

BIMM 143

Introduction to Bioinformatics Lecture 2

Barry Grant
UC San Diego

<http://thegrantlab.org/bimm143>

Recap From Last Time:

- Bioinformatics is computer aided biology.
 - ▶ Deals with the collection, archiving, organization, and interpretation of a wide range of biological data.
- The NCBI and EBI are major online bioinformatics service providers.
- Introduced via **hands-on session** the BLAST, Entrez, GENE, OMIM, UniProt, Muscle and PDB bioinformatics tools and databases.
 - Muddy point assessment (see [results](#))
- There are a large number of bioinformatics databases (see [handout!](#)).
- Also covered: Course structure; Supporting course website, Ethics code, and Introductions...

Today's Menu

Classifying Databases

Primary, secondary and composite Bioinformatics databases

Using Databases

Vignette demonstrating how major Bioinformatics databases intersect

Major Biomolecular Formats

How nucleotide and protein sequence and structure data are represented

Alignment Foundations

Introducing the *why* and *how* of comparing sequences

Alignment Algorithms

Hands-on exploration of alignment algorithms and applications

Primary, secondary & composite databases

Bioinformatics databases can be usefully classified into *primary*, *secondary* and *composite* according to their data source.

- **Primary databases** (or archival databases) consist of data derived experimentally.
 - **GenBank**: NCBI's primary nucleotide sequence database.
 - **PDB**: Protein X-ray crystal and NMR structures.
- **Secondary databases** (or derived databases) contain information derived from a primary database.
 - **RefSeq**: non redundant set of curated reference sequences primarily from GenBank
 - **PFAM**: protein sequence families primarily from UniProt and PDB
- **Composite databases** (or *metadatabases*) join a variety of different primary and secondary database sources.
 - **OMIM**: catalog of human genes, genetic disorders and related literature
 - **GENE**: molecular data and literature related to genes with extensive links to other databases.

DATABASE VIGNETTE

You have just come out a seminar about gastric cancer and one of your co-workers asks:

“What do you know about that ‘Kras’ gene the speaker kept taking about?”

You have some recollection about hearing of ‘Ras’ before. How would you find out more?

- Google?
- Library?
- **Bioinformatics databases at NCBI and EBI!**

<http://www.ncbi.nlm.nih.gov/>

<http://www.ncbi.nlm.nih.gov/>

NCBI National Center for Biotechnology Information

All Databases Search

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical information.

About the NCBI | Mission | Organization | NCBI News

Get Started

- [Data](#): Search and analyze data using NCBI software
- [Tools](#): Get NCBI data or software
- [How Tos](#): Learn how to accomplish specific tasks at NCBI
- [Submissions](#): Submit data to GenBank or other NCBI databases

Genotypes and Phenotypes

Data from Genome Wide Association studies that link genes and diseases. See study variables, protocols, and analysis.

Resources

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI Announcements

RefSeq release 69 available on

The full RefSeq release 69 is now available on the FTP site with 74 records describing 50,276,469 ..

Hands on demo (or see following slides)

Example Vignette Questions:

- What chromosome location and what genes are in the vicinity of a given query gene? NCBI **GENE**
- What can you find out about molecular functions, biological processes, and prominent cellular locations? EBI **GO**
- What amino acid positions in the protein are responsible for ligand binding? EBI **UniProt**
- What variants of this gene are associated with gastric cancer and other human diseases? NCBI **OMIM**
- What is known about the protein family, its species distribution, number in humans and residue-wise conservation? EBI **PFAM**
- Are high resolution protein structures available to examine the details of these mutations? How might we explain their potential molecular effects? RCSB **PDB**

ras - GQuery: Global Cross X

www.ncbi.nlm.nih.gov/gquery/?term=ras

NCBI Resources How To Sign in to NCBI

Search NCBI databases

Help

ras

Search

About 2,978,774 search results for "ras"

Literature			Genes		
Books	1,677	books and reports	EST	3,985	expressed sequence tag sequences
MeSH	402	ontology used for PubMed indexing	Gene	87,165	collected information about gene loci
NLM Catalog	223	books, journals and more in the NLM Collections	GEO DataSets	3,732	functional genomics studies
PubMed	54,672	scientific & medical abstracts/citations	GEO Profiles	1,622,789	gene expression and molecular abundance profiles
PubMed Central	96,114	full-text journal articles	HomoloGene	696	homologous gene sets for selected organisms
Health			PopSet	2,254	sequence sets from phylogenetic and population studies
ClinVar	759	human variations of clinical significance	UniGene	4,770	clusters of expressed transcripts
dbGaP	120	genotype/phenotype interaction studies	Proteins		
GTR	1,879	genetic testing registry			

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ras - Gene - NCBI

www.ncbi.nlm.nih.gov/gene/?term=ras

NCBI Resources How To Sign in to NCBI

Gene Gene ras Search Save search Advanced Help

Show additional filters Hide sidebar >>

Display Settings: Tabular, 20 per page, Sorted by Relevance Send to:

Filters: Manage Filters

Did you mean ras as a gene symbol?
Search Gene for [ras](#) as a symbol.

<< First < Prev Page 1 of 4282 Next > Last >>

Results: 1 to 20 of 85633

i Filters activated: Current only. [Clear all](#) to show 87165 items.

Name/Gene ID	Description	Location	Aliases
<input type="checkbox"/> ras ID: 19412	resistance to audiogenic seizures [<i>Mus</i> <i>musculus</i> (house mouse)]		asr
<input type="checkbox"/> ras ID: 43873	rasberry [<i>Drosophila</i> <i>melanogaster</i> (fruit fly)]	Chromosome X, NC_004354.4 (10744502..10749097)	Dmel_CG1799, CG11485, CG1799, Dmel\CG1799, EP(X)1093,

Top Organisms [Tree]

- Homo sapiens (1126) **(highlighted)**
- Mus musculus (823)
- Rattus norvegicus (625)
- Oreochromis niloticus (533)
- Neolamprologus brichardi (507)
- All other taxa (82019)

More...

Find related data

Database: Select

Find items

Search details

ras [All Fields] AND alive [property]

(ras) AND "Homo sapiens" | [Save search](#) [Advanced](#)

Gene [Gene](#) (ras) AND "Homo sapiens"[porgn:_txid9606] [Search](#)

Show additional filters [Display Settings:](#) Tabular, 20 per page, Sorted by Relevance [Send to:](#) [Hide sidebar >>](#)

[Clear all](#)

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

Filters activated: Current only. [Clear all](#) to show 1499 items.

Name/Gene ID	Description	Location	Aliases
<input type="checkbox"/> NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [Homo sapiens (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
<input type="checkbox"/> KRAS ID: 3845	Kirsten rat sarcoma viral oncogene homolog [Homo sapiens (human)]	Chromosome 12, NC_000012.12 (25205246..25250923, complement)	C-K-RAS, CFC2, K-RAS2A, K-RAS2B, K-RAS4A, K-RAS4B, K-RAS1, KRAS2, NS, NS2, RAKS2

Filters: Manage Filters

Find related data

Database: Select

Find items

Search details

```
ras[All Fields] AND "Homo sapiens"[porgn] AND alive[property]
```

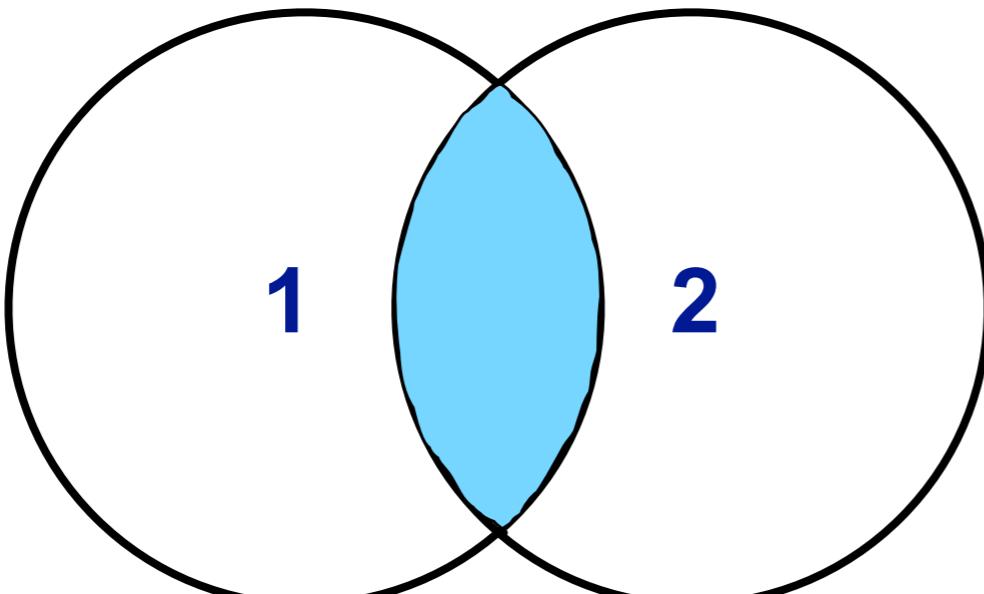
Search See more...

Recent activity

Turn Off Clear

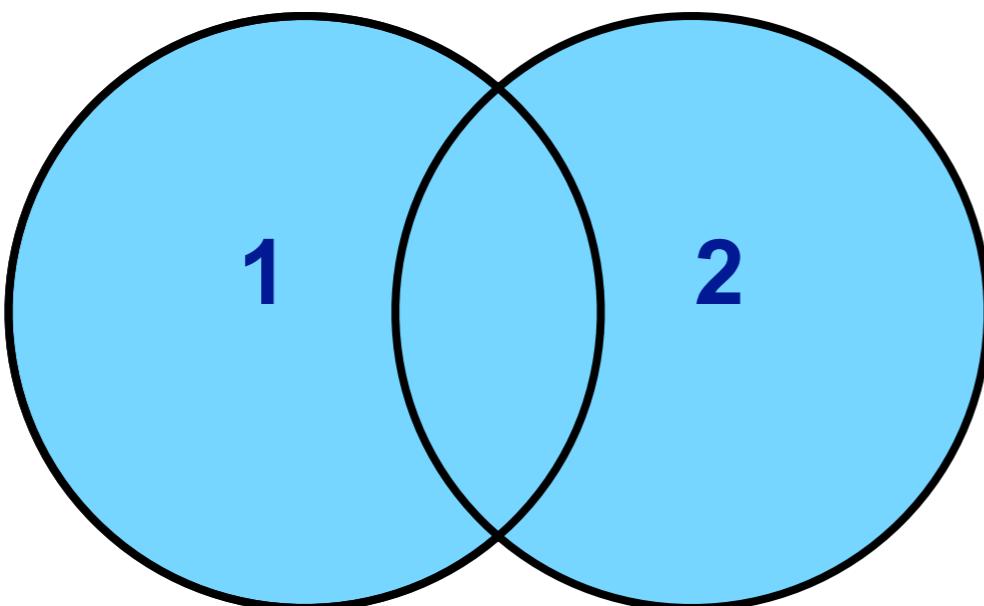
10

1 AND 2



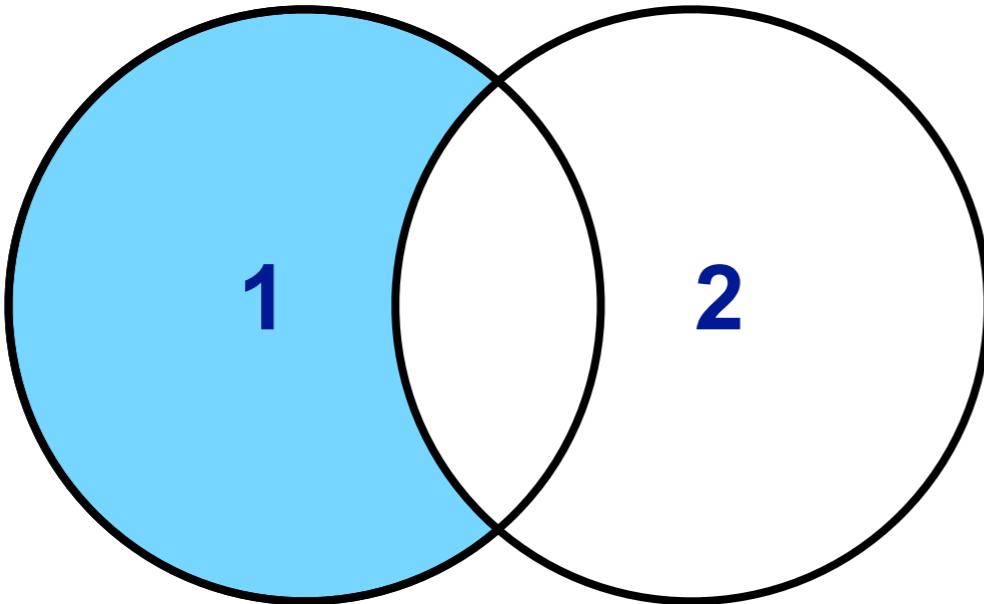
**ras AND disease
(1185 results)**

1 OR 2



**ras OR disease
(134,872 results)**

1 NOT 2



**ras NOT disease
(84,448 results)**

(ras) AND "Homo sapiens" | X

www.ncbi.nlm.nih.gov/gene

NCBI Resources How To Sign in to NCBI

Gene Gene (ras) AND "Homo sapiens"[porgn:txid9606] Search Save search Advanced Help

Show additional filters Hide sidebar >>

Display Settings: Tabular, 20 per page, Sorted by Relevance Send to:

Results: 1 to 20 of 1126 << First < Prev Page 1 of 57 Next > Last >>

i Filters activated: Current only. Clear all to show 1499 items.

Gene sources Genomic Categories

Alternatively spliced Annotated genes Non-coding Protein-coding Pseudogene

Sequence content CCDS Ensembl RefSeq Status clear

✓ Current only Chromosome locations Select

Name/Gene ID Description Location Aliases

<input type="checkbox"/> NRAS ID: 4893	neuroblastoma RAS viral (v-ras) oncogene homolog [Homo sapiens (human)]	Chromosome 1, NC_000001.11 (114704464..114716894, complement)	RP5-1000E10.2, ALPS4, CMNS, N-ras, NCMS1, NS6, NRAS
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Filters: Manage Filters

Find related data

Database: Select

Find items

Search details

```
ras[All Fields] AND "Homo sapiens"[porgn] AND alive[property]
```

Search See more...

Recent activity Turn Off Clear

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KRAS Kirsten rat sarcoma viral oncogene homolog [*Homo sapiens* (human)]

Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070;
Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

Organism *Homo sapiens*

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini;
Hominidae; Homo

Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

Table of contents

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- Genomic context
- Genomic regions, transcripts, and products
- Bibliography
- Phenotypes
- Variation
- HIV-1 interactions
- Pathways from BioSystems
- Interactions
- General gene information
 - Markers, Related pseudogene(s), Homology, Gene Ontology
- General protein information
- NCBI Reference Sequences (RefSeq)

KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845

NCBI Resources How To Sign in to NCBI

Gene Search Help Hide sidebar >>

Example Questions:

What chromosome location and what genes are in the vicinity?

Display S KRAS (human) Gene ID: 3845, updated on 4-Jan-2015

Summary

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070; Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

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Markers, Related pseudogene(s), Homology, Gene Ontology

General protein information

NCBI Reference Sequences (RefSeq)

Related documents

14

KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845#genomic-context

Genomic context

Location: 12p12.1 **Exon count:** 6

See KRAS in [Epigenomics](#), [MapViewer](#)

Annotation release	Status	Assembly	Chr	Location
106	current	GRCh38 (GCF_000001405.26)	12	NC_000012.12 (25205246..25250923, complement)
105	previous assembly	GRCh37.p13 (GCF_000001405.25)	12	NC_000012.11 (25358180..25403870, complement)

Chromosome 12 - NC_000012.12

[25052101 ►] [25436297 ►]

LRMP → LYRM5 ← CASC1 ← KRAS → LOC100421617 ← RPL39P27

Genomic regions, transcripts, and products

Go to [reference sequence details](#)

Genomic Sequence: NC_000012.12 chromosome 12 reference GRCh38 Primary Assembly

Go to nucleotide: [Graphics](#) [FASTA](#) [GenBank](#)

BioAssay by Target (List)
BioAssay by Target (Summary)
BioAssay, by Gene target
BioAssays, RNAi Target, Active
BioAssays, RNAi Target, Tested
BioProjects
BioSystems
Books
CCDS
ClinVar
Conserved Domains
dbVar
EST
Full text in PMC
Full text in PMC_nucleotide
Gene neighbors
Genome
GEO Profiles
GTR
HomoloGene
Map Viewer
MedGen
Nucleotide

KRAS Kirsten rat sarcoma

www.ncbi.nlm.nih.gov/gene/3845

NCBI Resources How To Sign in to NCBI

Gene

Display Settings

KRAS Ki (human)] Gene ID: 3845

Summary

Example Questions:

What 'molecular functions', 'biological processes', and 'cellular component' information is available?

Official Symbol KRAS provided by HGNC

Official Full Name Kirsten rat sarcoma viral oncogene homolog provided by HGNC

Primary source HGNC:HGNC:6407

See related Ensembl:ENSG00000133703; HPRD:01817; MIM:190070; Vega:OTTHUMG00000171193

Gene type protein coding

RefSeq status REVIEWED

Organism Homo sapiens

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo

Also known as NS; NS3; CFC2; KRAS1; KRAS2; RASK2; KI-RAS; C-K-RAS; K-RAS2A; K-

Search Help Hide sidebar >>

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NCBI Reference Sequences (RefSeq)

Related documents

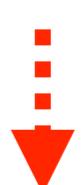
KRAS Kirsten rat sarcoma

Gene Ontology [Provided by GOA](#)

Function	Evidence Code	Pubs
GDP binding	IEA	
GMP binding	IEA	
GTP binding	IEA	
LRR domain binding	IEA	
protein binding	IPI	PubMed
protein complex binding	IDA	PubMed

Items 1 - 25 of 33 < Prev Page 1 of 2 Next >

Process	Evidence Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	



GO: Gene Ontology

GO provides a controlled vocabulary of terms for describing gene product characteristics and gene product annotation data

The screenshot shows a web browser window with the UniProt-GOA database. The address bar shows 'www.ebi.ac.uk/GOA'. The page has a dark header with 'EMBL-EBI' and a green circular logo. Below the header is a teal banner with the text 'UniProt-GOA'. A search bar contains 'Examples: GO:0006915, tropomyosin, P06727' and a 'Search' button. The main content area features a large title 'Gene Ontology Annotation (UniProt-GOA) Database'. Below it is a paragraph about the UniProt GO annotation program. To the right is a 'Menu' sidebar with links to various resources.

