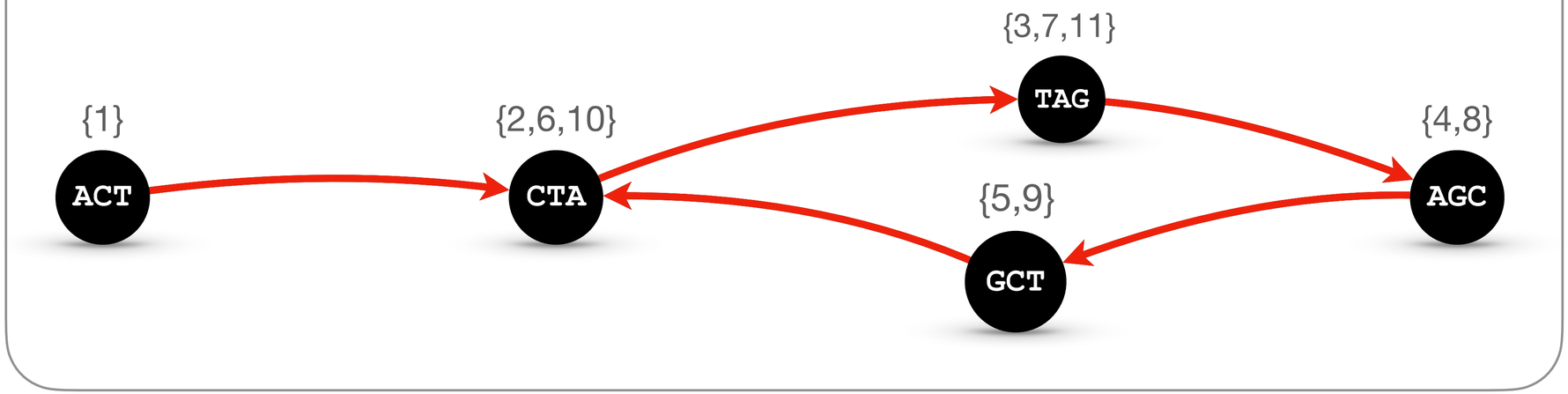

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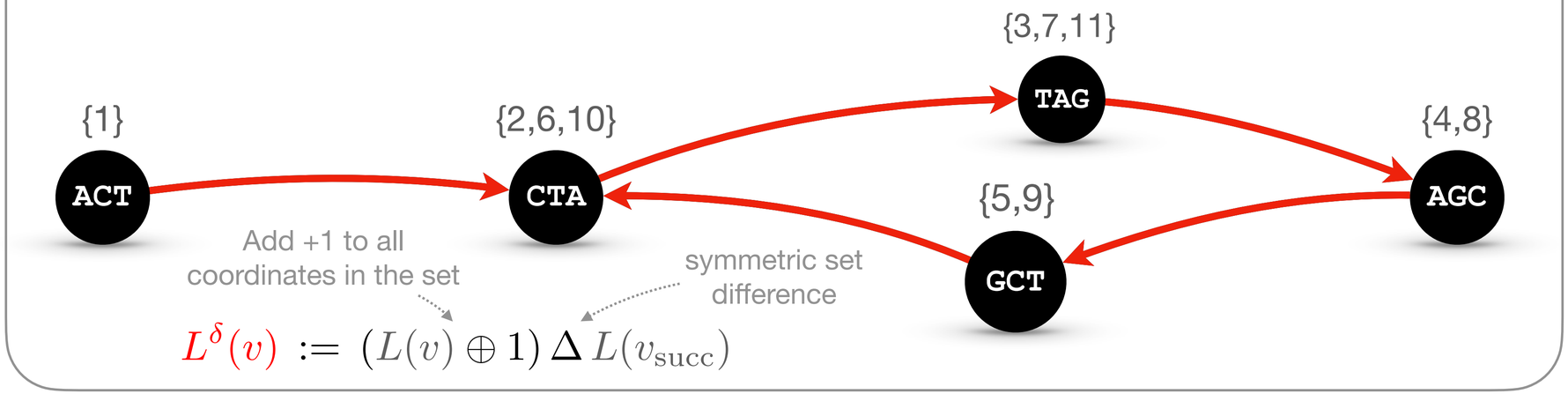

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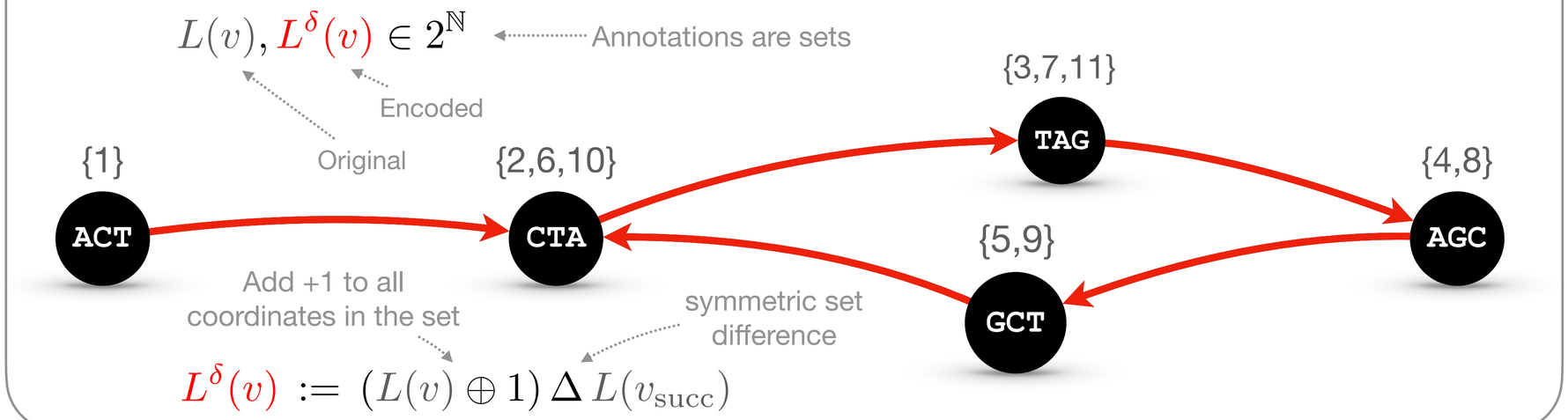