KRAS Kirsten rat sarcoma × UniProt-GOA < EMBL-EBI ×

www.ebi.ac.uk/GOA

EMBL-EBI

Services Research Training About us

UniProt-GOA

Search

Examples: GO:0006915, tropomyosin, P06727

Overview New to UniProt-GOA FAQ Contact Us

Gene Ontology Annotation (UniProt-GOA) Database

The UniProt GO annotation program aims to provide high-quality Gene Ontology (GO) annotations to proteins in the UniProt Knowledgebase (UniProtKB). The assignment of GO terms to UniProt records is an integral part of [UniProt biocuration](#). UniProt manual and electronic GO annotations are supplemented with manual annotations supplied by external collaborating GO Consortium groups, to ensure a comprehensive GO annotation dataset is supplied to users .

UniProt is a member of the [GO Consortium](#).

Menu

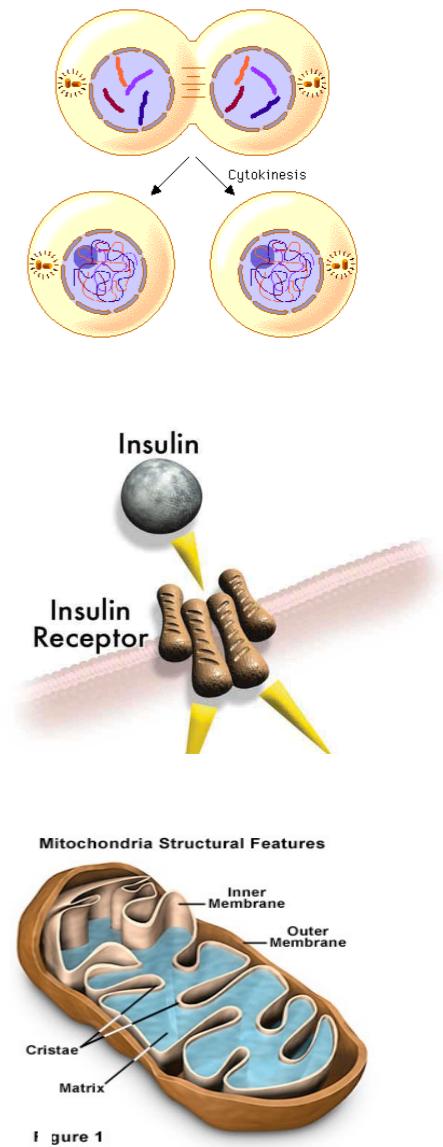
- [Downloads](#)
- [Searching UniProt-GOA](#)
- [Annotation Methods](#)
- [Annotation Tutorial](#)
- [Manual Annotation Efforts](#)
 - [Reference Genome Annotation Initiative](#)
 - [Cardiovascular Gene Ontology Annotation Initiative](#)
 - [Renal Gene Ontology Annotation Initiative](#)
 - [Exosome Gene](#)

Why do we need Ontologies?

- Annotation is essential for capturing the understanding and knowledge associated with a sequence or other molecular entity
- Annotation is traditionally recorded as “free text”, which is easy to read by humans, but has a number of disadvantages, including:
 - ▶ Difficult for computers to parse
 - ▶ Quality varies from database to database
 - ▶ Terminology used varies from annotator to annotator
- Ontologies are annotations using standard vocabularies that try to address these issues
- GO is integrated with UniProt and many other databases including a number at NCBI

GO Ontologies

- There are three ontologies in GO:
 - ▶ **Biological Process**
A commonly recognized series of events
e.g. cell division, mitosis,
 - ▶ **Molecular Function**
An elemental activity, task or job
e.g. kinase activity, insulin binding
 - ▶ **Cellular Component**
Where a gene product is located
e.g. mitochondrion, mitochondrial membrane



KRAS Kirsten rat sarcoma

Gene Ontology Provided by GOA

Function

	Evidence Code	Pubs
GDP binding		
GMP binding		
GTP binding		
LRR domain binding		
protein binding		
protein complex binding		

Process

	Code	Pubs
Fc-epsilon receptor signaling pathway	TAS	
GTP catabolic process	IEA	
MAPK cascade	TAS	
Ras protein signal transduction	TAS	
actin cytoskeleton organization	IEA	
activation of MAPKK activity	TAS	
axon guidance	TAS	
blood coagulation	TAS	

The ‘Gene Ontology’ or GO is actually maintained by the EBI so lets switch or link over to UniProt also from the EBI.

⋮ Scroll down to
↓ **UniProt** link

UniProt will detail much more information for protein coding genes such as this one

KRAS Kirsten rat sarcoma X www.ncbi.nlm.nih.gov/gene/3845#gene-ontology

genomic X01669.1 CAA25828.1

Items 1 - 25 of 43 < Prev Page 1 of 2 Next >

Protein Accession	Links
P01116.1	GenPept Link UniProtKB Link GenPept UniProtKB/Swiss-Prot:P01116

Additional links

You are here: NCBI > Genes & Expression > Gene Write to the Help Desk

GETTING STARTED

- NCBI Education
- NCBI Help Manual
- NCBI Handbook
- Training & Tutorials

RESOURCES

- Chemicals & Bioassays
- Data & Software
- DNA & RNA
- Domains & Structures
- Genes & Expression
- Genetics & Medicine
- Genomes & Maps
- Homology
- Literature
- Proteins
- Sequence Analysis
- Taxonomy

POPULAR

- PubMed
- Bookshelf
- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

FEATURED

- Genetic Testing Registry
- PubMed Health
- GenBank
- Reference Sequences
- Gene Expression Omnibus
- Map Viewer
- Human Genome
- Mouse Genome
- Influenza Virus
- Primer-BLAST
- Sequence Read Archive

NCBI INFORMATION

- About NCBI
- Research at NCBI
- NCBI News
- NCBI FTP Site
- NCBI on Facebook
- NCBI on Twitter
- NCBI on YouTube

UniProtKB/Swiss-Prot:P01116

UniProtKB/Swiss-Prot link

Scroll down to
Very bottom for
UniProt link

UniProt will detail much more information for protein coding genes

KRAS - GTPase KRas prec

www.uniprot.org/uniprot/P01116

UniProtKB Advanced

BLAST Align Retrieve/ID Mapping Help Contact

Basket

P01116 - RASK_HUMAN

Protein: GTPase KRas
Gene: KRAS
Organism: Homo sapiens (Human)
Status: Reviewed - Experimental evidence at protein levelⁱ

Display: None

BLAST Align Format Add to basket History Feedback Help video

FUNCTION
 NAMES & TAXONOMY
 SUBCELL. LOCATION
 PATHOL/BIOTECH
 PTM / PROCESSING
 EXPRESSION
 INTERACTION
 STRUCTURE
 FAMILY & DOMAINS
 SEQUENCES (2)
 CROSS-REFERENCES

Functionⁱ

Ras proteins bind GDP/GTP and possess intrinsic GTPase activity. Plays an important role in the regulation of cell proliferation (PubMed:23698361, PubMed:22711838). 2 Publications Curated

Enzyme regulationⁱ

Alternates between an inactive form bound to GDP and an active form bound to GTP. Activated by a guanine nucleotide-exchange factor (GEF) and inactivated by a GTPase-activating protein (GAP). Interaction with SOS1 promotes exchange of bound GDP by GTP. 3 Publications

Regions

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding ⁱ	10 – 18	9	GTP 2 Publications			
Nucleotide binding ⁱ	29 – 35	7	GTP 2 Publications			
Nucleotide binding ⁱ	59 – 60	2	GTP 2 Publications			

UniProt will detail much more information for protein coding genes

KRAS - GTPase KRas prec

www.uniprot.org/uniprot/P01116

UniProtKB Advanced

BLAST Align Retrieve/ID Mapping Help Contact Basket

P01116 - RASK_HUMAN

Protein: GTPase KRas
Gene: KRAS
Organism: Homo sapiens (Human)
Status: Reviewed - Experimental evidence at protein level

Display: None

FUNCTION NAMES & TAXONOMY SUBCELL. LOCATION PATHOL/BIOTECH PTM / PROCESSING EXPRESSION INTERACTION STRUCTURE FAMILY & DOMAINS SEQUENCES (2) CROSS-REFERENCES

Format

Function
Ras proteins bind GDP/GTP and promote cell proliferation (PubMed: 23698361, 23698362)

Enzyme regulation
Alternates between an inactive form and an active form as a nucleotide-exchange factor (GEF). Promotes exchange of bound GDP by GTP. 3 Publications

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Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding	10 – 18	9	GTP	2 Publications		
Nucleotide binding	29 – 35	7	GTP	2 Publications		
Nucleotide binding	59 – 60	2	GTP	2 Publications		

>sp|P01116|RASK_HUMAN GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1 MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG QEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSEDVPMVLVGNKCDL PSRTVDTKQAQDLARSYGYIPFIETSAKTRQRVEDAFYTLVREIRQYRLKKISKEEKTPGC VKIKKCIIM

UniProt will detail much more information for protein coding genes

KRAS - GTPase KRas prec

www.uniprot.org/uniprot/P01116

UniProtKB Advanced

BLAST Align Retrieve/ID Mapping Help Contact

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BLAST Align Format Add to basket History Feedback Help video

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Nucleotide binding ⁱ	59 – 60	2	GTP 2 Publications			

KRAS - GTPase KRas prec x

www.uniprot.org/uniprot/P01116

UniProt

UniProtKB Advanced

BLAST Align Retrieve/ID Mapping Help Contact

P01116 - RASK_HUMAN

Protein GTPase KRas
Gene KRAS
Organism Homo sapiens (Human)
Status Reviewed - ○○○○○

Display None

BLAST Align Format Add to basket History Feedback Help video

Example Questions:

What positions in the protein are responsible for GTP binding?

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Nucleotide binding ⁱ	10 – 18	9	GTP 2 Publications			
Nucleotide binding ⁱ	29 – 35	7	GTP 2 Publications			
Nucleotide binding ⁱ	59 – 60	2	GTP 2 Publications			

Example Questions:

What variants of this enzyme are involved in gastric cancer and other human diseases?

KRAS - GTPase KRas prec x

www.uniprot.org/uniprot/P01116

Display None

FUNCTION

NAMES & TAXONOMY

SUBCELL. LOCATION

PATHOL/BIOTECH

PTM / PROCESSING

EXPRESSION

INTERACTION

STRUCTURE

FAMILY & DOMAINS

SEQUENCES (2)

CROSS-REFERENCES

PUBLICATIONS

ENTRY INFORMATION

MISCELLANEOUS

SIMILAR PROTEINS

▲ Top

Pathology & Biotech¹

Involvement in diseaseⁱ

LEUKEMIA, ACUTE MYELOGENOUS (AML)

[MIM:601626]: A subtype of acute leukemia, a cancer of the white blood cells. AML is a malignant disease of bone marrow characterized by maturational arrest of hematopoietic precursors at an early stage of development. Clonal expansion of myeloid blasts occurs in bone marrow, blood, and other tissue. Myelogenous leukemias develop from changes in cells that normally produce neutrophils, basophils, eosinophils and monocytes. 1 Publication ▾

Note: The disease is caused by mutations affecting the gene represented in this entry.

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier	Actions
Natural variant ⁱ	10 – 10		1 G → GG in one individual with AML; expression in 3T3 cell causes cellular transformation; expression in COS cells activates the Ras-MAPK signaling pathway; lower GTPase activity; faster GDP dissociation rate. 1 Publication ▾		VAR_034601	

LEUKEMIA, JUVENILE MYELOMONOCYTIC (JMML)

[MIM:607785]: An aggressive pediatric myelodysplastic syndrome/myeloproliferative disorder characterized by malignant transformation in the hematopoietic stem cell compartment with proliferation of differentiated progeny. Patients have splenomegaly, enlarged lymph nodes, rashes, and hemorrhages.

Note: The disease is caused by mutations affecting the gene represented in this entry.

NOONAN SYNDROME 3 (NS3)

[MIM:609942]: A form of Noonan syndrome, a disease characterized by short stature, facial dysmorphic features such as hypertelorism, a downward eyeslant and low-set posteriorly rotated ears, and a high incidence of congenital heart

Example Questions:

Are high resolution protein structures available to examine the details of these mutations?

The screenshot shows the Uniprot protein entry page for KRAS (P01116). The 'STRUCTURE' section is highlighted with a red box. A blue box highlights the secondary structure visualization, showing a sequence of green, blue, and pink bars representing beta strands, helices, and turns respectively. A red arrow points to the '4EPV' link in the 3D structure database table, which is also highlighted with a green box. A red box with the text 'Open link in a new tab!' surrounds the '4EPV' row.

Display None

Structure¹

Secondary structure

1 Legend: Helix Turn Beta strand 189

Show more details

3D structure databases

Select the link destinations:

PDBⁱ RCSB PDBⁱ PDBjⁱ

Entry	Method	Resolution (Å)	Chain	Positions	PDBsum
1D8D	X-ray	2.00	P	178-188	[»]
1D8E	X-ray	3.00	P	178-188	[»]
1KZO	X-ray	2.20	C	169-173	[»]
1KZP	X-ray	2.10	C	169-173	[»]
3GFT	X-ray	2.27	A/B/C/D/E/F	1-164	[»]
4DSN	X-ray	2.03	A	2-164	[»]
4DSO	X-ray	1.85	A	2-164	[»]
4EPR	X-ray	2.00	A	1-164	[»]
4EPT	X-ray	2.00	A	1-164	[»]
4EPV	X-ray	1.35	A	1-164	[»]
4EPW	X-ray	1.70	A	1-1	
4EPX	X-ray	1.76	A	1-1	
4EPY	X-ray	1.80	A	1-1	
4L8G	X-ray	1.52	A	1-1	
4LDJ	X-ray	1.15	A	1-164	[»]
4LPK	X-ray	1.50	A/B	1-169	[»]

▲ Top

Open link in a new tab!

Lets view the 3D structure:

Can we find where in the structure our mutations are located and infer their potential molecular effects?

The screenshot shows the RCSB PDB website interface. At the top, there is a navigation bar with links for Home, Gmail, Deposit, Search, Visualize, and Analyze. Below this is the main header with the RCSB PDB logo and a search bar. The search bar contains the text "Search by PDB ID, author, macromolecule, sequence, or ligand" and a "Go" button. There are also links for Advanced Search and Browse by Annotations. To the right of the search bar is a map of the world with various protein structures visualized as spheres.

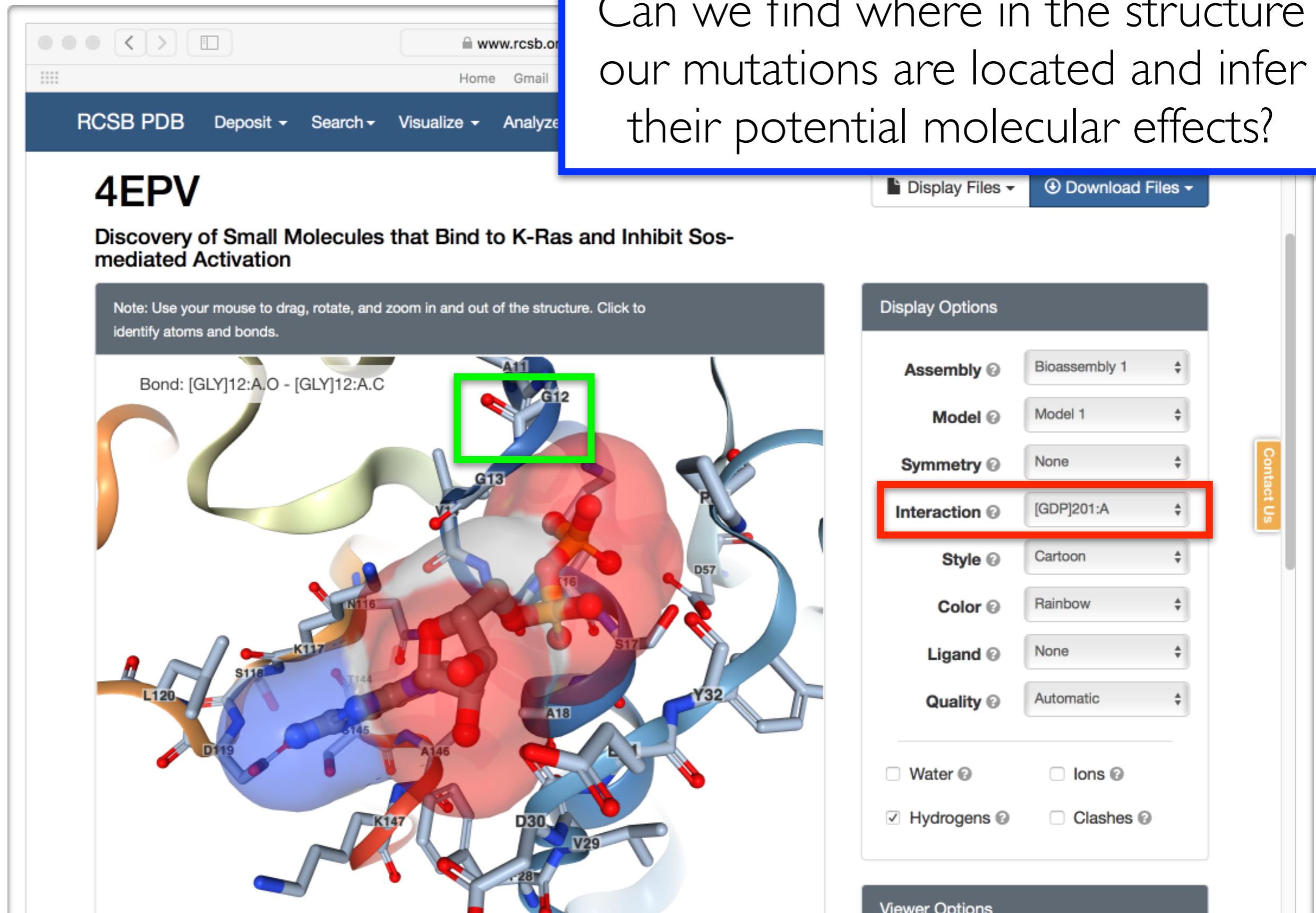
Below the header, there is a banner for "PDB-101" and other related databases like EMDDataBank and Nucleic Acid Database (NDB). A green speech bubble points to the "3D View" button in the navigation menu, which is highlighted with a red border. The menu also includes Structure Summary, Annotations, Sequence, Sequence Similarity, and Structure.

The main content area displays the structure summary for "Biological Assembly 1" of the protein 4EPV. The title "4EPV" is prominently displayed, along with the subtitle "Discovery of Small Molecules that Bind to K-Ras and Inhibit Sos-mediated Activation". The DOI is listed as 10.22110/pdb4epv/pdb. The classification is "HYDROLASE". The deposition date is 2012-04-17 and the release date is 2012-05-23. The deposition authors are Sun, Q., Burke, J.P., Phan, J., Burns, M.C., Olejniczak, E.T., Waterson, A.G., Lee, T., Rossanese, O.W., Fesik, S.W. The organism is Homo sapiens, the expression system is Escherichia coli, and there is 1 mutation. On the right side of the assembly viewer, there are buttons for "Display Files" (highlighted with a green border) and "Download Files". A green speech bubble points to the "Display Files" button with the text "View PDB file format".

At the bottom of the page, there are links for "View in 3D: NGL or JSmol (in Browser)" and "Experimental Data Snapshot" and "wwPDB Validation". There are also buttons for "3D Report" and "Full Report".

Lets view the 3D structure:

Can we find where in the structure our mutations are located and infer their potential molecular effects?



Back to UniProt:

What is known about the protein family,
its species distribution, number in humans
and residue-wise conservation, etc... ?

KRAS - GTPase KRas prec X www.uniprot.org/uniprot/P01116

Display None

FUNCTION

NAMES & TAXONOMY

SUBCELL. LOCATION

PATHOL/BIOTECH

PTM / PROCESSING

EXPRESSION

INTERACTION

STRUCTURE

FAMILY & DOMAINS

SEQUENCES (2)

CROSS-REFERENCES

PUBLICATIONS

ENTRY INFORMATION

MISCELLANEOUS

SIMILAR PROTEINS

▲ Top

OrthoDB

PhylomeDBⁱ P01116

TreeFamⁱ TF3

Family and domain databases

Gene3D ⁱ	3.40.50.300. 1 hit.
InterPro ⁱ	IPR027417. P-loop_NTPase. IPR005225. Small_GTP-bd_dom. IPR001806. Small_GTPase. IPR020849. Small_GTPase_Ras. [Graphical view]
PANTHER ⁱ	PTHR24070. PTHR24070. 1 hit.
Pfam ⁱ	PF00071. Ras. 1 hit. [Graphical view]
PRINTS ⁱ	PR00449. RASTRNSFRMNG.
SMART ⁱ	SM00173. RAS. 1 hit. [Graphical view]
SUPFAM ⁱ	SSF52540. SSF52540. 1 hit.
TIGRFAMs ⁱ	TIGR00231. small_GTP. 1 hit.
PROSITE ⁱ	PS51421. RAS. 1 hit. [Graphical view]

Sequences (2)ⁱ

Sequence statusⁱ: Complete.

Sequence processingⁱ: The displayed sequence is further processed into a mature form.

This entry describes 2 isoformsⁱ produced by alternative splicing. Align

PFAM is one of the best
protein family databases

Example Questions:

What is known about the protein family, its **species distribution**, number in humans and residue-wise conservation, etc... ?

The screenshot shows a web browser window with the URL pfam.xfam.org/family/PF00071. The page header includes the EMBL-EBI logo and a navigation bar with links like HOME, SEARCH, and HELP. The main content area displays information for the protein family PF00071, specifically KRAS - GTPase KRas precursor. It includes a summary table with columns for architectures, sequences, interactions, species, and structures, and a detailed description of the Ras family.

Family: Ras (PF00071)

Summary

Domain organisation

Clan

Alignments

HMM logo

Trees

Curation & model

Species (highlighted with a red box)

Interactions

Structures

Jump to... ⓘ

enter ID/acc Go

Summary: Ras family

Pfam includes annotations and additional family information from a range of different sources. These sources can be accessed via the tabs below.

[Wikipedia: Ras subfamily](#) [Wikipedia: Ras superfamily](#) [Pfam](#) [InterPro](#)

This is the Wikipedia entry entitled "[Ras subfamily](#)". [More...](#)

Ras subfamily [Edit Wikipedia article](#)

This article is about p21/Ras protein. For the p21/waf1 protein, see [p21](#).

Ras is the name given to a [family of related proteins](#) which is ubiquitously expressed in all cell lineages and organs. All Ras protein family members belong to a class of protein called [small GTPase](#), and are involved in transmitting signals within cells ([cellular signal transduction](#)). Ras is the prototypical member of the [Ras superfamily](#) of proteins, which are all related in 3D structure and regulate diverse cell behaviours.

The name 'Ras' is an abbreviation of 'Rat sarcoma', reflecting the way the first members of the protein family were discovered. The name ras is also used to refer to the family of [genes](#) encoding those proteins.

When Ras is 'switched on' by incoming signals, it subsequently switches on other proteins, which ultimately turn on genes involved in [cell growth](#), [differentiation](#) and [survival](#). As a result, mutations in ras genes can lead to the production of permanently activated Ras proteins. This can cause unintended and overactive signalling inside the cell, even in the absence of incoming signals.

Because these signals result in cell growth and division, overactive Ras signaling can ultimately lead to [cancer](#).^[1] The 3 Ras genes in humans ([HRAS](#), [KRAS](#), and [NRAS](#)) are the most common [oncogenes](#) in human [cancer](#); mutations that permanently activate Ras are found in 20% to 25% of all human tumors and up to 90% in certain types of cancer (e.g., [pancreatic cancer](#)).^[2] For this reason, Ras inhibitors are being studied as a treatment for cancer, and other diseases with Ras overexpression.

[Contents](#) [hide]

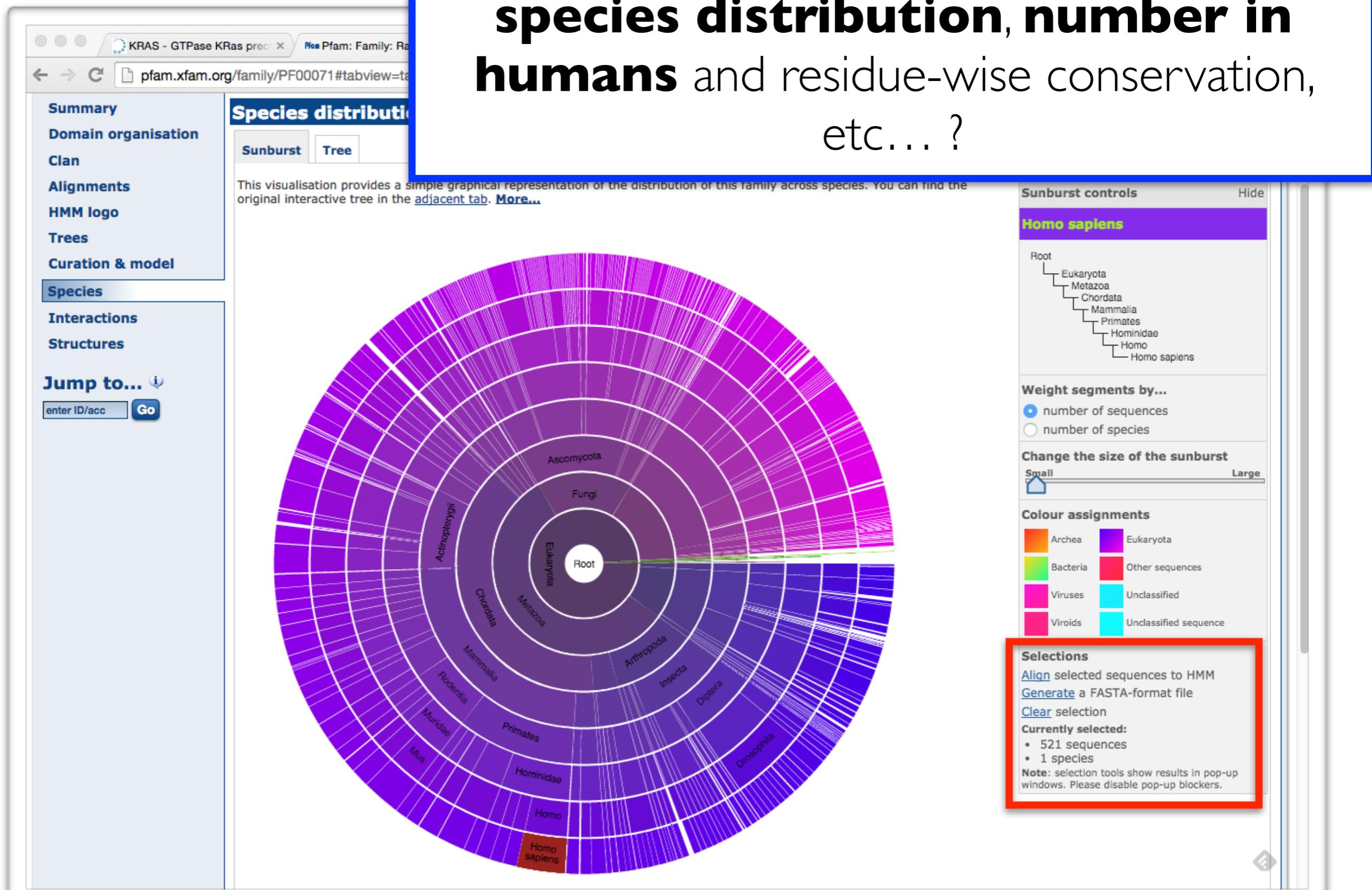
1 History
2 Structure
3 Function
 3.1 Activation and deactivation
 3.2 Membrane attachment
4 Members
5 Ras in cancer
 5.1 Inappropriate activation
 5.2 Constitutively active Ras

Identifiers

Symbol	Ras
Pfam	PF00071 ⓘ
InterPro	IPR013753 ⓘ
PROSITE	PDOC00017 ⓘ
SCOP	5p21 ⓘ
SUPERFAMILY	5p21 ⓘ

Example Questions:

What is known about the protein family, its
species distribution, number in humans and residue-wise conservation,
etc... ?



Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc... ?

KRAS - GTPase KRas prec X More Pfam: Family: Re...

← → C pfam.xfam.org/family/PF00071#tabview=tab1

Summary Species distribution

Domain organisation Sunburst Tree

Clan Alignment HMM log Trees Curation Species Interactions Structures

Jump to enter ID/acc

Pfam: Pfam alignment viewer pfam.xfam.org/family/PF00071/alignment/view?jobId=EDCA403E-9836-11E4-B360-10B3298E2F76

EMBL-EBI

Alignment for selected sequences

Currently showing rows 1 to 30 of 536 rows in this alignment. Show 30 rows of alignment

P11234/16-178 . KVIMVGSCGGVGKSAITL Q . . FM . . . Y . D . EF . V . . . E . DYEPPIK . -AD . . . SYRKVVLD . . .
P01112/5-165 . KLVVVGAGGVGKSAITI Q . . LI . . . Q . N . HF . V . . . D . EYDPPI . -ED . . . SYRKQVVID . . .
Q14088/38-204 . KIIIVIGDSNVGKTCILTF R . . FC . . . G . . TF . P . . . D . KTEAII . GVD . . . FREAKTVEIE . . .
Q9BW83/7-173 . KCILAGDPAVGKTAIIAQ I . . FR . . . S . DgaHF . Q . . K . SYTLLT . GMD . . . LVVKTVPVPd . . .
P15153/7-178 . KCVVVGDDGAVGKTCILLI S . . YT . . . T . N . AF . P . . . G . EYIPTV . -FD . . . NYSAVMVD . . .
D00194/11-183 . KLLALGDSCGVGKTCILLY R . . YT . . . D . N . KF . N . . . P . KFITTIV . GID . . . FREAKRVVYNaaqgn . . .
Q15907/13-174 . KVVVLIGDSGVGKSNLIS R . . FT . . . R . N . EF . N . . . L . ESKSII . GVE . . . FATRSIQVD . . .
P10114/5-166 . KVVVLIGDSGVGKSAITV Q . . FV . . . T . G . . TF . I . . . E . KYDPPI . -ED . . . FYRKEIEVD . . .
P51153/10-171 . KLLLIGDSCGVGKTCILLI R . . FA . . . E . D . NF . N . . . N . TYISII . GID . . . FKIRTVDIE . . .
P55040/77-241 . RVVLLIGEQQGVGKSTLAN I . . FA . . . Gvhd . . SM . D . . . S . D . CEVL . GED . . . TYERTLMVD . . .
P55042/93-253 . KVLLLGAPGVGKSAALAR I . . FG . . . G . V . . ED . G . . . P . EAEAAG . --H . . . TYDRSIVVD . . .
P01116/5-165 . KLVVVGAGGVGKSAITI Q . . LI . . . Q . N . HF . V . . . D . EYDPPI . -ED . . . SYRKQVVID . . .
Q9H07/21-182 . KLVLLGSGSGVGKSSLAL R . . YV . . . K . N . DF . K . . . S . ILPTIV . GCA . . . FFTKVVDVCG . . .
Q9ULC3/11-171 . KMVVVGNGAVVGKSSMIQ R . . YC . . . K . G . . IF . T . . . K . DYKKTII . GVD . . . FLERQIQVN . . .
Q14807/15-177 . KLVVVGDGGVGKSAITI Q . . FF . . . Q . K . . IF . V . . . P . DYDPPI . -ED . . . SYLKHTEID . . .
Q9NX57/7-202 . KIVVLLGDMNVGKTSILQ R . . YM . . . E . R . . RF . P . . . D . T . VS . V . GGA . . . FYLKQW . . .
Q9H082/35-201 . KIIIVIGDSNVGKTCILTY R . . FC . . . A . G . . RF . P . . . D . RTEAII . GVD . . . FRERAVEID . . .
Q969Q5/9-174 . KVVMLGKEYVGKTSILVE R . . YV . . . H . D . . RFIV . . . G . PYQNTII . GAA . . . FVAKVMSVC . . .
P51149/10-175 . KVIIILGDSCGVGKTSILMN Q . . YV . . . N . K . . KF . S . . . N . QYKAI . GAD . . . FLTKEVMVD . . .
Q9ULW5/65-227 . KVMLVGDSCGVGKTCILV R . . FK . . . D . G . . AF . L . . . AgTFISIV . GID . . . FRNKVLDVD . . .
P57735/14-175 . KVVLIGECSGVGKTNLLS R . . FT . . . R . N . . EF . S . . . H . DSRTII . GVE . . . FSTRTVMLCG . . .
P51159/11-183 . KFLALGDSCGVGKTSVLY Q . . YT . . . D . G . . KF . N . . . S . KFITTIV . GID . . . FREAKRVVYRasgpd . . .
P01111/5-165 . KLVVVGAGGVGKSAITI Q . . LI . . . Q . N . HF . V . . . D . EYDPPI . -ED . . . SYRKQVVID . . .
P11233/16-177 . KVIMVGSCGGVGKSAITL Q . . FM . . . Y . D . EF . V . . . E . DYEPPIK . -AD . . . SYRKVVLD . . .
Q9UL25/21-182 . KVVLIGECSGVGKTSILV R . . YC . . . E . N . . KF . N . . . D . KHITII . QAS . . . FLTKKLNICG . . .
Q9NP72/10-171 . KILIIGECSGVGKSSL R . . FT . . . D . D . . TF . D . . . P . ELAATII . GVD . . . FKVKTISVD . . .
Q9HOU4/10-171 . KLLLGAGDSCGVGKSCILL R . . FA . . . D . D . . TY . T . . . E . SYISII . GVD . . . FKIRTIELD . . .
Q9UL26/7-168 . KVCLLIGDTGVGKSSIVW R . . FV . . . E . D . . SF . D . . . P . NINPI . GAS . . . FMTKTVQYQ . . .
Q9UBK7/23-179 . KIICLGDSAVGKSILME R . . FL . . . M . D . . GF . Q . . . P . QQLSY . ALT . . . LYKHTATVD . . .
P51157/14-179 . KIVVLGDCASGKTSIT C . . FA . . . Q . E . . TF . G . . . K . QYKQII . GLD . . . FFLRRITLP . . .

1 2 3 4 5 6 7 8 9 10 11 ...

There are 18 pages in this alignment. Show page 1

Download this alignment.

Close window

can find the

Sunburst controls Hide

Homo sapiens

Root
Eukaryota
Metazoa
Chordata
Mammalia
Primates
Hominidae
Homo
Homo sapiens

Weight segments by...
 number of sequences
 number of species

Change the size of the sunburst
Small Large

Colour assignments

Archaea	Eukaryota
Bacteria	Other sequences
Viruses	Unclassified
Viroids	Unclassified sequence

Selections

Align selected sequences to HMM
Generate a FASTA-format file
Clear selection
Currently selected:

- 521 sequences
- 1 species

Note: selection tools show results in pop-up windows. Please disable pop-up blockers.

Example Questions:

What is known about the protein family, its species distribution, number in humans and **residue-wise conservation**, etc... ?

KRAS - GTPase KRas prec X More Pfam: Family: Ra

← → C pfam.xfam.org/family/PF00071#tabview=tab4

EMBL-EBI 

HOME | SEARCH | BROWSE | FTP | HELP | ABOUT

Pfam keyword search Go

Family: Ras (PF00071)

Summary Domain organisation Clan Alignments **HMM logo** (highlighted with a red box) Trees Curation & model Species Interactions Structures

Jump to... enter ID/acc Go

HMM logo

HMM logos is one way of visualising profile HMMs. Logos provide a quick overview of the properties of an HMM in a graphical form. You can see a more detailed description of HMM logos and find out how you can interpret them [here](#). [More...](#)

Contribution

332 architectures 21243 sequences 30 interactions 1006 species 663 structures

Family: Kinesin (PF00225)

126 architectures
4150 sequences
6 Interactions
248 species
114 structures
Summary**Domain organisation****Clans****Alignments****HMM logo****Trees****Curation & models****Species****Interactions****Structures****Jump to...**

enter ID/acc

Structures

For those sequences which have a structure in the [Protein DataBank](#), we use the mapping between [UniProt](#), PDB and Pfam coordinate systems from the [PDBe](#) group, to allow us to map Pfam domains onto UniProt sequences and three-dimensional protein structures. The table below shows the structures on which the **Kinesin** domain has been found.