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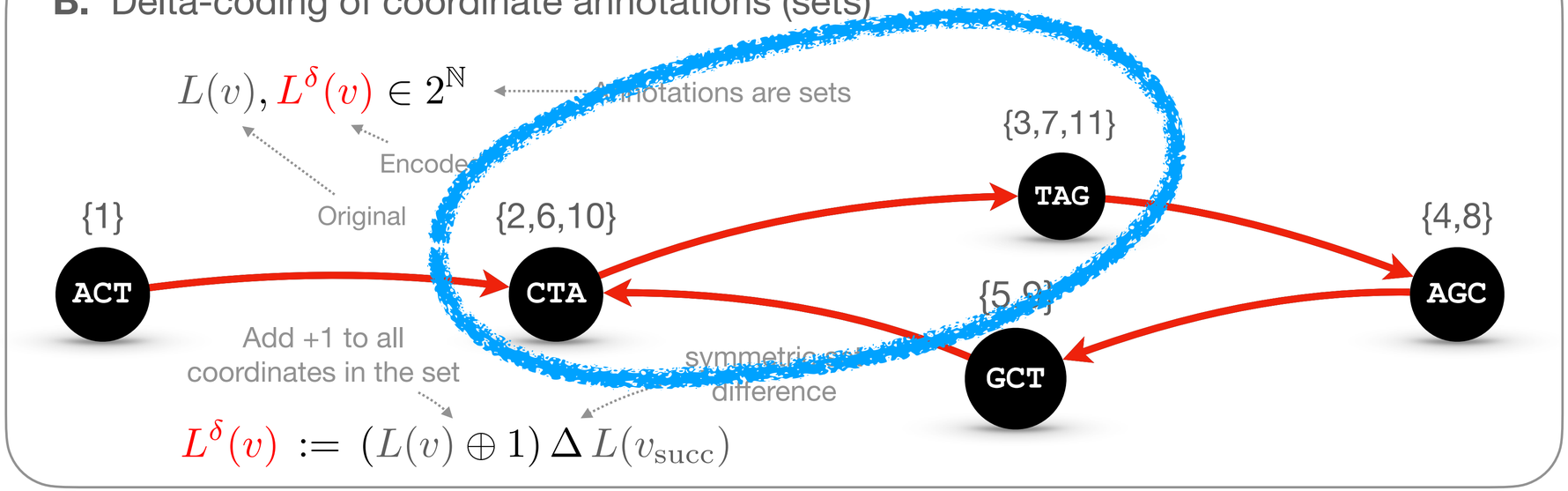

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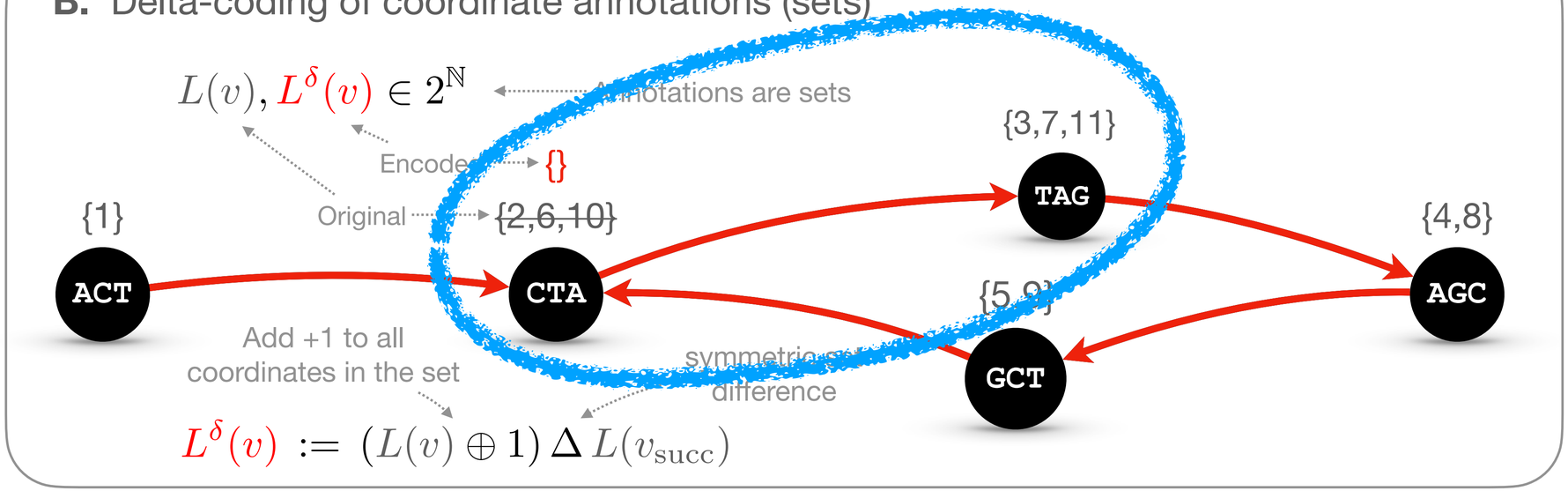

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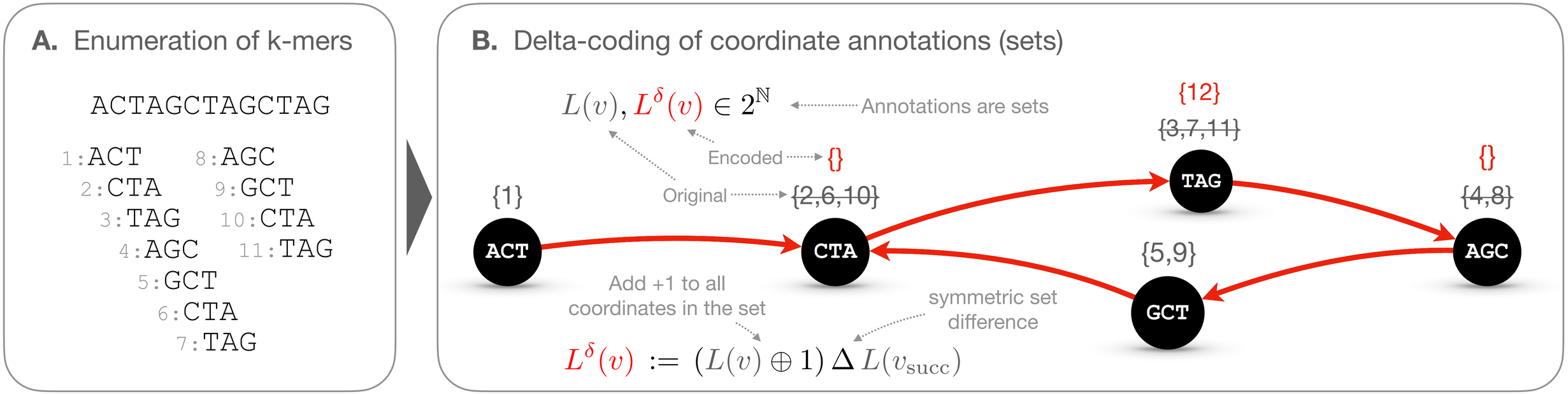

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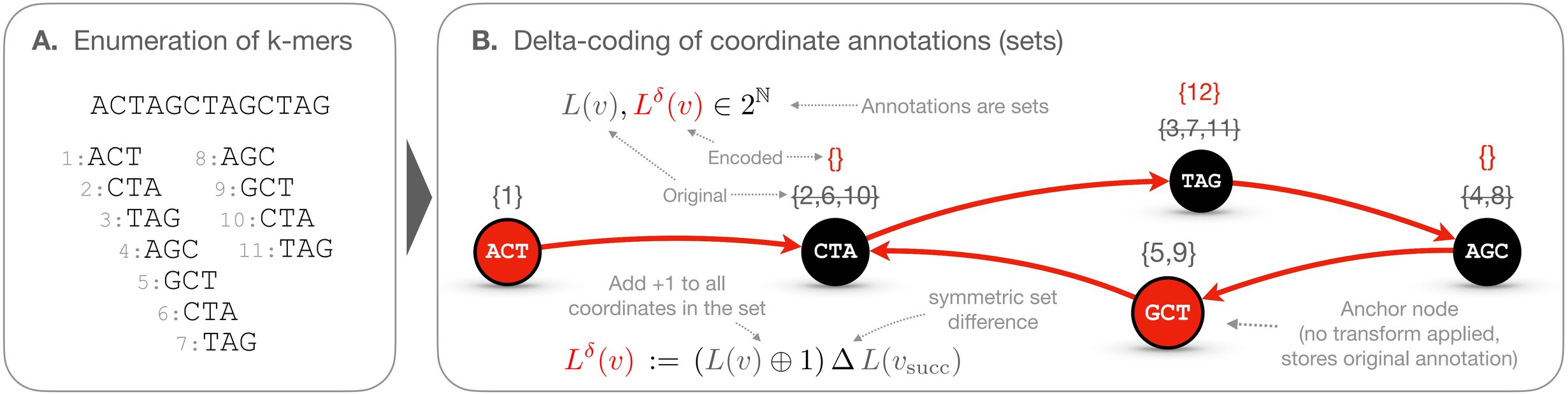