UniProt entry	UniProt residues	PDB ID	PDB chain ID	PDB residues	View
A8BKD1_GIALA	11 - 335	2vvg	A	11 - 335	Jmol AstexViewer SPICE
			B	11 - 335	Jmol AstexViewer SPICE
CENPE_HUMAN	12 - 329	1t5c	A	12 - 329	Jmol AstexViewer SPICE
			B	12 - 329	Jmol AstexViewer SPICE
KAR3_YEAST	392 - 723	1f9t	A	392 - 723	Jmol AstexViewer SPICE
		1f9u	A	392 - 723	Jmol AstexViewer SPICE
		1f9v	A	392 - 723	Jmol AstexViewer SPICE
		1f9w	A	392 - 723	Jmol AstexViewer SPICE
		3kar	A	392 - 723	Jmol AstexViewer SPICE
KI13B_HUMAN	11 - 352	3qbj	A	11 - 352	Jmol AstexViewer SPICE
			B	11 - 352	Jmol AstexViewer SPICE
			C	11 - 352	Jmol AstexViewer SPICE
		1ii6	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1q0b	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1x88	A	24 - 359	Jmol AstexViewer SPICE
			B	24 - 359	Jmol AstexViewer SPICE
		1	A	24 - 359	Jmol AstexViewer SPICE

Recap: Major NCBI and EBI databases

- What chromosome location and what genes are in the vicinity of a given query gene? **NCBI GENE**
- What can you find out about molecular functions, biological processes, and prominent cellular locations? **EBI GO**
- What amino acid positions in the protein are responsible for ligand binding? **EBI UniProt**
- What variants of this gene are associated with gastric cancer and other human diseases? **NCBI OMIN**
- What is known about the protein family, its species distribution, number in humans and residue-wise conservation? **EBI PFAM**
- Are high resolution protein structures available to examine the details of these mutations? How might we explain their potential molecular effects? **RCSB PDB**

Today's Menu

Classifying Databases

Primary, secondary and composite Bioinformatics databases

Using Databases

Vignette demonstrating how major Bioinformatics databases intersect

Major Biomolecular Formats

How nucleotide and protein sequence and structure data are represented

Alignment Foundations

Introducing the *why* and *how* of comparing sequences

Alignment Algorithms

Hands-on exploration of alignment algorithms and applications

ALIGNMENT FOUNDATIONS

- **Why...**
 - ▶ Why compare biological sequences?
- **What...**
 - ▶ Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
- **How...**
 - ▶ Dot matrices
 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

ALIGNMENT FOUNDATIONS

- **Why...**
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 - ▶ Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
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 - ▶ Dot matrices
 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

Basic Idea: Display one sequence above another with spaces (termed gaps) inserted in both to reveal similarity of nucleotides or amino acids.

Seq1 : C A T T C A C

Seq2 : C T C G C A G C

Basic Idea: Display one sequence above another with spaces (termed gaps) inserted in both to reveal similarity of nucleotides or amino acids.

Seq1 : C A T T C A C
 | | |
Seq2 : C T C G C A G C



Two types of character correspondence

Basic Idea: Display one sequence above another with spaces (termed gaps) inserted in both to reveal similarity of nucleotides or amino acids.

Seq1 : C A T - T C A - C

Seq2 : | | | | |

C - T C G C A G C

Add gaps to increase number of matches

gaps

match mismatch

The diagram illustrates the basic idea of sequence alignment. Seq1 and Seq2 are shown as two horizontal lines of text. Vertical blue lines connect the second 'A' in Seq1 to the first 'T' in Seq2, and the third 'A' in Seq1 to the fourth 'C' in Seq2. A curved grey arrow labeled 'gaps' points to the '-' symbol in Seq1 and the 'C' in Seq2. Another curved grey arrow labeled 'match mismatch' points to the 'G' in Seq2. The text 'Add gaps to increase number of matches' is located at the bottom left.

Basic Idea: Display one sequence above another with spaces (termed gaps) inserted in both to reveal similarity of nucleotides or amino acids.

Seq1 : C A T - T C A - C

Seq2 : | | | | |
C - T C G C A G C

Gaps represent 'indels'
mismatch represent mutations
match
mismatch } mutation
insertion
deletion } indels

Why compare biological sequences?

- To obtain functional or mechanistic insight about a sequence by inference from another potentially better characterized sequence
- To find whether two (or more) genes or proteins are evolutionarily related
- To find structurally or functionally similar regions within sequences (e.g. catalytic sites, binding sites for other molecules, etc.)
- Many practical bioinformatics applications...

Practical applications include...

- Similarity searching of databases
 - Protein structure prediction, annotation, etc...
- Assembly of sequence reads into a longer construct such as a genomic sequence
- Mapping sequencing reads to a known genome
 - "Resequencing", looking for differences from reference genome - SNPs, indels (insertions or deletions)
 - Mapping transcription factor binding sites via ChIP-Seq (chromatin immuno-precipitation sequencing)
 - Pretty much all next-gen sequencing data analysis

Practical applications include...

- Similarity searching of databases
 - Protein structure prediction
- Assembly of sequences such as a bacterial genome
- Mapping of new sequences to a known genome
 - Looking for differences from reference sequence: SNPs, indels (insertions or deletions)
 - Mapping transcription factor binding sites via ChIP-Seq (chromatin immuno-precipitation sequencing)
 - Pretty much all next-gen sequencing data analysis

N.B. Pairwise sequence alignment is arguably the most fundamental operation of bioinformatics!

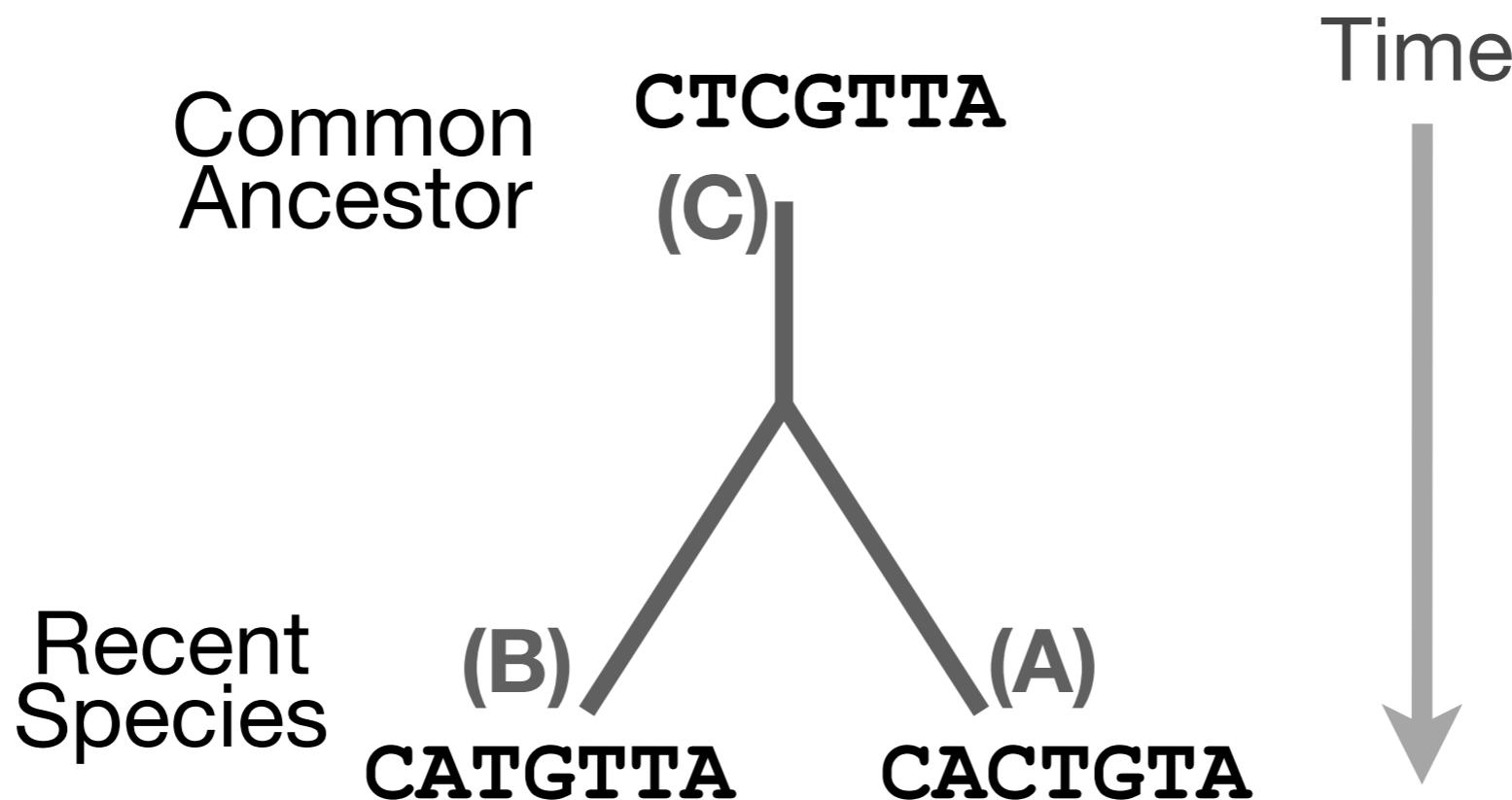
ALIGNMENT FOUNDATIONS

- Why...
 - Why compare biological sequences?
- What...
 - ▶ Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
- How...
 - ▶ Dot matrices
 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

Sequence changes during evolution

There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- Deletions
- Insertions

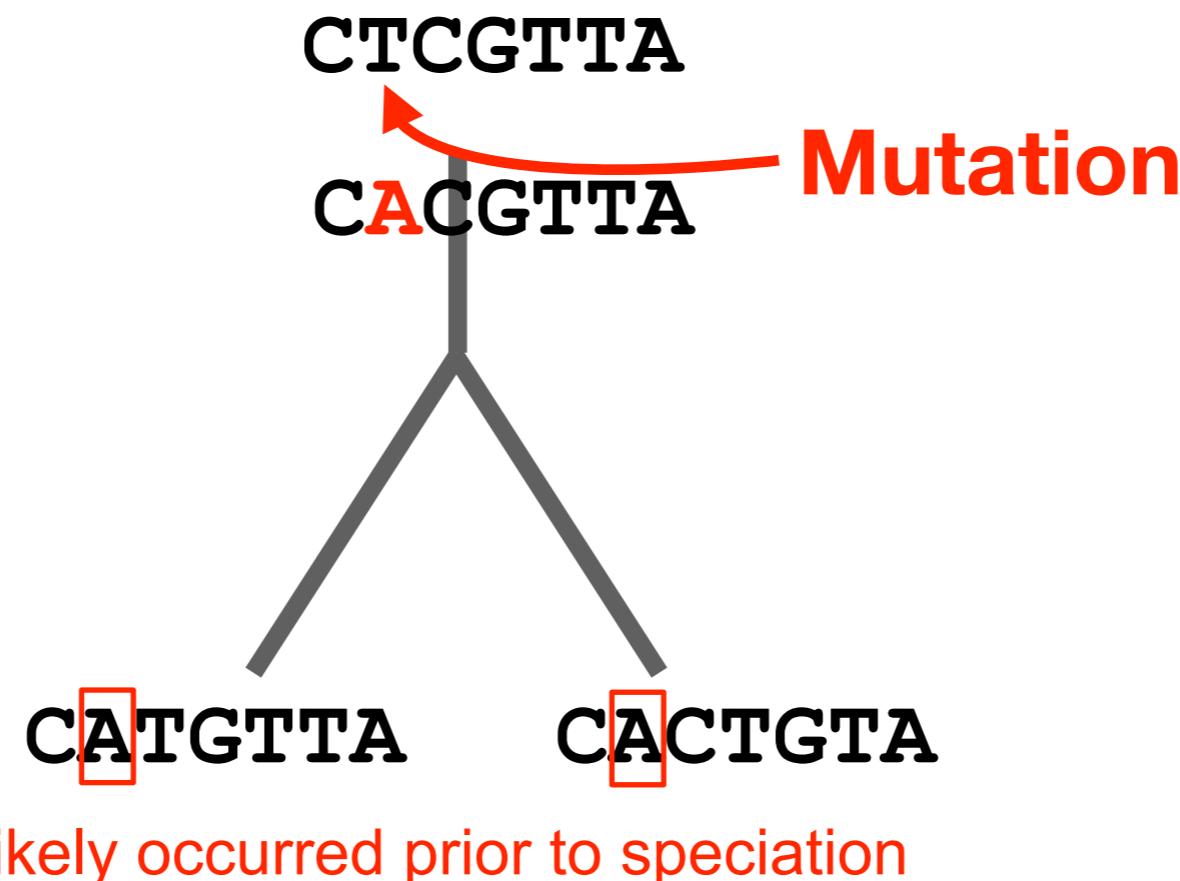


Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- Deletions
- Insertions

CTCGTTA → CACGTTA

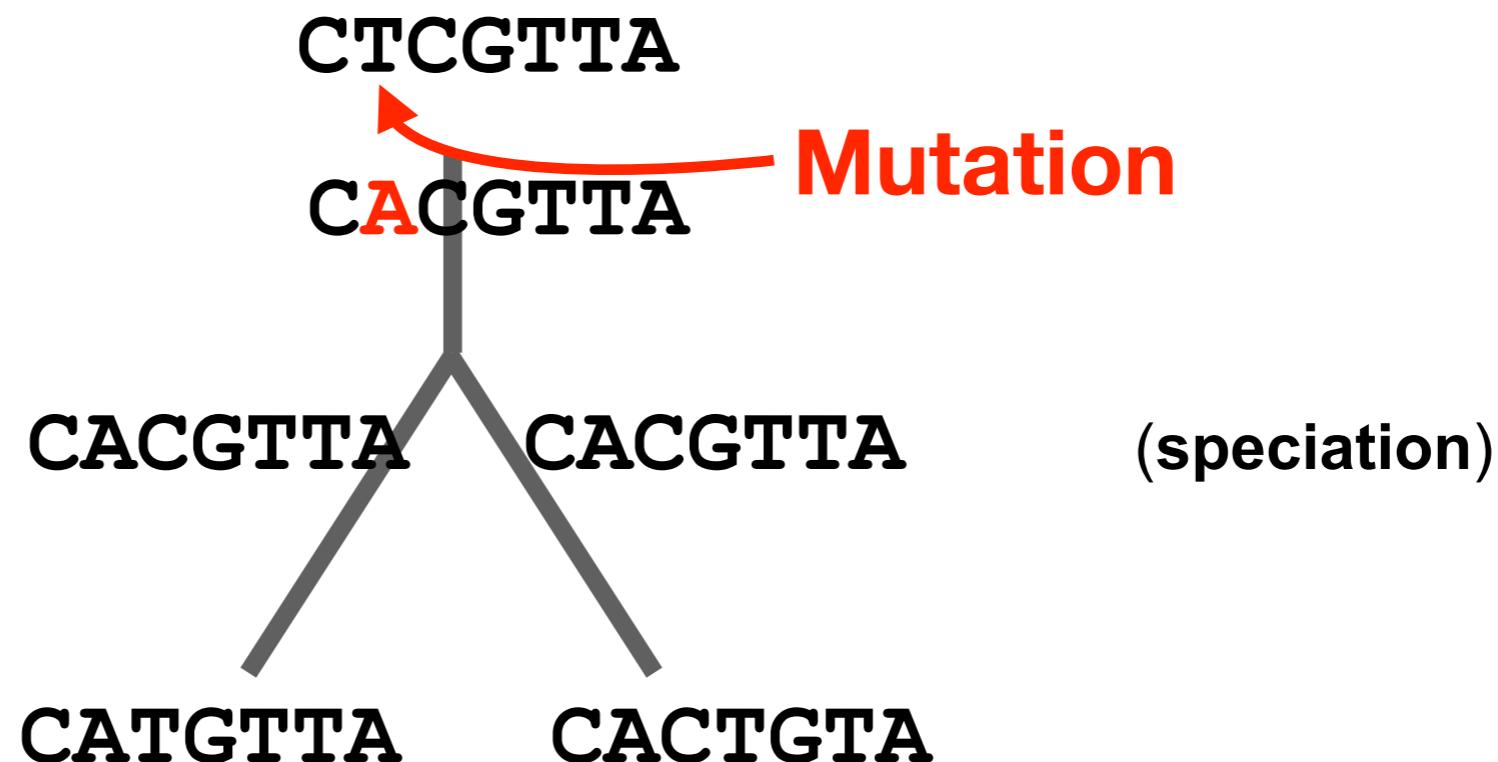


Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

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- Deletions
- Insertions

CTCGTTA → CACGTTA

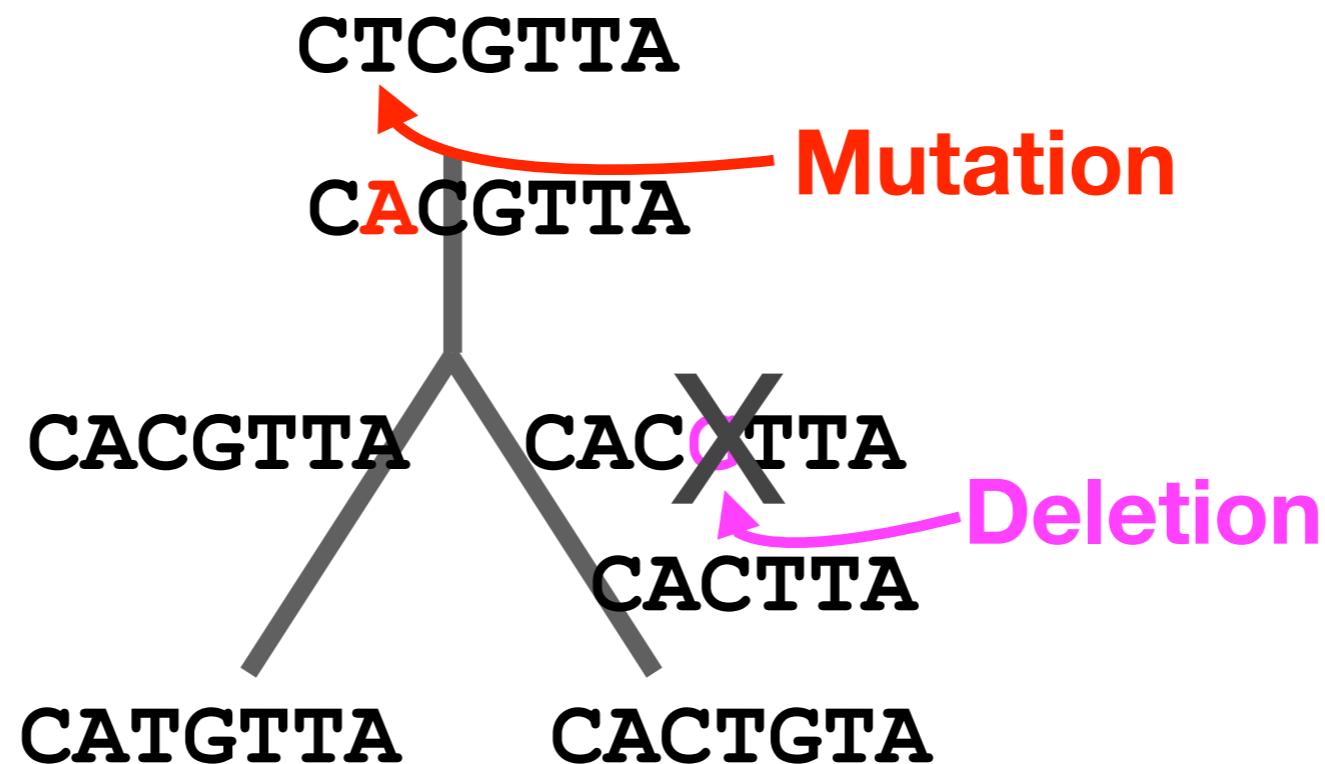


Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- Deletions
- Insertions

CTCGTTA → **CACGTTA**
CACGTTA → **CACTTA**

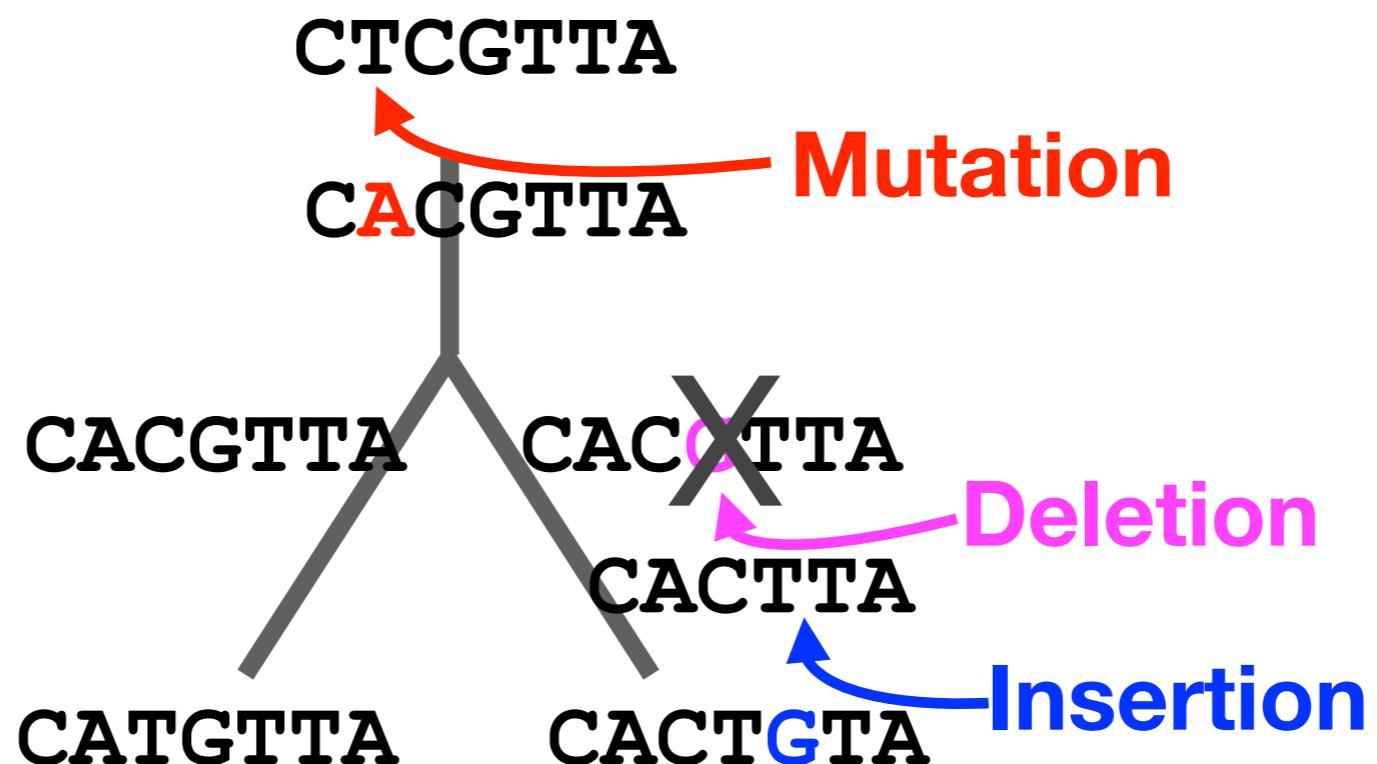


Mutations, deletions and insertions

There are three major types of sequence change that can occur during evolution.

- Mutations/Substitutions
- Deletions
- Insertions

CTCGTTA → CACGTTA
CACGTTA → CACTTA
CACTTA → CACTGTA

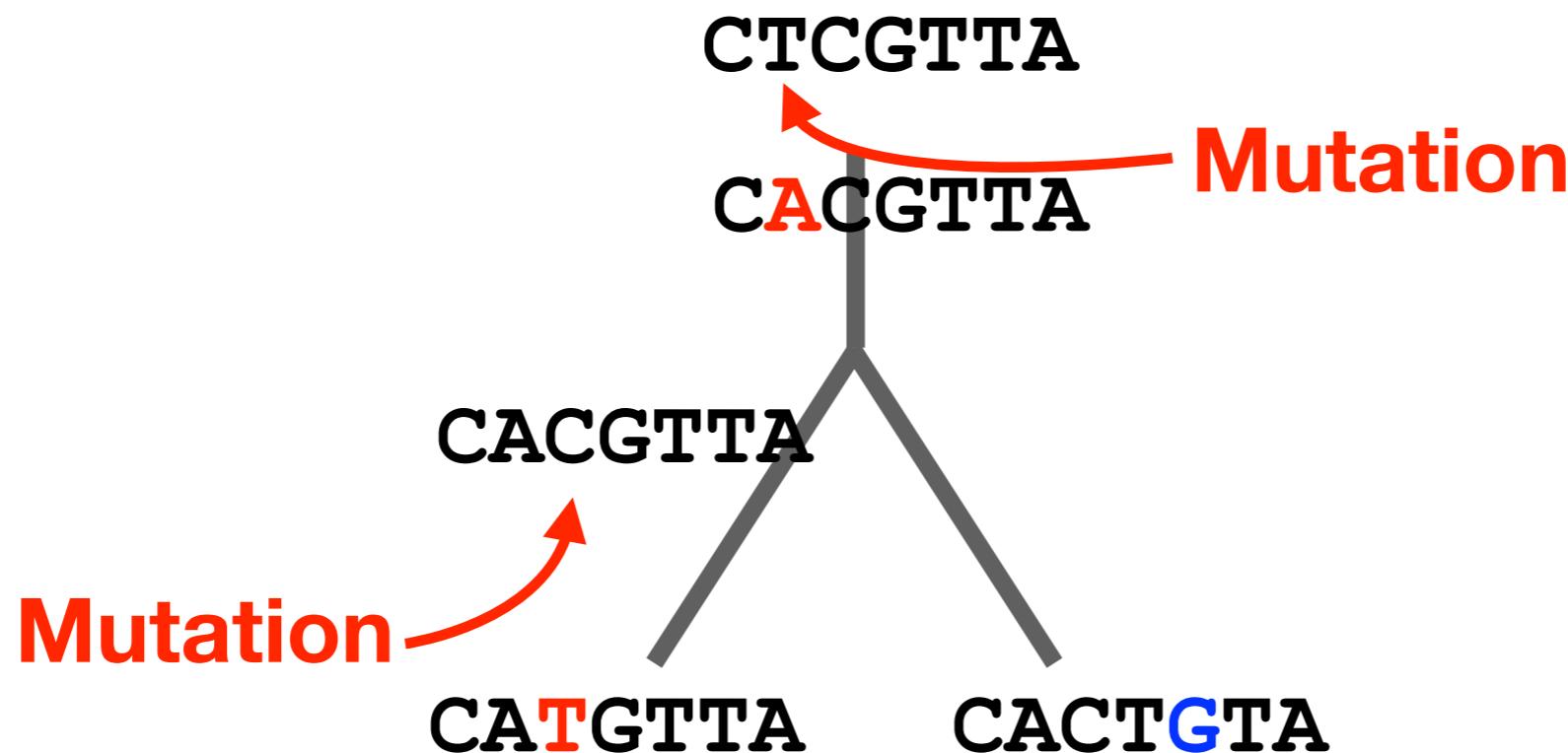


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- Deletions
- Insertions

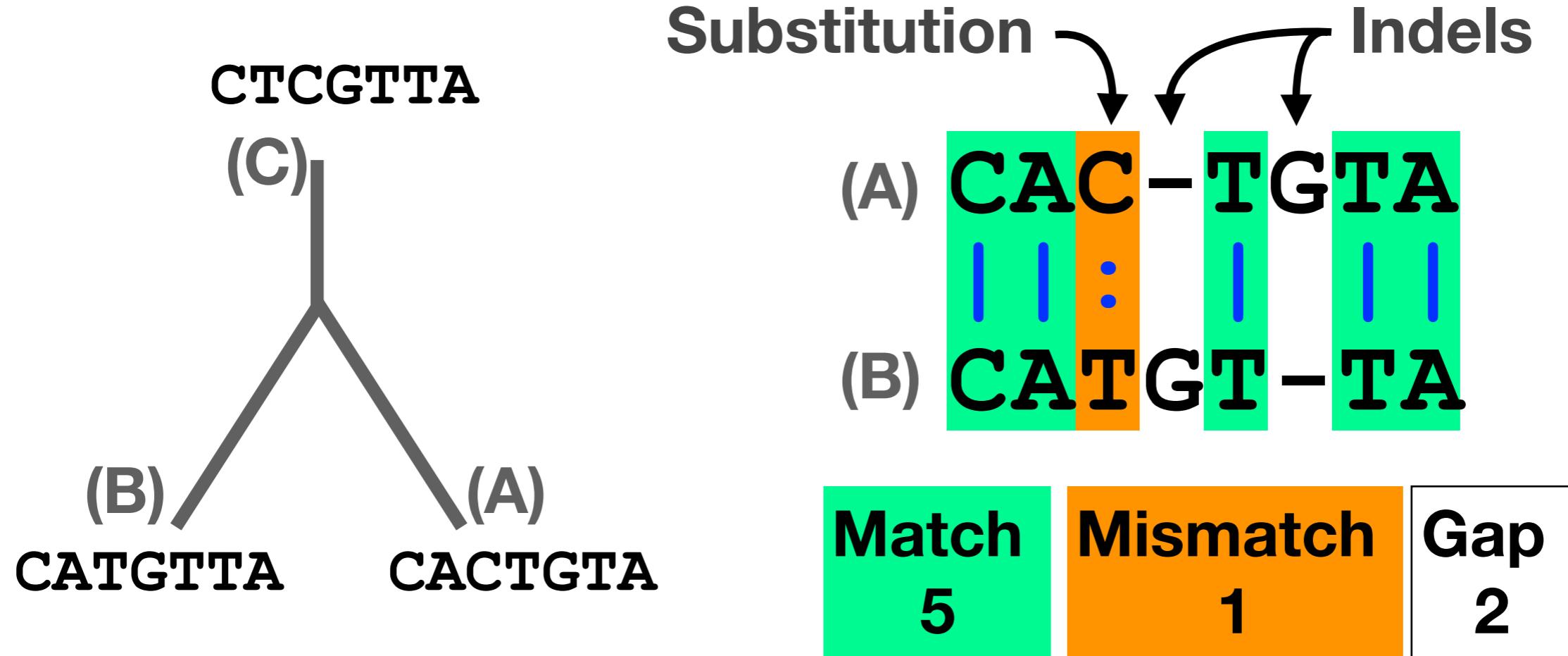
CTCGTTA → **CACGTTA**
CACGTTA → **CATGTTA**



Alignment view

Alignments are great tools to visualize sequence similarity and evolutionary changes in homologous sequences.

- Mismatches represent mutations/substitutions
- Gaps represent insertions and deletions (indels)



Alternative alignments

- Unfortunately, finding the correct alignment is difficult if we do not know the evolutionary history of the two sequences

Q. Which of these 3 possible alignments is best?

1.

CA	CTG	TA
	:	:
CAT	TGT	TA

2.

CA	CTG	T	-	A
CA	-T	G	T	TA

3.

CAC	-T	G	TA
	:		
CAT	TGT	-T	A

Alternative alignments

- One way to judge alignments is to compare their number of matches, insertions, deletions and mutations

● 4 matches
● 3 mismatches
○ 0 gaps

● 6 matches
● 0 mismatches
○ 2 gaps

● 5 matches
● 1 mismatch
○ 2 gaps

CACTGTA
|| : : : ||
CATGTAA

This sequence alignment shows a green box for 'CACTGTA' and an orange box for 'CATGTAA'. There are 4 matches (green), 3 mismatches (orange), and 0 gaps (white). A vertical blue bar is positioned between the two sequences.

CACTGT-A
|| | | | |
CA-TGTAA

This sequence alignment shows a green box for 'CACTGT-A' and an orange box for 'CA-TGTAA'. There are 6 matches (green), 0 mismatches (orange), and 2 gaps (white). A vertical blue bar is positioned between the two sequences.

CAC-TGTA
| | : | |
CATGT-TA

This sequence alignment shows a green box for 'CAC-TGTA' and an orange box for 'CATGT-TA'. There are 5 matches (green), 1 mismatch (orange), and 2 gaps (white). A vertical blue bar is positioned between the two sequences.

Scoring alignments

- We can assign a score for each match (+3), mismatch (+1) and indel (-1) to identify the optimal alignment for this scoring scheme

● 4 (+3)
● 3 (+1)
○ 0 (-1) = 15

● 6 (+3)
● 0 (+1)
○ 2 (-1) = 16

● 5 (+3)
● 1 (+1)
○ 2 (-1) = 14

Sequence alignment diagram showing two rows of DNA sequence. The top row is CACTGTA and the bottom row is CATGTAA. Vertical blue lines indicate matches between A, C, T, G, T, and A. Vertical orange lines indicate a mismatch between the second C and the first A. Vertical green lines indicate indels (deletions) in the bottom sequence.

Sequence alignment diagram showing two rows of DNA sequence. The top row is CACTGT-A and the bottom row is CA-TGTAA. Vertical blue lines indicate matches between C, A, C, T, G, T, and A. Vertical orange lines indicate a mismatch between the second C and the first A. Vertical green lines indicate indels (deletions) in the bottom sequence.

Sequence alignment diagram showing two rows of DNA sequence. The top row is CAC-TGTA and the bottom row is CATGT-TA. Vertical blue lines indicate matches between C, A, C, T, G, T, and A. Vertical orange lines indicate a mismatch between the second C and the first A. Vertical green lines indicate indels (deletions) in the bottom sequence.

Optimal alignments

- Biologists often prefer parsimonious alignments, where the number of postulated sequence changes is minimized.

- 4 matches
- 3 mismatches
- 0 gaps

CA	CTG	TA
	:	:
CAT	TGT	TA

- 6 matches
- 0 mismatches
- 2 gaps

CA	CTG	T	-	A
CA	-	TGT	T	A

- 5 matches
- 1 mismatch
- 2 gaps

CA	C	-	T	G	T	A
		:				
CAT	G	T	-	T	A	

Optimal alignments

- Biologists often prefer parsimonious alignments, where the number of postulated sequence changes is minimized.

- 4 matches
- 3 mismatches
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CA	CTG	TA
	:	:
CAT	TGT	TA

- 6 matches
- 0 mismatches
- 2 gaps

CA	CTG	T	-	A
CA	-	TGT	TA	

- 5 matches
- 1 mismatch
- 2 gaps

CA	C	-	T	G	TA
		:			
CAT	G	T	-	TA	

Optimal alignments

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- 4 matches
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CA	CTG	TA
	:	:
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- 6 matches
- 0 mismatches
- 2 gaps

CA	CTG	-	TA
CA	-TGT	TA	

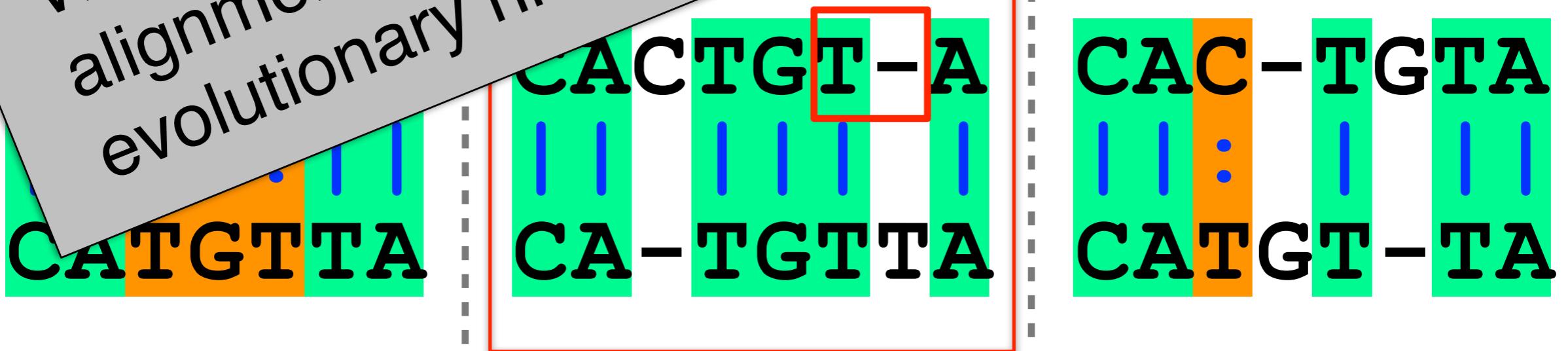
- 5 matches
- 1 mismatch
- 2 gaps

CAC	-	TG	TA
	:		
CAT	G	T	-TA

Optimal alignments

- Biologists often prefer parsimonious alignments, where the number of sequence changes is minimized.

- 4 matches
- 3 mismatches
- 2 gaps



Warning: There may be more than one optimal alignment and these may not reflect the true evolutionary history of our sequences!

- 4 matches
- 3 mismatches
- 2 gaps

ALIGNMENT FOUNDATIONS

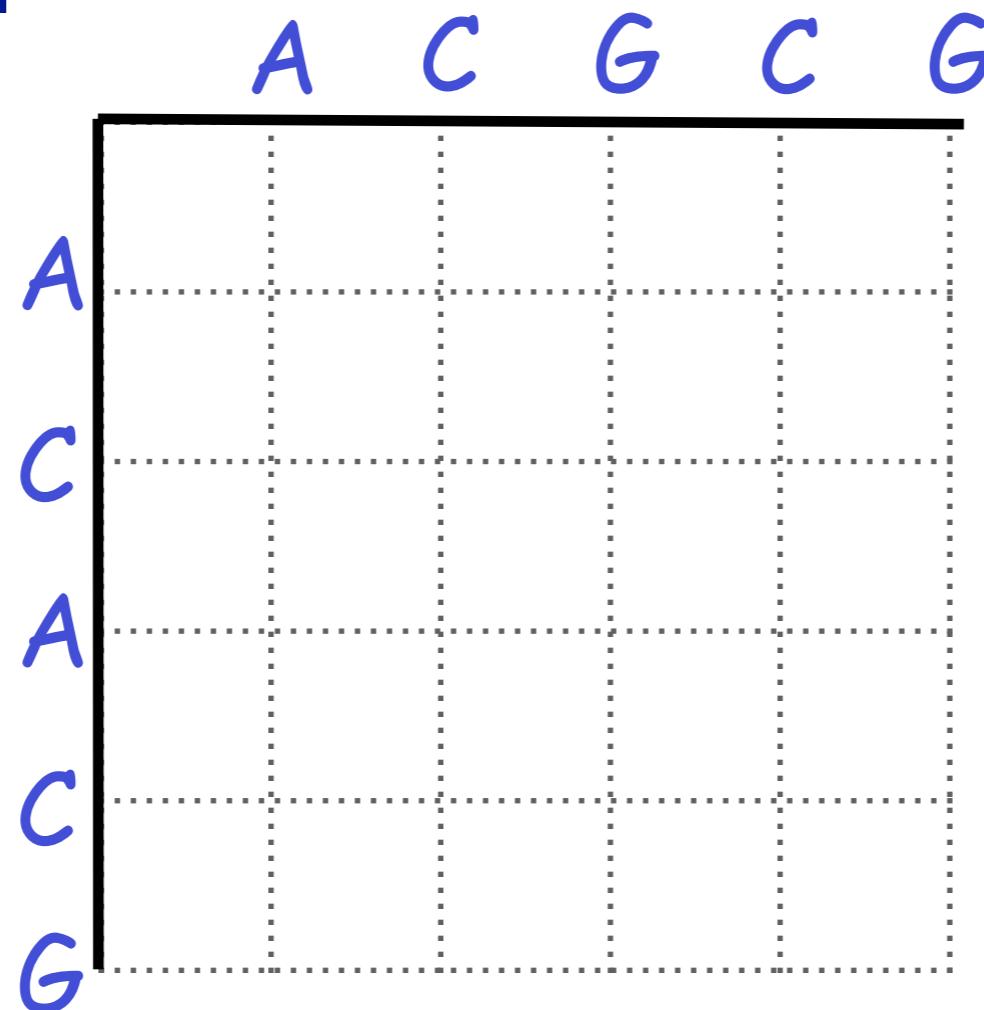
- **Why...**
 - Why compare biological sequences?
- **What...**
 - Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
- **How...**
 - ▶ Dot matrices
 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

ALIGNMENT FOUNDATIONS

- Why...
 - Why compare biological sequences?
 - What...
 - Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
 - How...
 - ▶ Dot matrices
 - ▶ D
 - ▶ B
- How do we compute the optimal alignment between two sequences?