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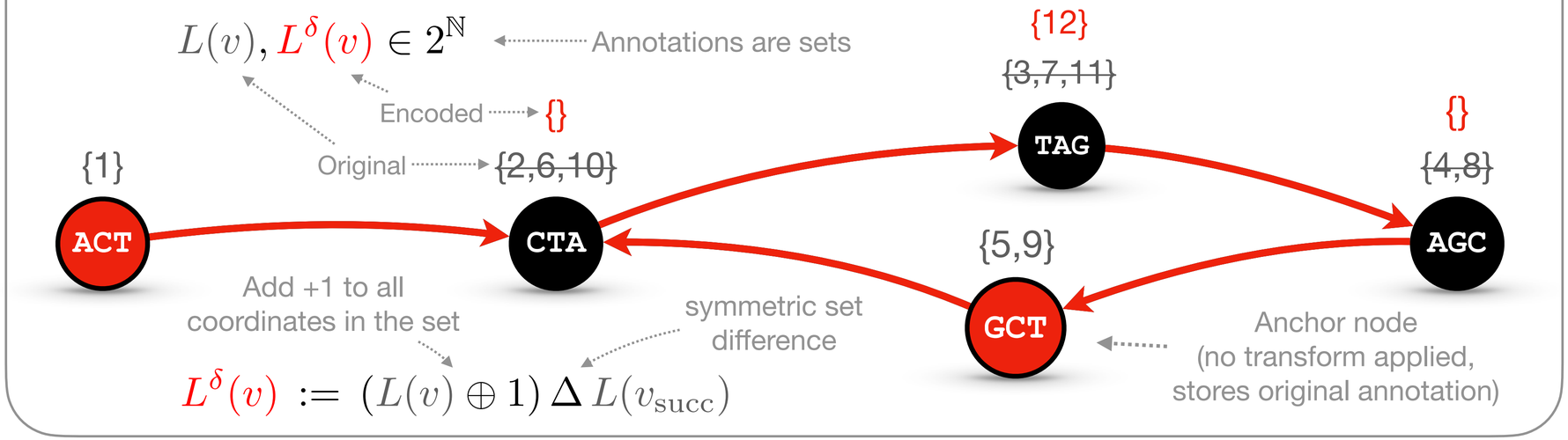
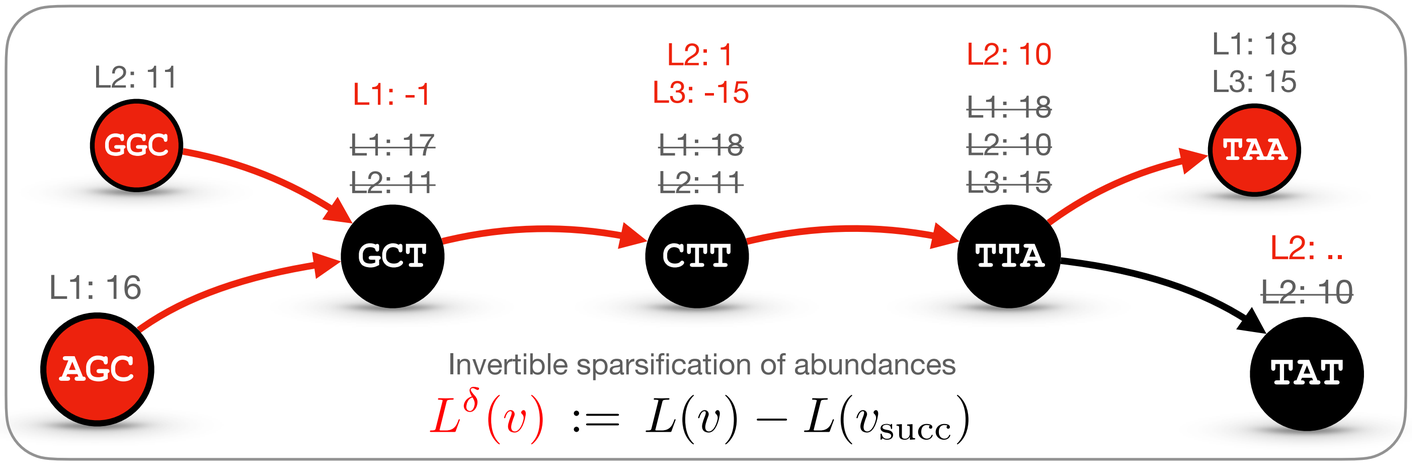
11:TAG

B. Delta-coding of coordinate annotations (sets)

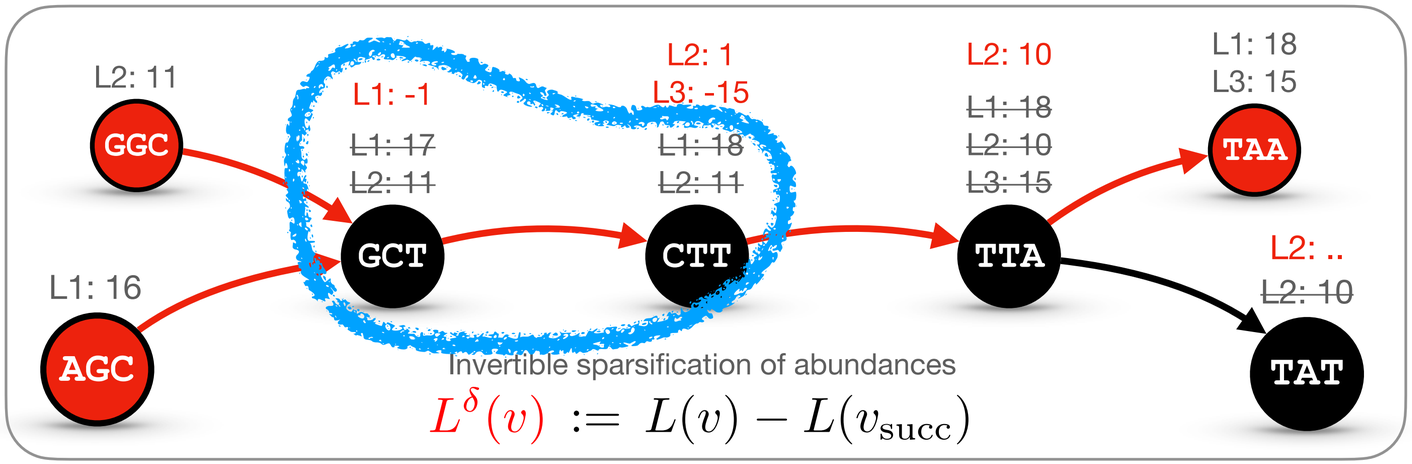


Decoding: $L(v) = (L^{\delta}(v) \,\Delta\, L(v_{\text{succ}})) \ominus 1$

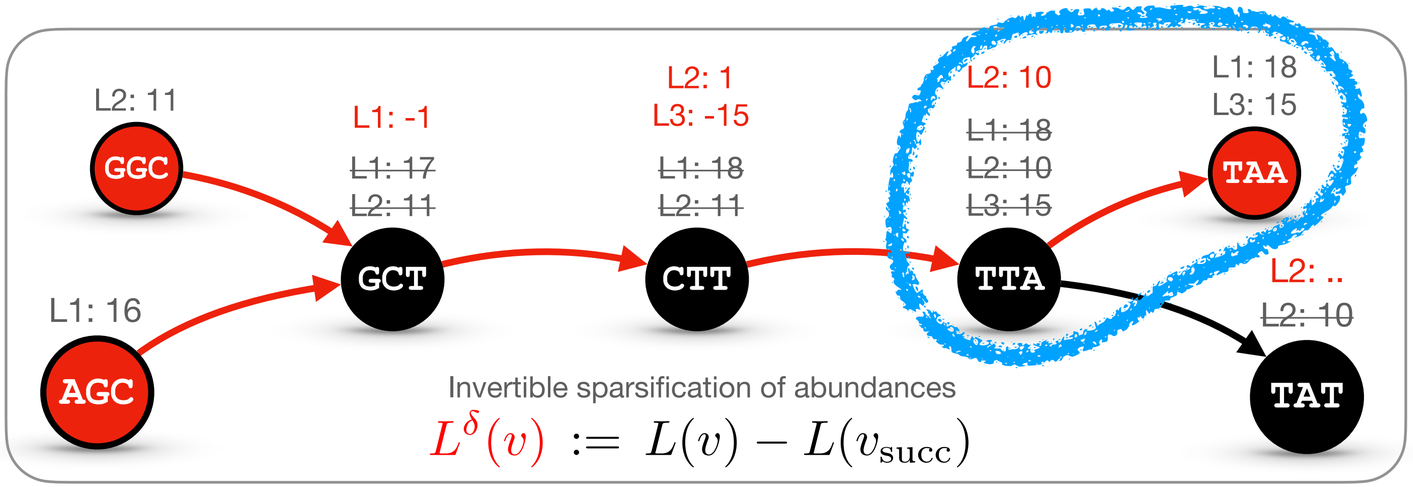
Delta coding for k-mer abundances



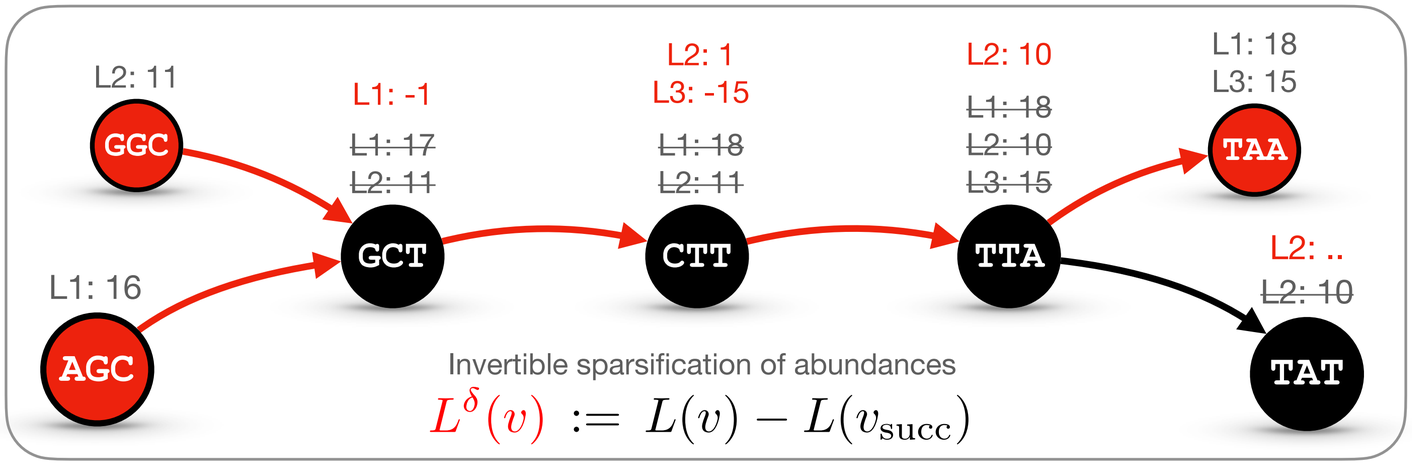
Delta coding for k-mer abundances



Delta coding for k-mer abundances

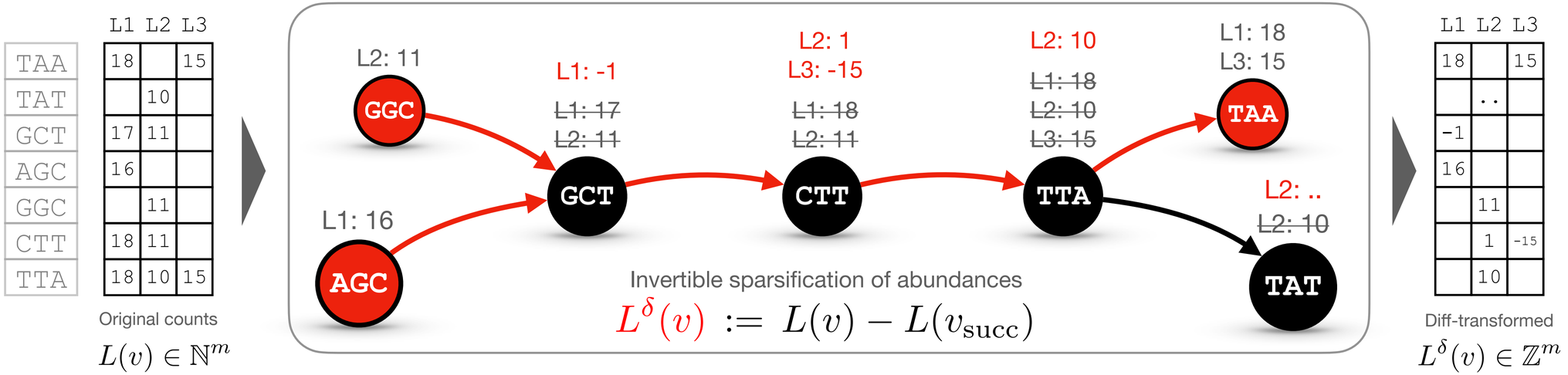


Delta coding for k-mer abundances



Decoding: $L(v) = L(v_{\text{succ}}) + L^{\delta}(v)$

Delta coding for k-mer abundances



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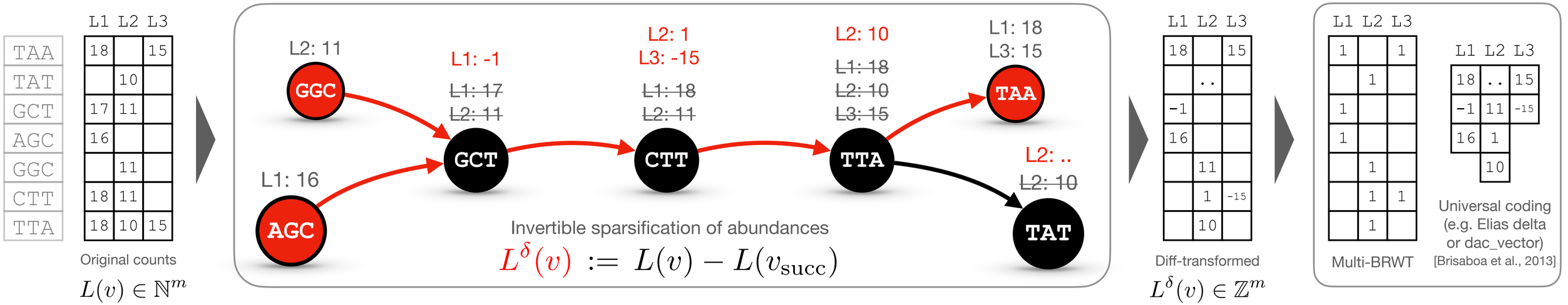

Decoding: $L(v) = L(v_{\text{succ}}) + L^\delta(v)$

Method

Counting DBG: Implementation

Repository: github.com/ratschlab/counting_dbg

Implemented as part of the MetaGraph framework

- succinct graph representations (based on the BOSS table Bowe *et al.*, 2012)
- graph annotation representations (e.g., `Multi-BRWT` Karasikov *et al.*, 2019)
- hybrid bit vector representations
- procedures for query and alignment

Base succinct data structures from sdsl-lite (Succinct Data Structure Library)

- compressed and packed bitmaps
- compressed integer arrays (`sdsl::dac_vector_dp<>`)

Experiments

1. Indexing k-mer abundances
2. Indexing k-mer coordinates
   - **Encoding traces** for lossless indexing of sequences