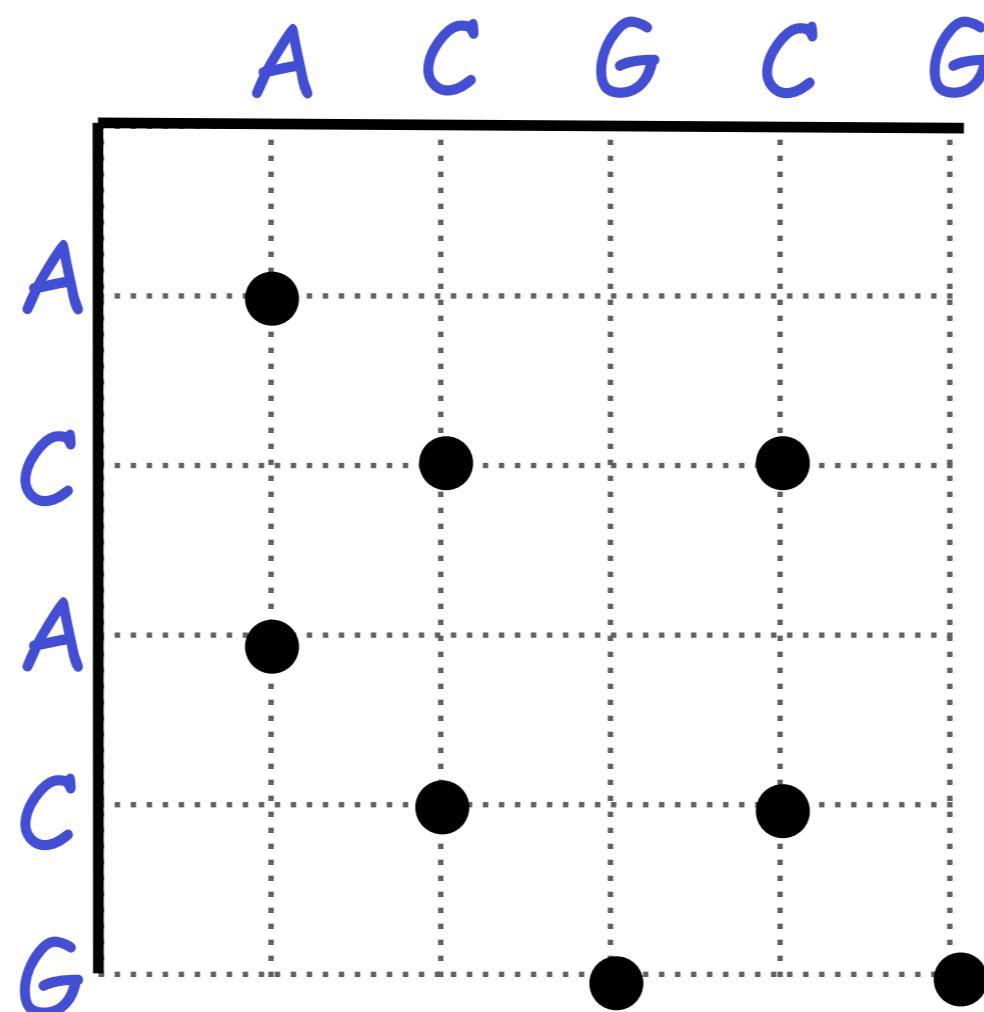
Dot plots: simple graphical approach

- Place one sequence on the vertical axis of a 2D grid (or matrix) and the other on the horizontal



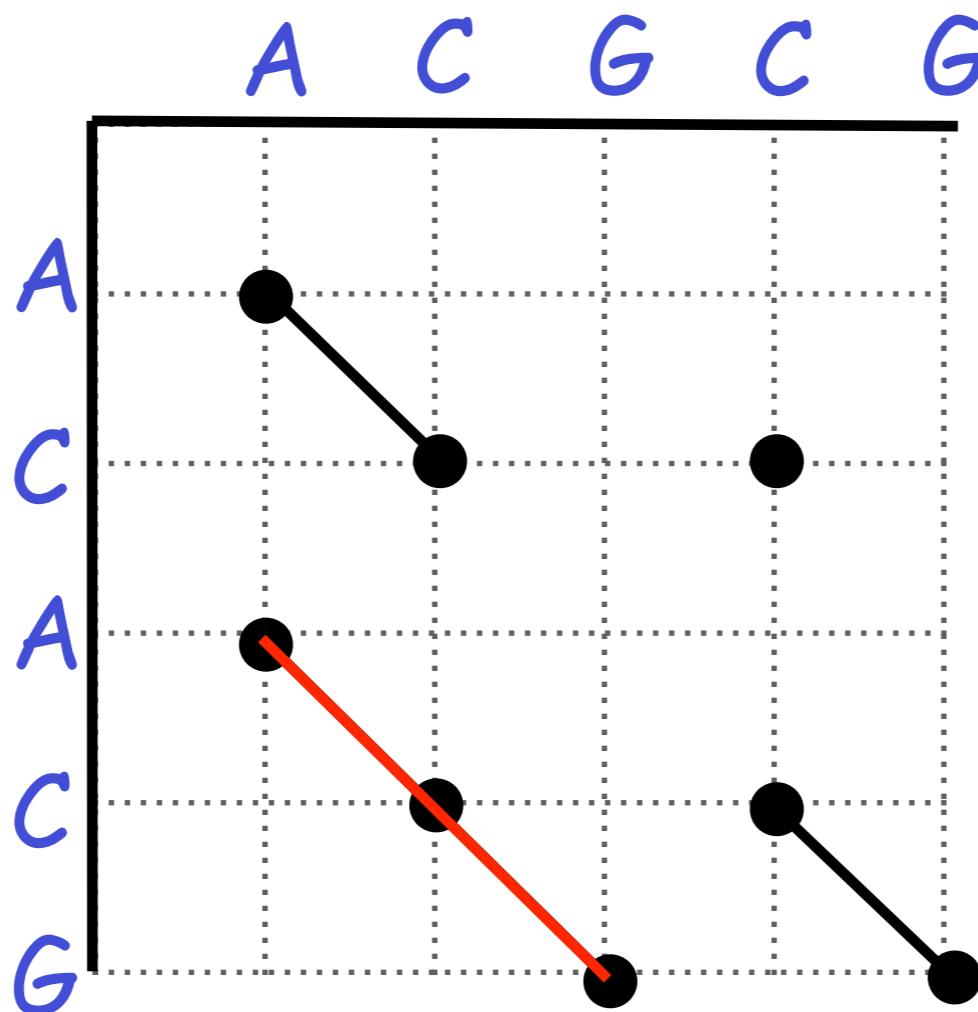
Dot plots: simple graphical approach

- Now simply put dots where the horizontal and vertical sequence values match



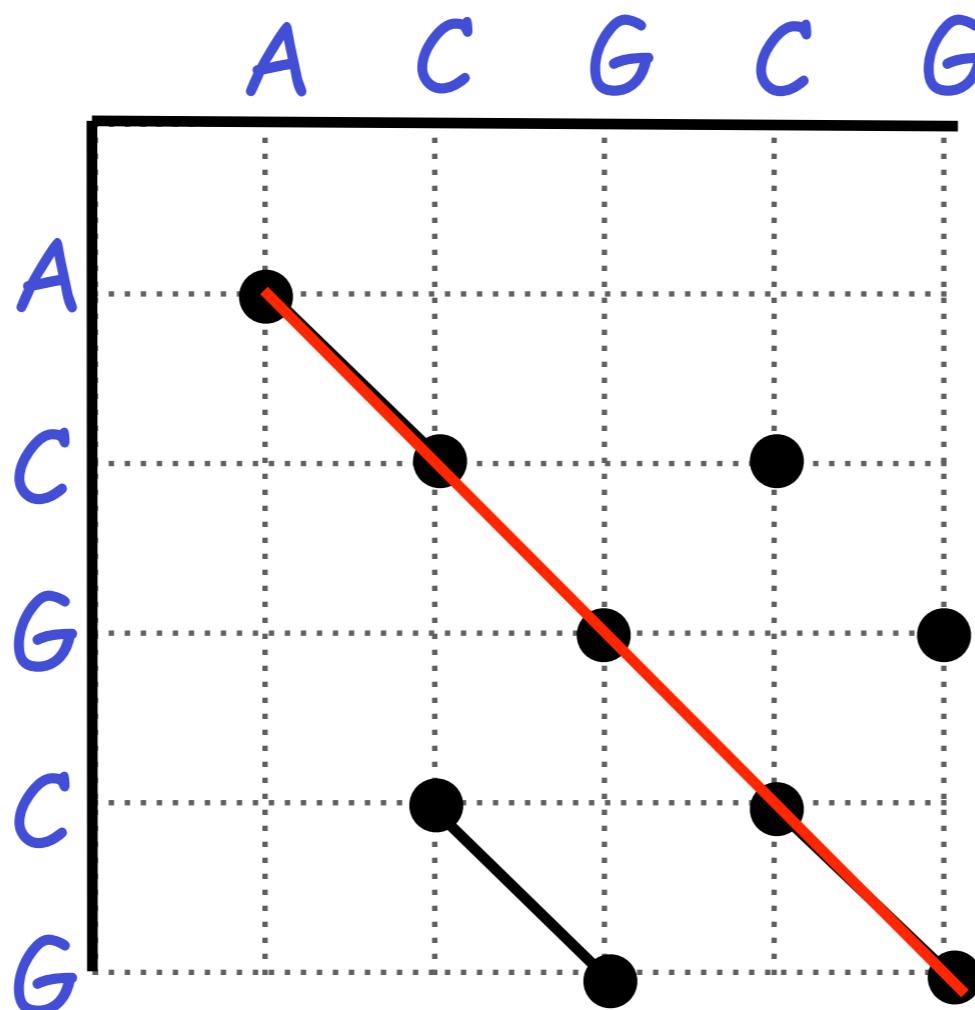
Dot plots: simple graphical approach

- Diagonal runs of dots indicate matched segments of sequence



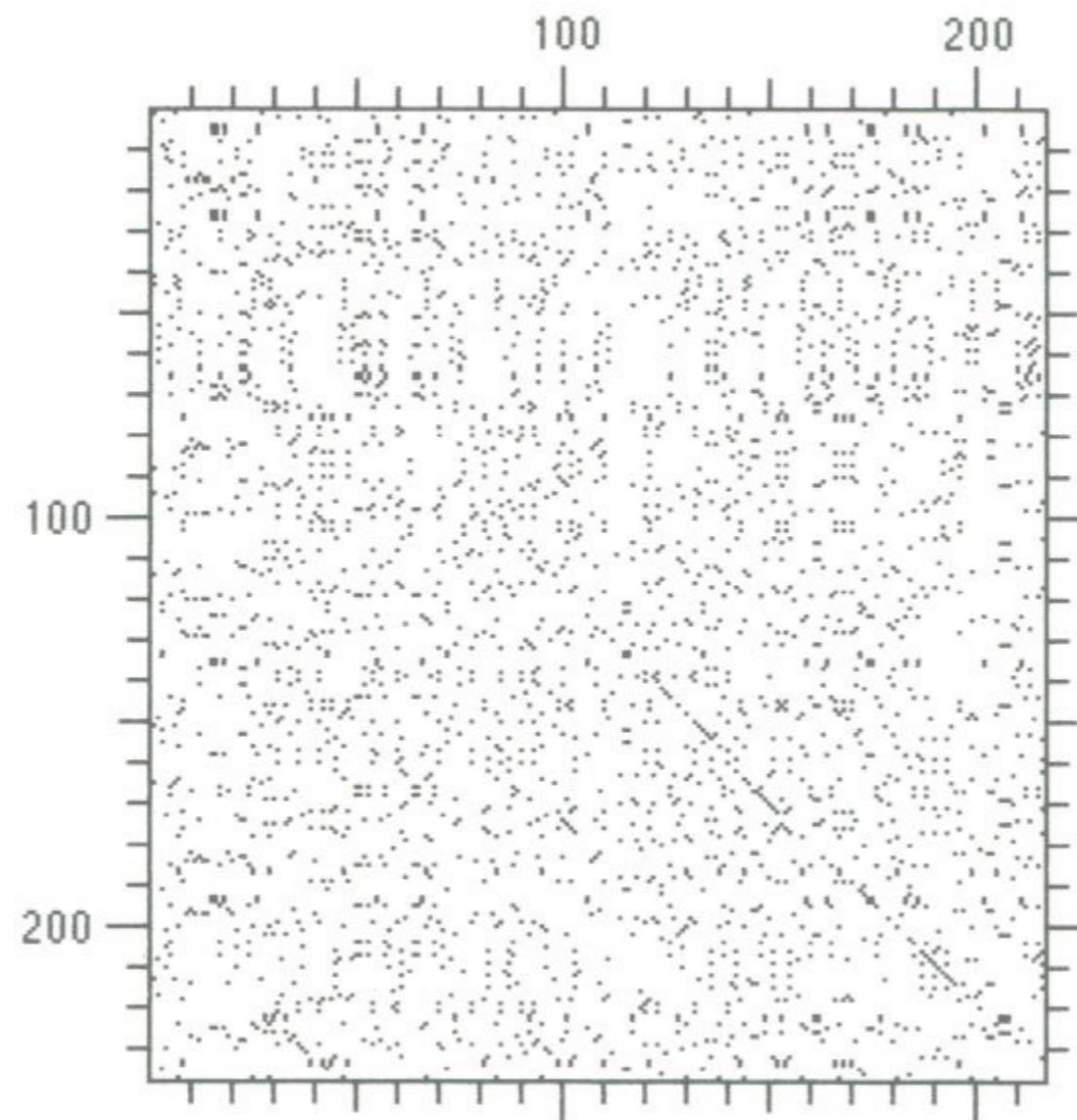
Dot plots: simple graphical approach

Q. What would the dot matrix of a two identical sequences look like?



Dot plots: simple graphical approach

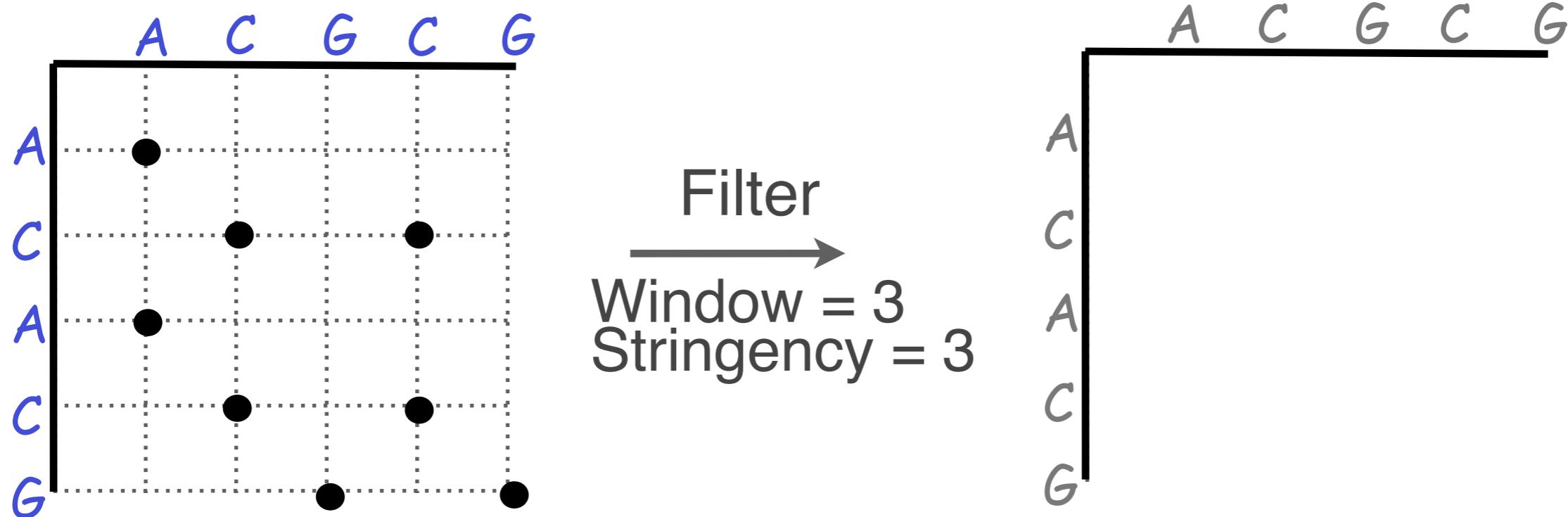
- Dot matrices for long sequences can be noisy



Dot plots: window size and match stringency

Solution: use a window and a threshold

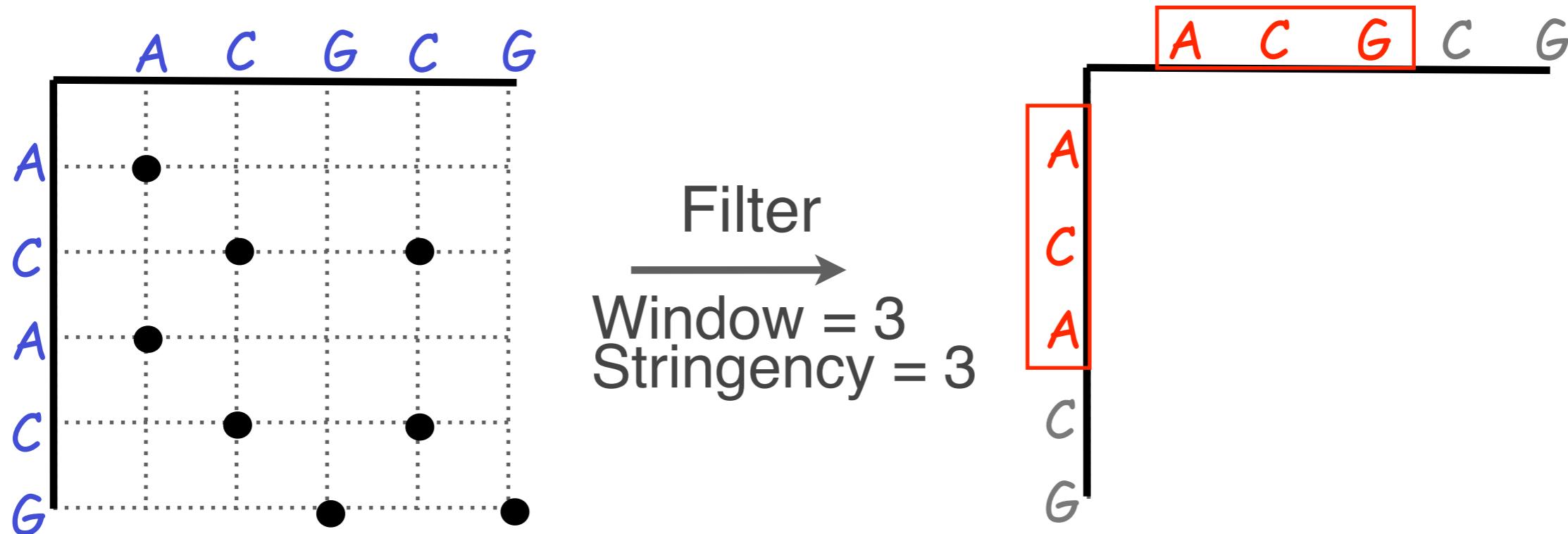
- compare character by character within a window
- require certain fraction of matches within window in order to display it with a dot.
 - You have to choose window size and stringency



Dot plots: window size and match stringency

Solution: use a window and a threshold

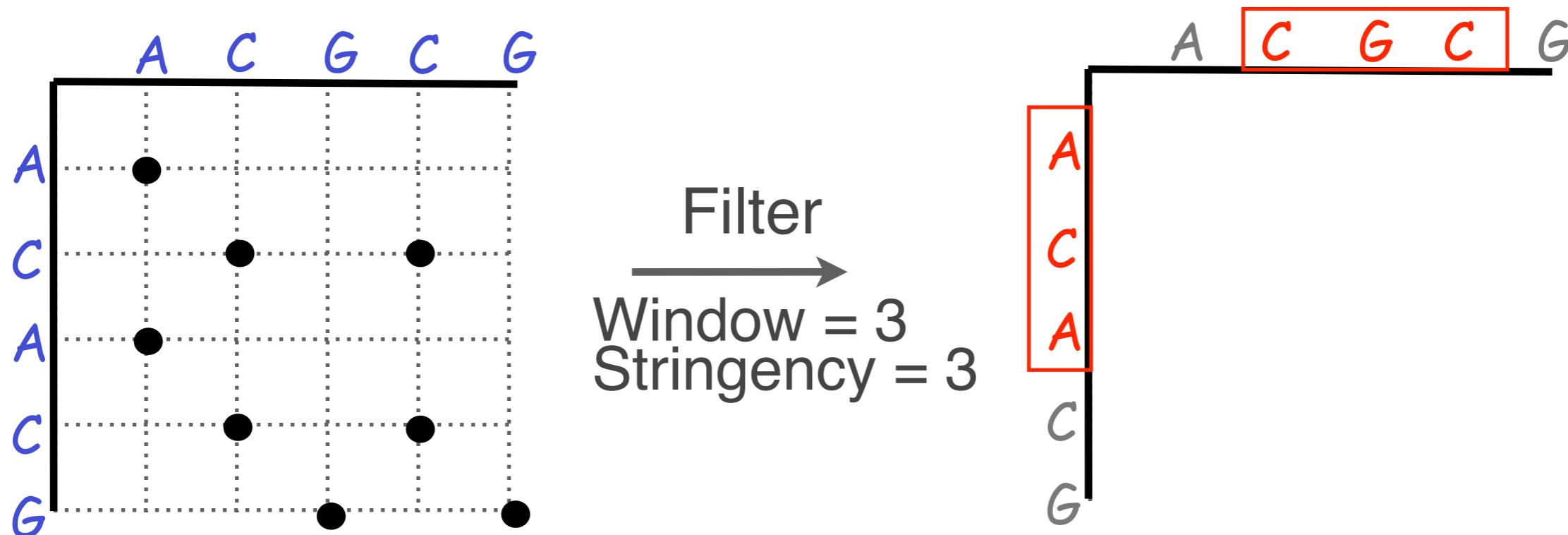
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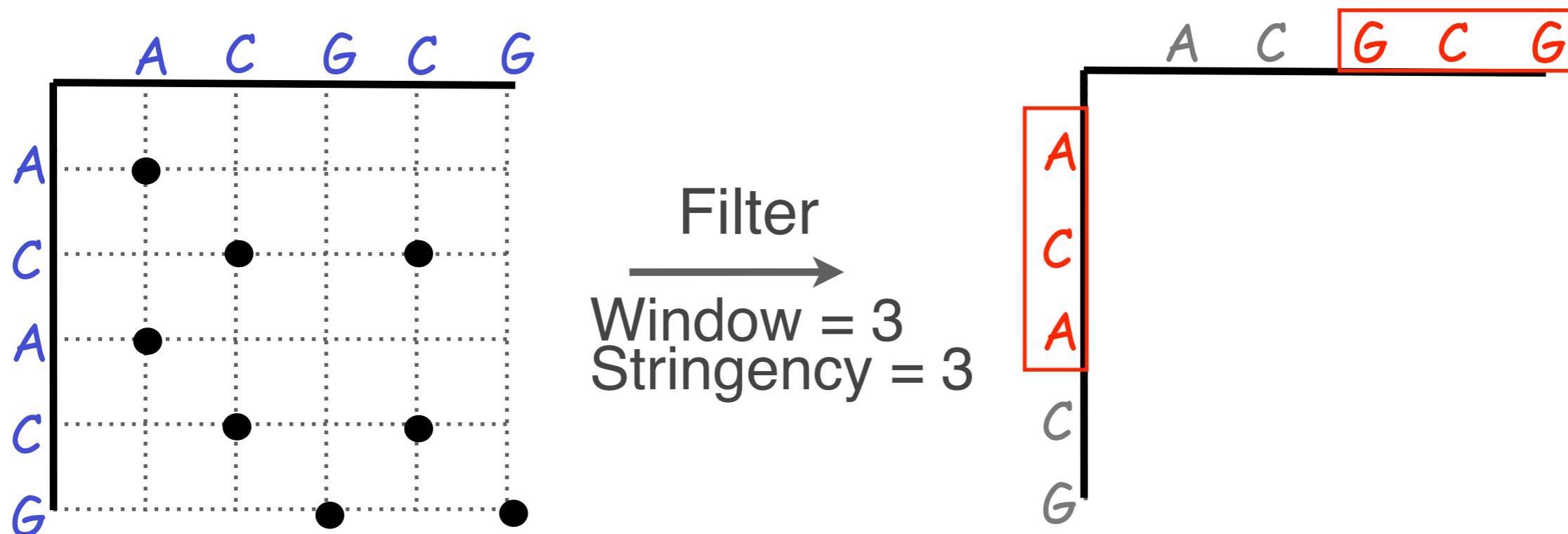
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Solution: use a window and a threshold

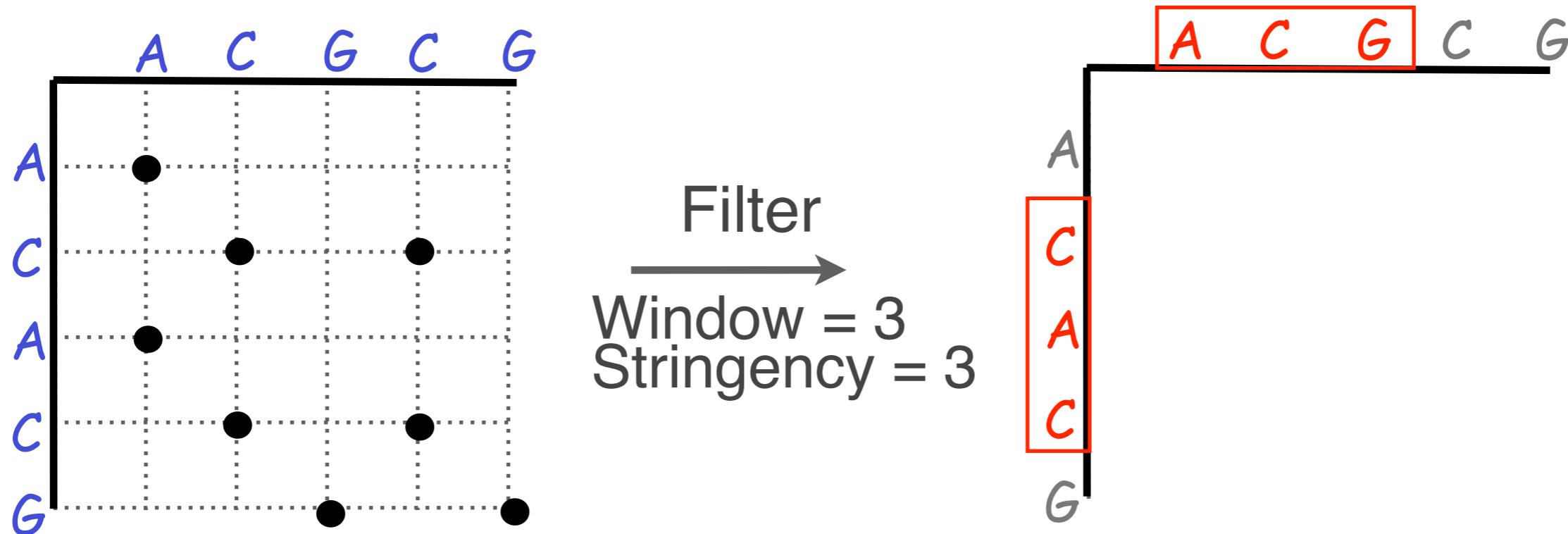
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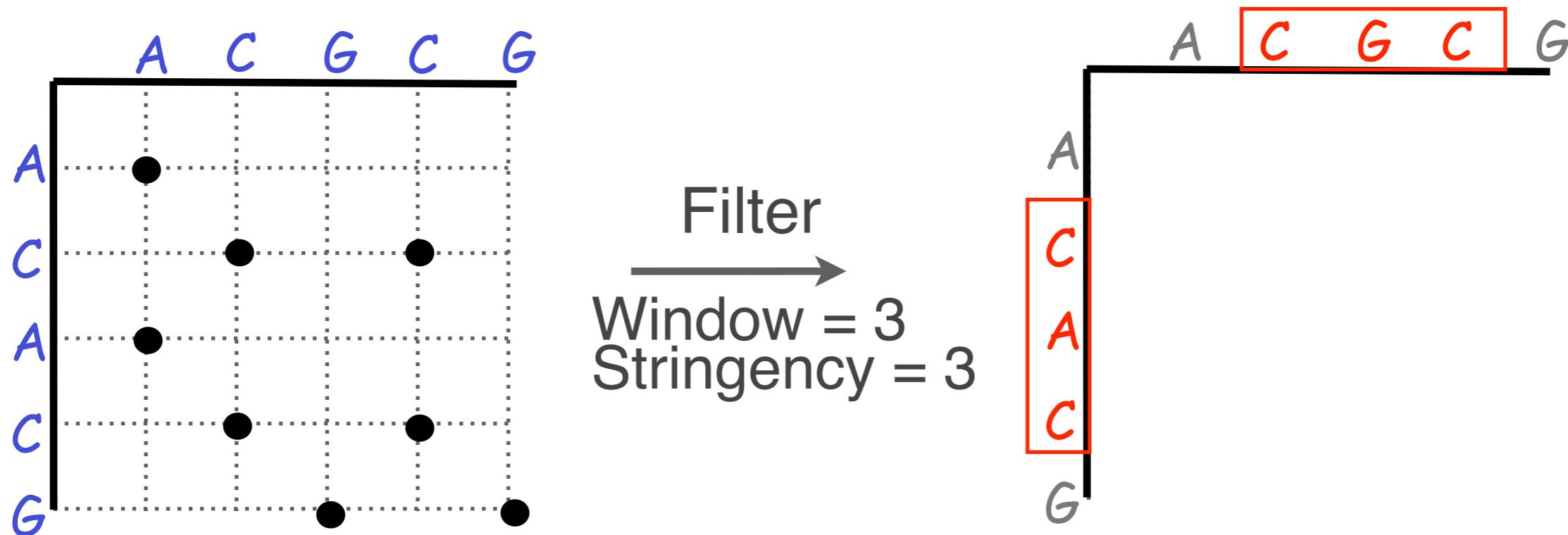
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Dot plots: window size and match stringency

Solution: use a window and a threshold

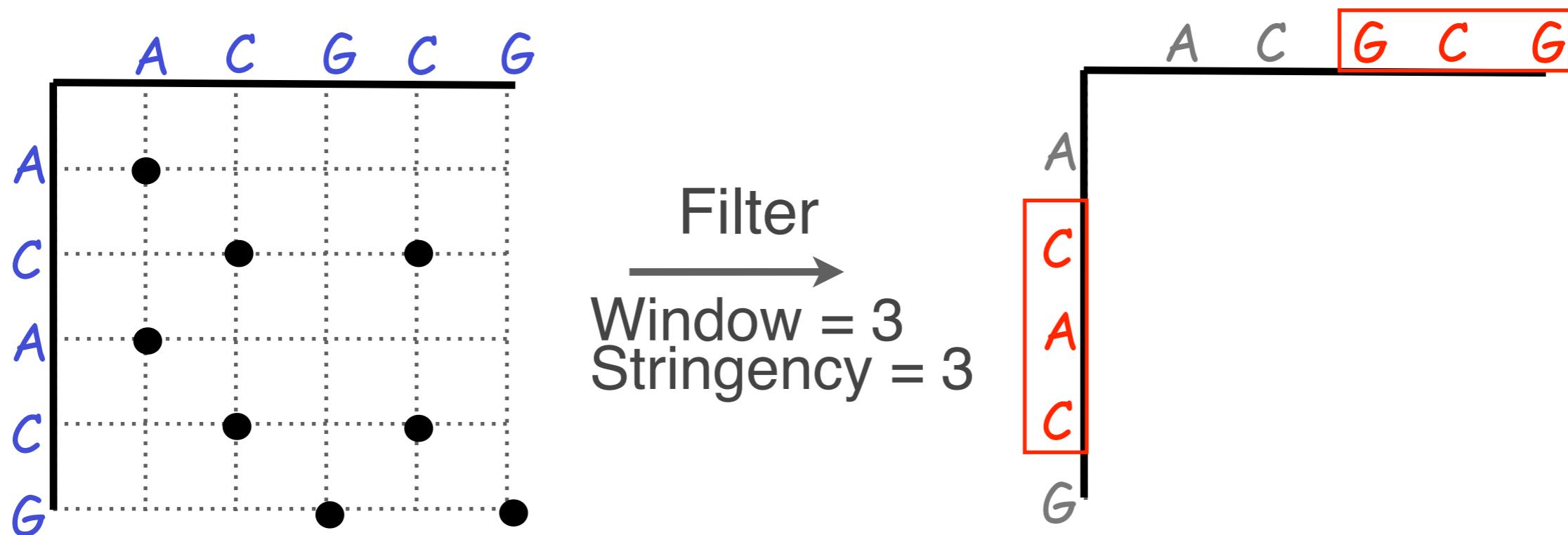
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Dot plots: window size and match stringency

Solution: use a window and a threshold

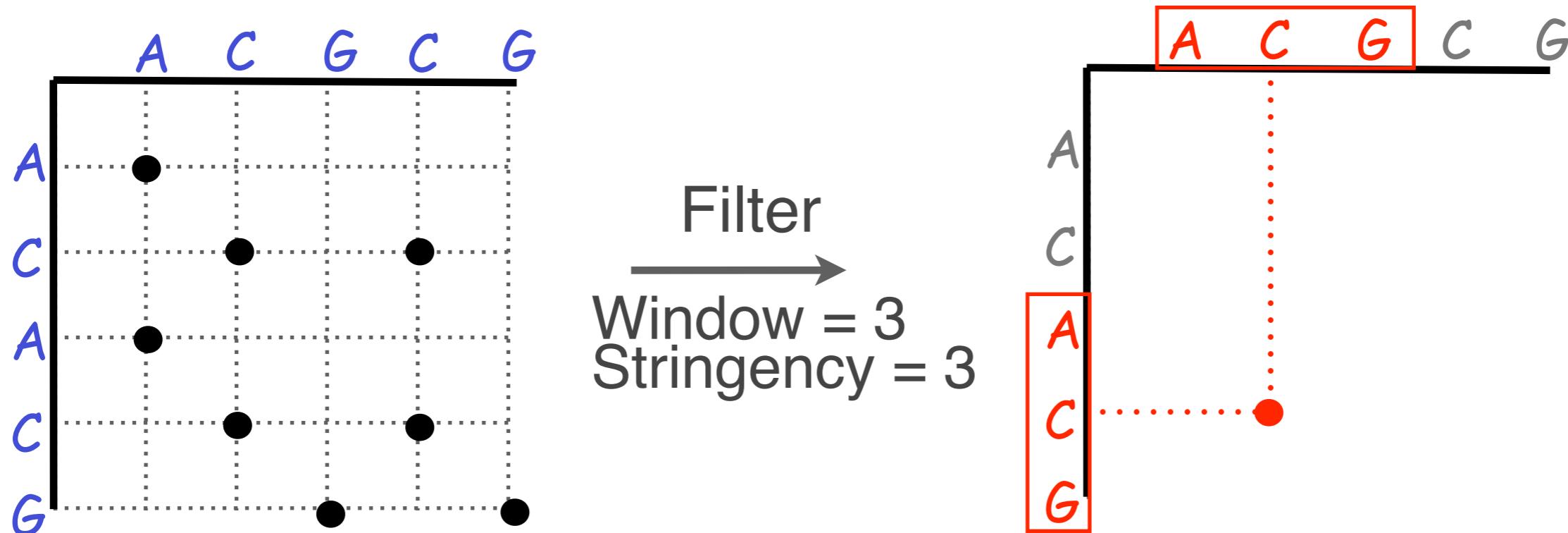
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Dot plots: window size and match stringency