   - Trace Consistent Graph Alignment **(TCG-Aligner)**

Indexing k-mer abundances

Data: 2,586 Illumina RNA-Seq read sets*

On querying 100 random human transcripts (≈ 90 kbp in total)

(excluding index loading)

	Index size			Peak RAM during query			Query time		
Method	**binary**	**smooth counts**	**raw counts**	**binary**	**smooth counts**	**raw counts**	**binary**	**smooth counts**	**raw counts**
Mantis-MST	24.9 GB	-	-	25.1 GB	-	-	**0.6 s**	-	-
RowDiff	7.7 GB	-	-	8.0 GB	-	-	8.6 s	-	-
REINDEER	30.3 GB	59 GB	-	58.9 GB	91 GB	-	53.1 s	56.5 s	-
This work	**6.6 GB**	**11 GB**	**21 GB**	**6.9 GB**	**11 GB**	**21 GB**	6.4 s	**17.6 s**	**21.2 s**

* read sets from [Solomon and Kingsford, 2018]

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- Generates **5x smaller** representations and uses **8x less RAM**

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- Generates **5x smaller** representations and uses **8x less RAM**
- **3-5x faster** to query

* read sets from [Solomon and Kingsford, 2018]

Experiments

1. Indexing k-mer abundances
2. Indexing k-mer coordinates
   - **Encoding traces** for lossless indexing of sequences
   - Trace Consistent Graph Alignment **(TCG-Aligner)**

Trace Consistent Graph (TCG-) Aligner

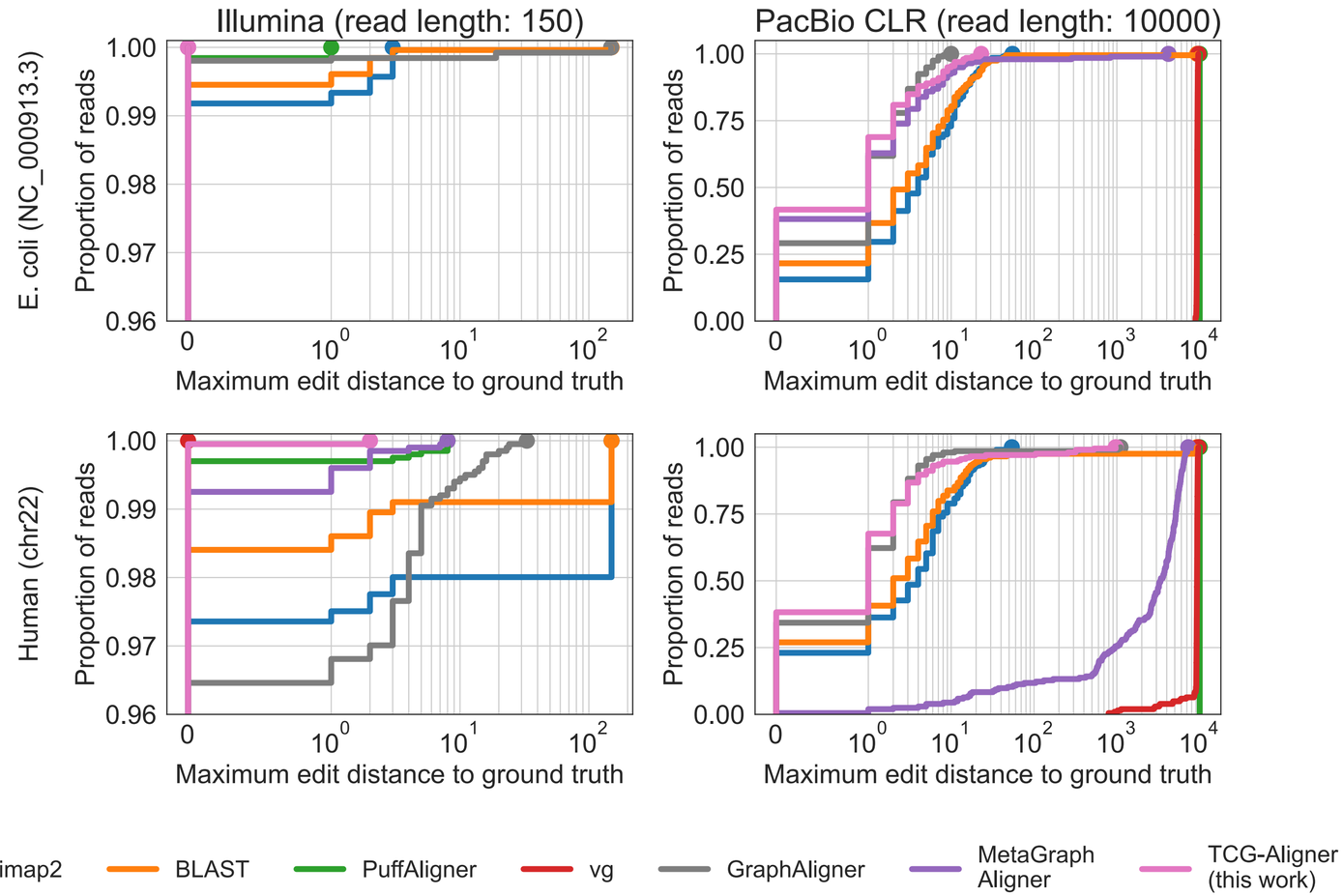
Sequence alignment on top of Counting DBG with k-mer coordinates with the **seed-chain-extend** approach:

1. Find seeds of size *k* or less
2. Chaining (inspired by Minimap2 [Li, 2018])
   - DP table for pairs (seed, coordinate) sorted by coordinates
   - Dynamic Programming + Backtracking
3. Extension algorithm
   - generalization of Needleman-Wunsch algorithm
   - similar to the MetaGraph aligner [Karasikov, Mustafa et al., 2020]

Alignment accuracy

Evaluation approach

1. Index a reference genome
2. Simulate reads from the same reference
3. Align reads and measure the distance between the alignments and their generating references



Alignment accuracy for **Counting DBG** and **state-of-the-art aligners** on simulated Illumina- and PacBio-type reads (E. coli NC 000913.3 and human chr22). The edit distance is measured between the alignment (the returned path in the graph) and the ground truth sequence. In the top left subplot, the curves of vg- and TCG-Aligner are superimposed.

Lossless indexing of RefSeq

RefSeq (33M accessions, 1.7 Tbp, 483 GB)

	BLAST	MegaBLAST	This work
Index size	**437 GB (2.05 bits/bp)**	2,358 GB (11.07 bits/bp)	509 GB (2.39 bits/bp)
Align 1 read (*)	353 sec, 417 GB	12.5 sec, **0.090 GB**	**0.66 sec**, 500 GB
Align 1,000 reads	1,857 sec, 428 GB	1,542 sec, **22.0 GB**	**575 sec**, 513 GB

The alignment speed was measured on reads taken from a metagenomic sequencing sample SRR10002688_1.

(*) For aligning single reads, the experiment is independently performed for the 100 first reads and the average time and RAM usage are presented.

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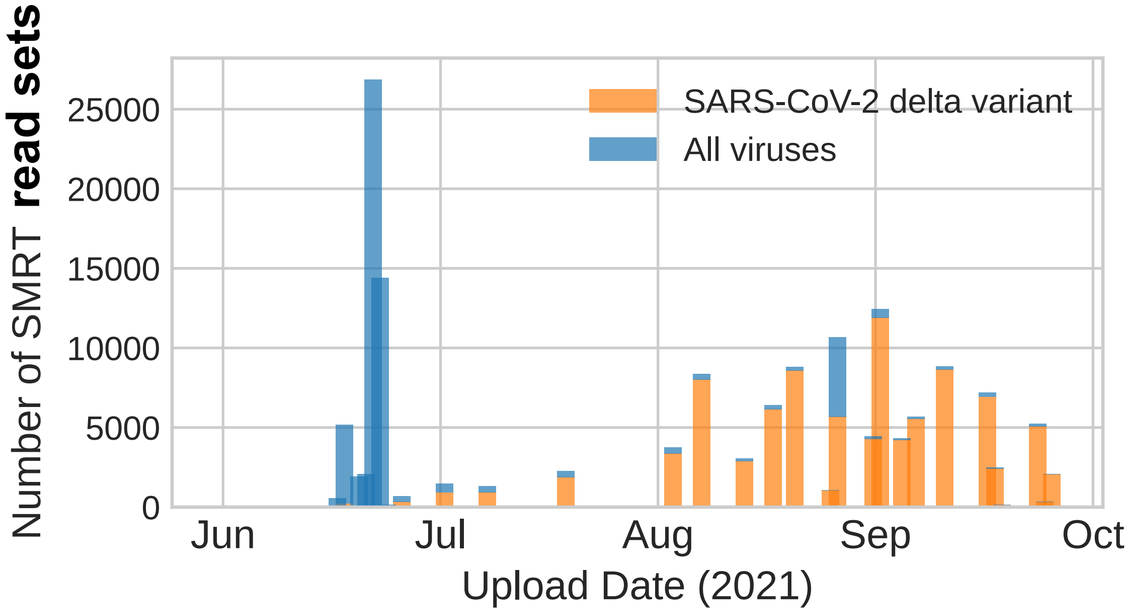
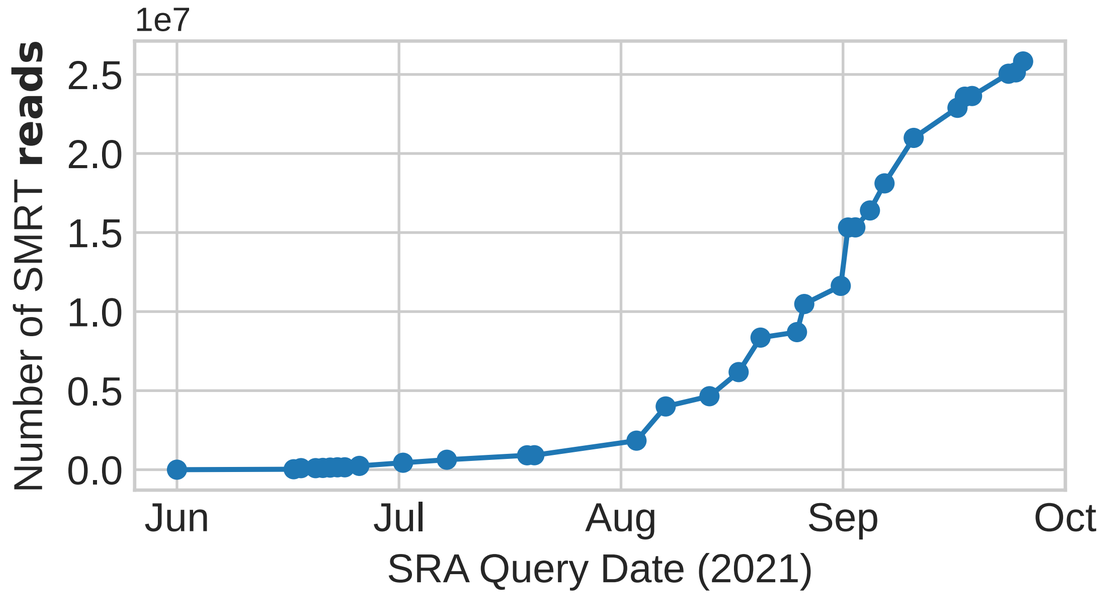
Query Delta variant of SARS-CoV-2

1. Constructed a joint index of **all 152,884 viral PacBio SMRT read sets from SRA**
2. Assembled a list of 9 defining mutations of the SARS-CoV-2 21A (Delta) variant spike protein
3. Retrieve all the occurrences of these specific mutations within the reads (took under 4 min)





Coordinates allow retrieving not only the number of read sets **(left)** but also single reads **(right)**

Conclusion

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Counting de Bruijn Graphs* generalize *Annotated de Bruijn graphs*

- Allow **efficiently encoding non-binary annotations**, e.g.:
  - k-mer abundances
  - k-mer coordinates
- **Scales to** very **large graphs**
  - constructs in linear time and constant memory
- Possible applications:
  - indexing and **querying k-mer abundances** (gene expression levels)
  - can be used as a **backend for aligners** (such as BLAST)
  - alignment with different error models (using k-mer abundances)

* Recently published in journal *Genome Research*

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- Predrag Krnetic

Thanks for your attention!

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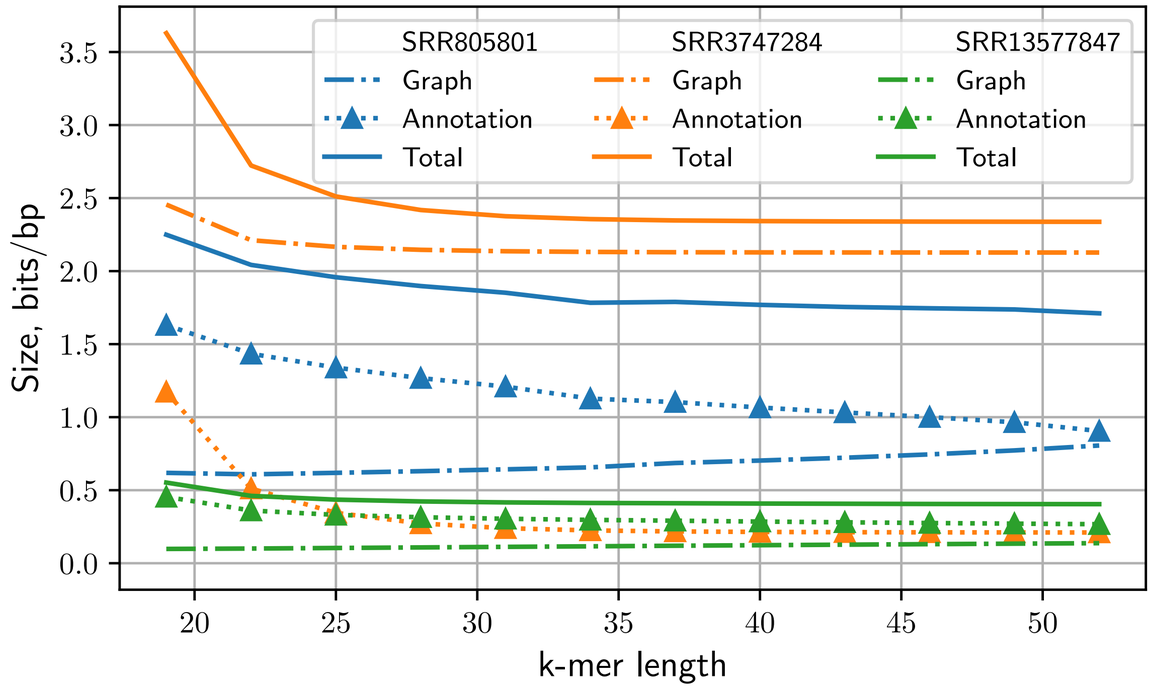
Swiss National Science Foundation

ETH zürich

Backup slides

Lossless indexing of k-mer coordinates

Dependence on k-mer length



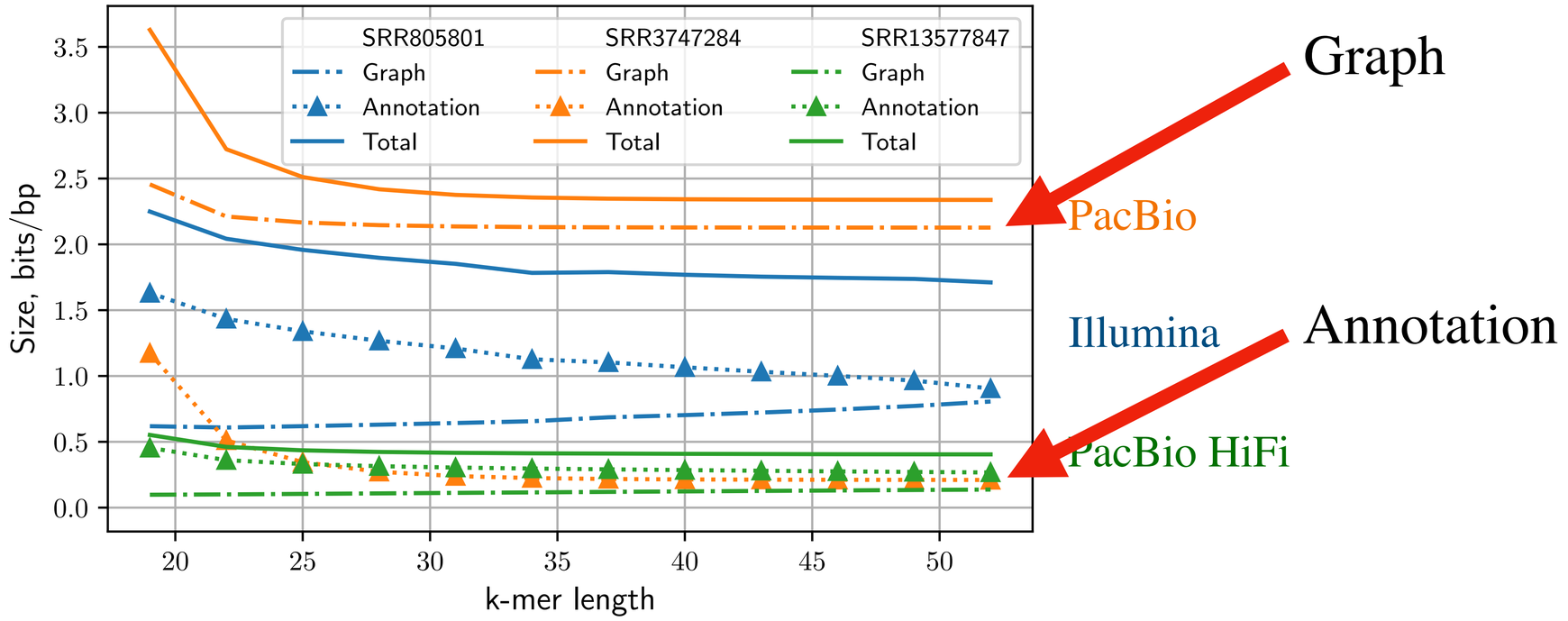
PacBio

Illumina

PacBio HiFi

Lossless indexing of k-mer coordinates

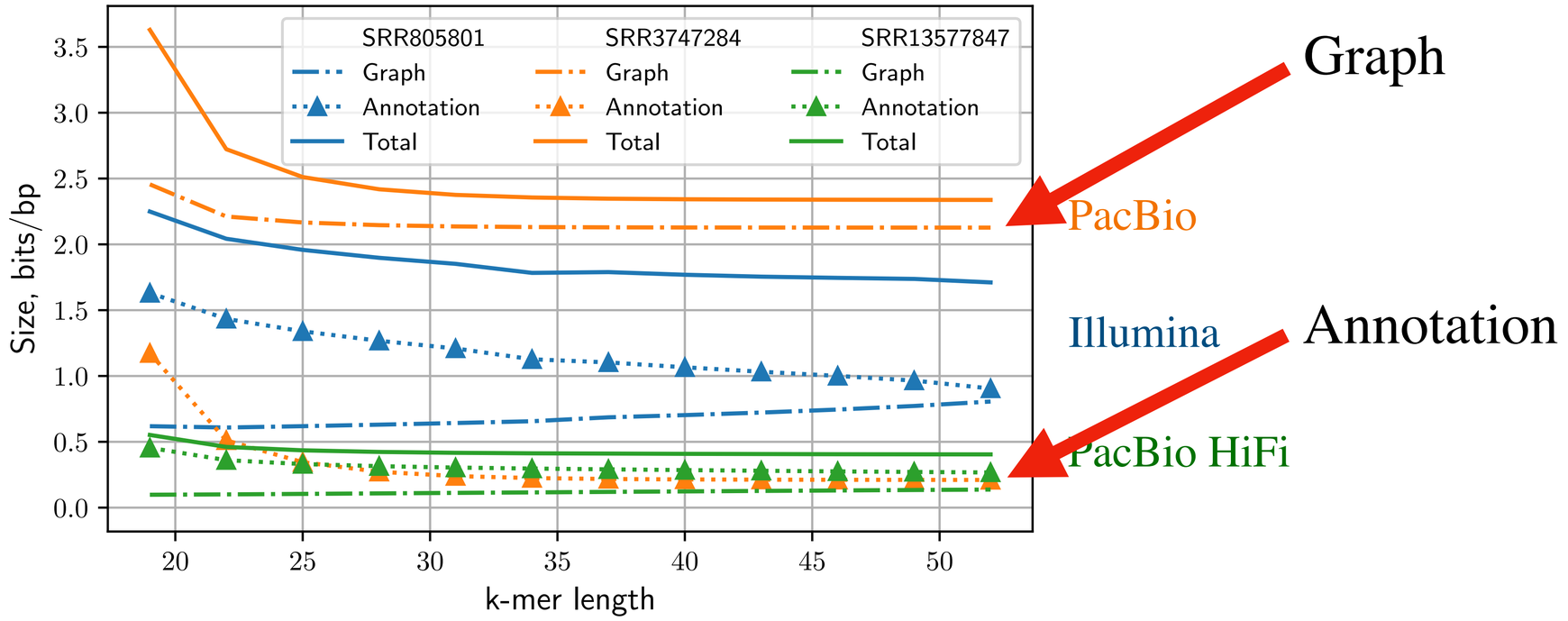
Dependence on k-mer length



1. For low-error reads (HiFi), annotation is tiny compared to graph

Lossless indexing of k-mer coordinates

Dependence on k-mer length



1. For low-error reads (HiFi), annotation is tiny compared to graph
2. Index size does not increase for larger values of k even for short Illumina reads

Construction time

Method	Construction time			Max. RAM		
	Binary	Smooth counts	Raw counts	Binary	Smooth counts	Raw counts
k-mer spectrum estimation with ntCard†	2.0 h	-	-	19 GB	-	-
k-mer counting with Squeakr†	35.4 h	-	-	333 GB	-	-
k-mer counting with Squeakr (single thread)†*	19.3 h	-	-	483 GB	-	-
Graph and annotation construction with Mantis*	9.6 h	-	-	42.7 GB	-	-
Annotation transform to MST	0.4 h	-	-	26.6 GB	-	-
Mantis-MST (all steps)	**29.3 h**	-	-	**483 GB**	-	-
k-mer counting with KMC† (with flag -m2)	3.2 h	-	-	41 GB	-	-
Assembling contigs from k-mers with MetaGraph†	0.7 h	-	-	51 GB	-	-
Graph construction and annotation with MetaGraph	1.7 h	-	-	52 GB	-	-
Annotation transform to RowDiff-MultiBRWT	1.3 h	-	-	58 GB	-	-
RowDiff (all steps)	**6.9 h**	-	-	**58 GB**	-	-
Assembling unitigs with BCALM† (with -max-memory 1000)	40.6 h	40.6 h	-	152 GB	152 GB	-
REINDEER (indexing)*	8.7 h	10.6 h	-	68.8 GB	59.4 GB	-
REINDEER (all steps)	**49.3 h**	**51.2 h**	-	**152 GB**	**152 GB**	-
k-mer counting with KMC† (with flag -m2)	3.2 h	3.2 h	3.2 h	41 GB	41 GB	41 GB
Assembling contigs from k-mers with MetaGraph†	0.7 h	0.9 h	0.8 h	51 GB	70 GB	70 GB
Graph construction and annotation with MetaGraph	1.6 h	2.2 h	2.3 h	52 GB	52 GB	52 GB
Annotation transformation (this work)	1.2 h	1.2 h	1.4 h	59 GB	88 GB	88 GB
This work (all steps)	**6.7 h**	**7.5 h**	**7.7 h**	**59 GB**	**88 GB**	**88 GB**

Alignment performance

Supplemental Table 2. Percentage of simulated reads mapping exactly to their respective ground-truth sequences (top) and total query time in seconds (bottom). For each reference, 2000 Illumina reads were simulated using ART and 200 PacBio CLR reads were simulated using pbsim, respectively. PuffAligner was unable to align the PacBio-type reads.

Reference	Minimap2	BLAST	PuffAligner	vg	GraphAligner	MetaGraph-Aligner	This work
Illumina: `E. coli`	99.18%	99.45%	99.84%	**100.00%**	99.8%	**100.00%**	**100.00%**
Illumina: `chr22`	97.36%	98.4%	99.70%	**100.00%**	96.46%	99.25%	99.95%
PacBio: `E. coli`	15.58%	21.61%	N/A	0.00%	29.15%	38.69%	**41.71%**
PacBio: `chr22`	23.04%	26.96%	N/A	0.00%	34.31%	0.49%	**40.20%**
Illumina: `E. coli`	0.13 s	0.39 s	**0.03 s**	1.16 s	3.22 s	1.13 s	1.47 s
Illumina: `chr22`	**0.47 s**	26.69 s	0.96 s	5.67 s	42.93 s	6.67 s	3.04 s
PacBio: `E. coli`	**1.11 s**	1.51 s	4.31 s	443.23 s	7.39 s	40.20 s	22.19 s
PacBio: `chr22`	**2.43 s**	34.80 s	4.91 s	1059.05 s	48.99 s	828.91 s	37.76 s

Data

Nine defining Delta gene variants of the SARS-CoV-2 spike protein

```
>OK091006.1:21536-25357:27-85
ACTAGTCTCTAGTCAGTGTGTTAATCTTAGAACCAGAACTCAATTACCCCCTGCATACA
>OK091006.1:21536-25357:444-502
CAACAAAAGTTGGATGGAAAGTGGAGTTTATTCTAGTGCGAATAATTGCACTT
>OK091006.1:21536-25357:1326-1384
TTCTAAGGTTGGTGGTAATTATAATTACCGGTATAGATTGTTTAGGAAGTCTAATCTCA
>OK091006.1:21536-25357:1404-1462
TTCAACTGAAATCTATCAGGCCGGTAGCAAACCTTGTAATGGTGTTGAAGGTTTTAATT
>OK091006.1:21536-25357:1812-1870
TTCTAACCAGGTTGCTGTTCTTTATCAGGGTGTTAACTGCACAGAAGTCCCTGTTGCTA
>OK091006.1:21536-25357:2013-2071
CGCTAGTTATCAGACTCAGACTAATTCTCGTCGGCGGGCACGTAGTGTAGCTAGTCAAT
>OK091006.1:21536-25357:2820-2878
CACAGCAAGTGCACTTGGAAAACTTCAAAATGTGGTCAACCAAAATGCACAAGCTTTAA
```