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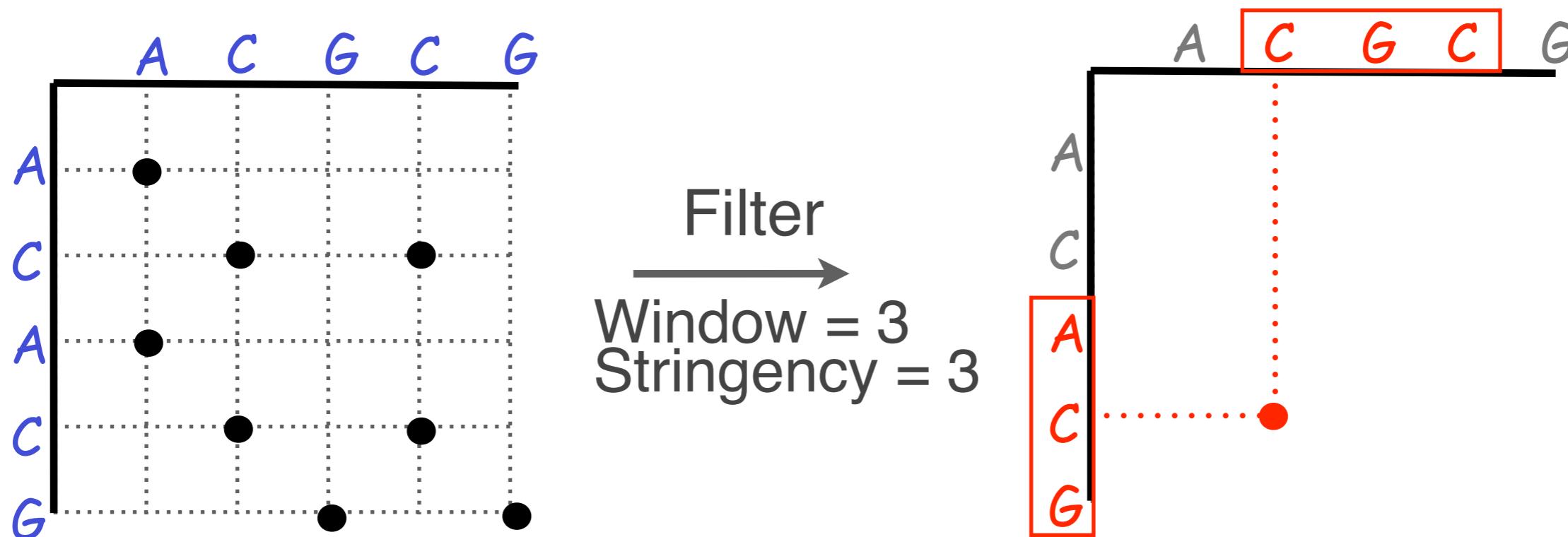
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Solution: use a window and a threshold

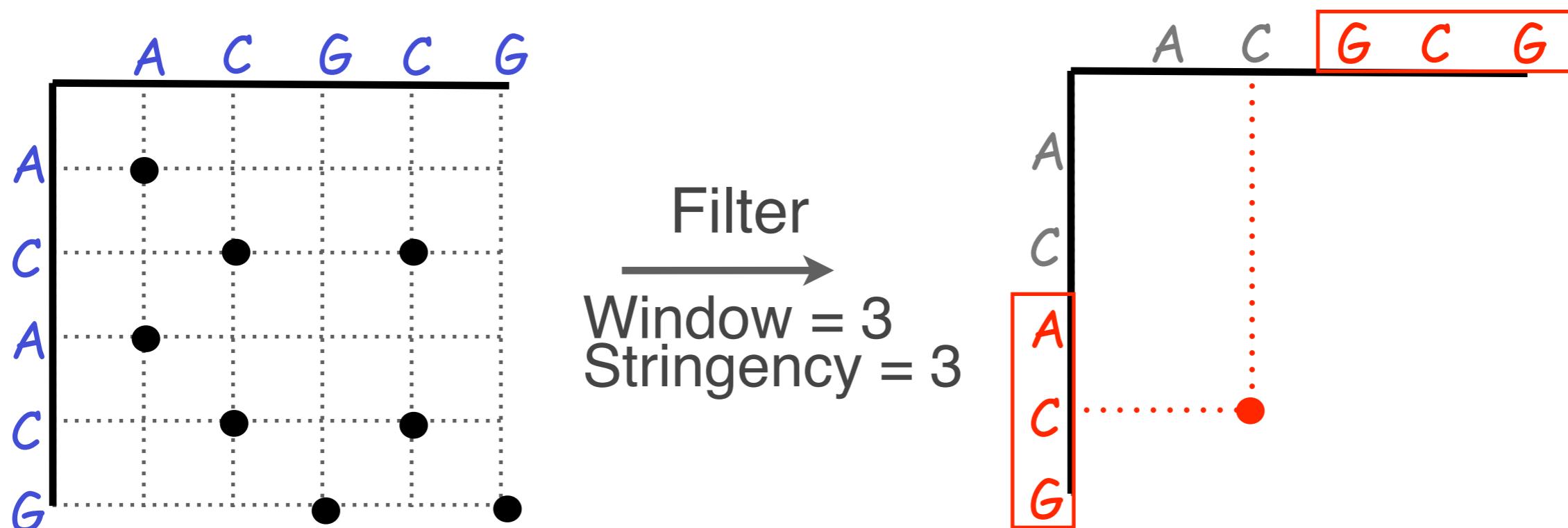
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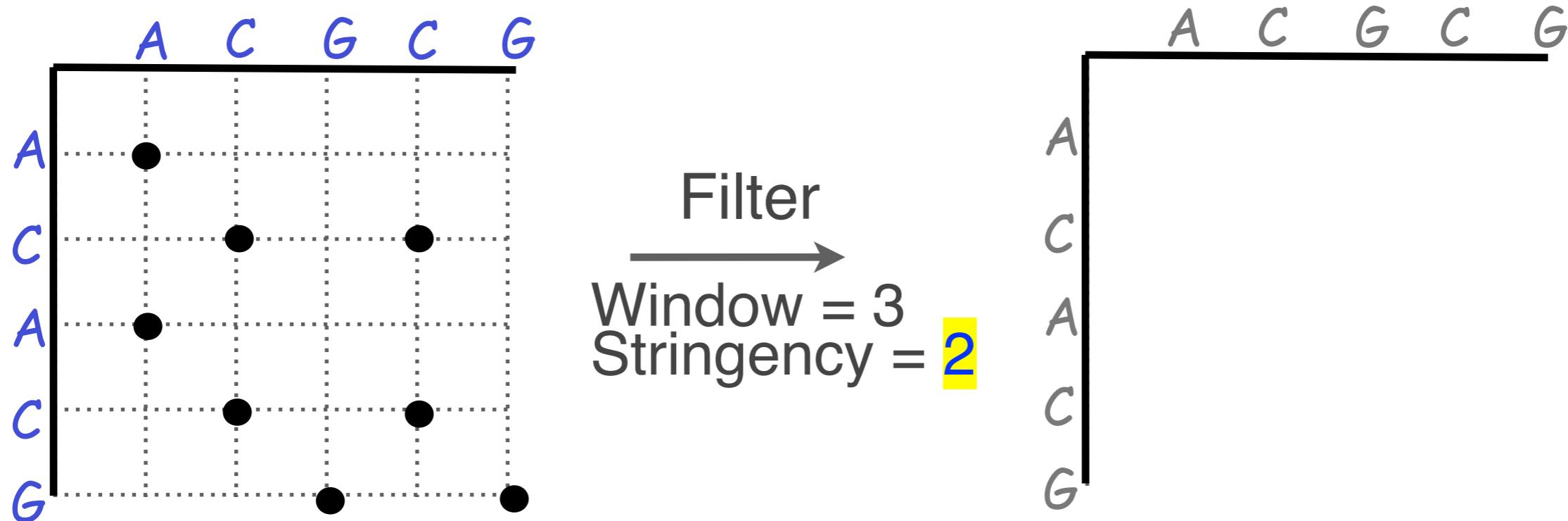
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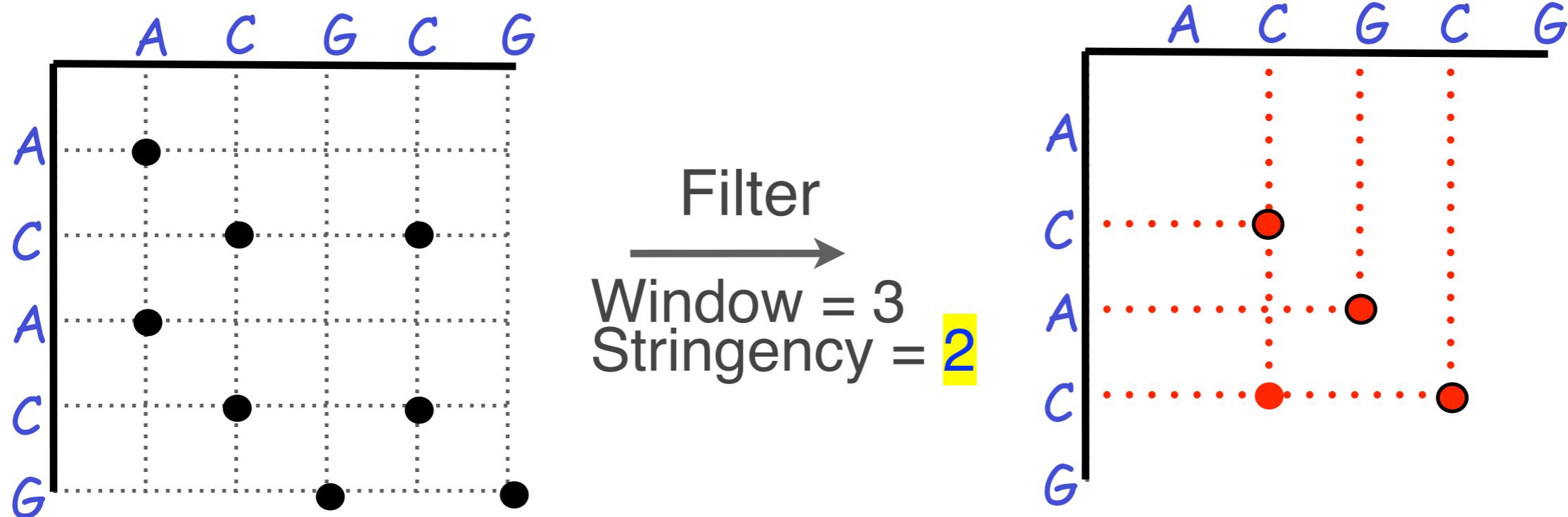
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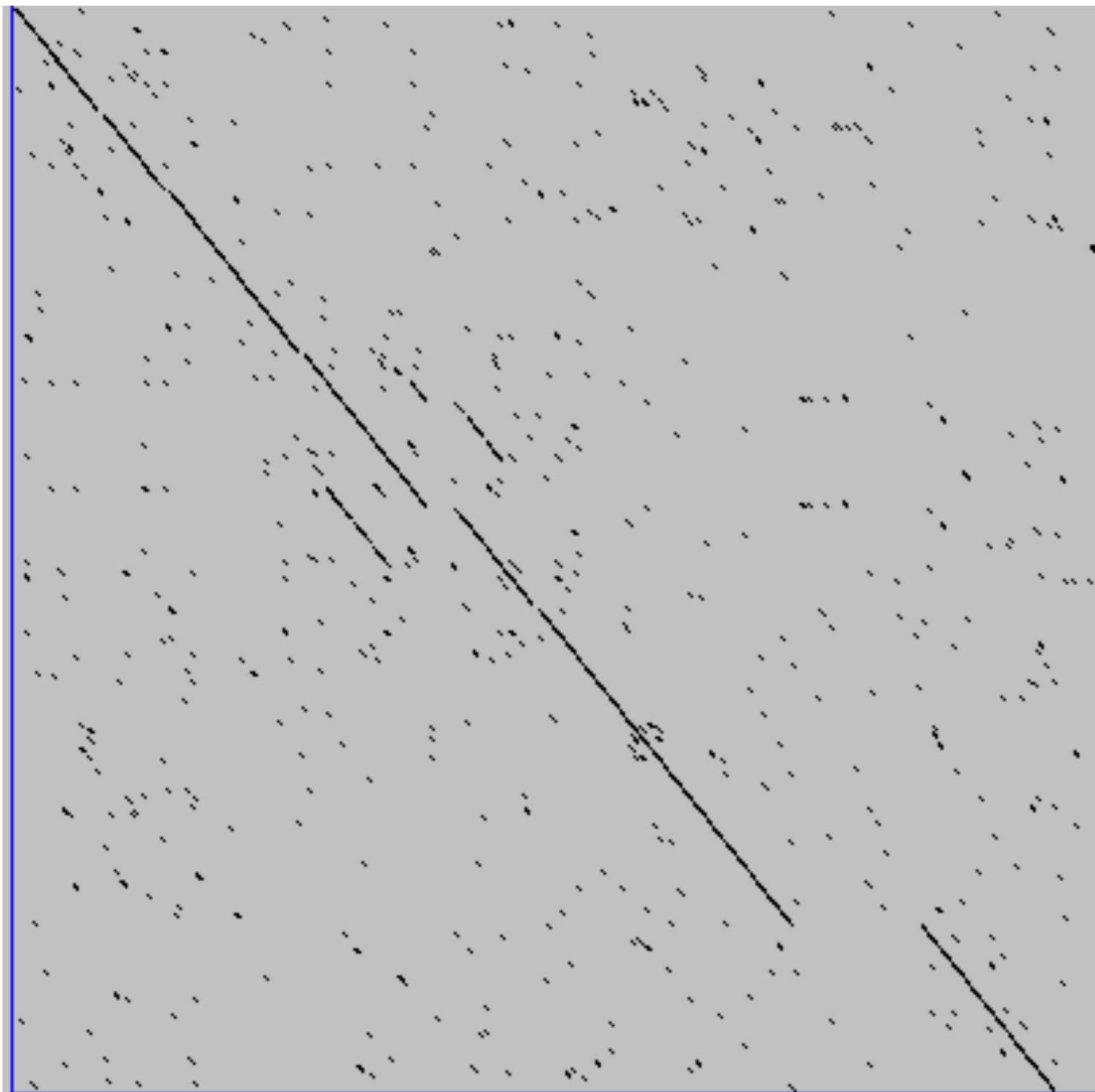
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Solution: use a window and a threshold

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- require certain fraction of matches within window in order to display it with a dot.
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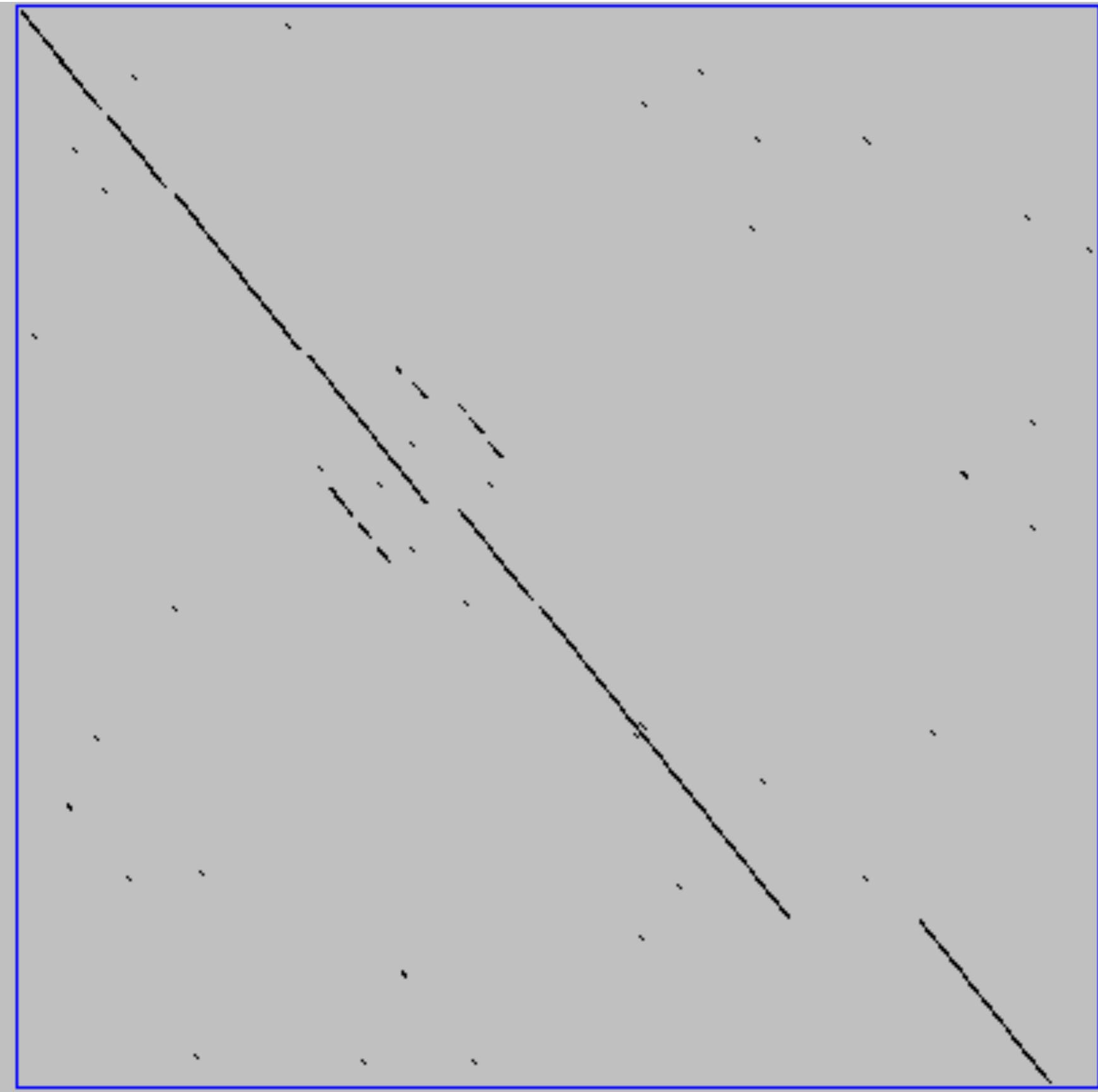
Window size = 5 bases



A dot plot simply puts a dot where two sequences match. In this example, dots are placed in the plot if 5 bases in a row match perfectly. Requiring a 5 base perfect match is a **heuristic** – only look at regions that have a certain degree of identity.

Do you expect evolutionarily related sequences to have more word matches (matches in a row over a certain length) than random or unrelated sequences?

Window size = 7 bases

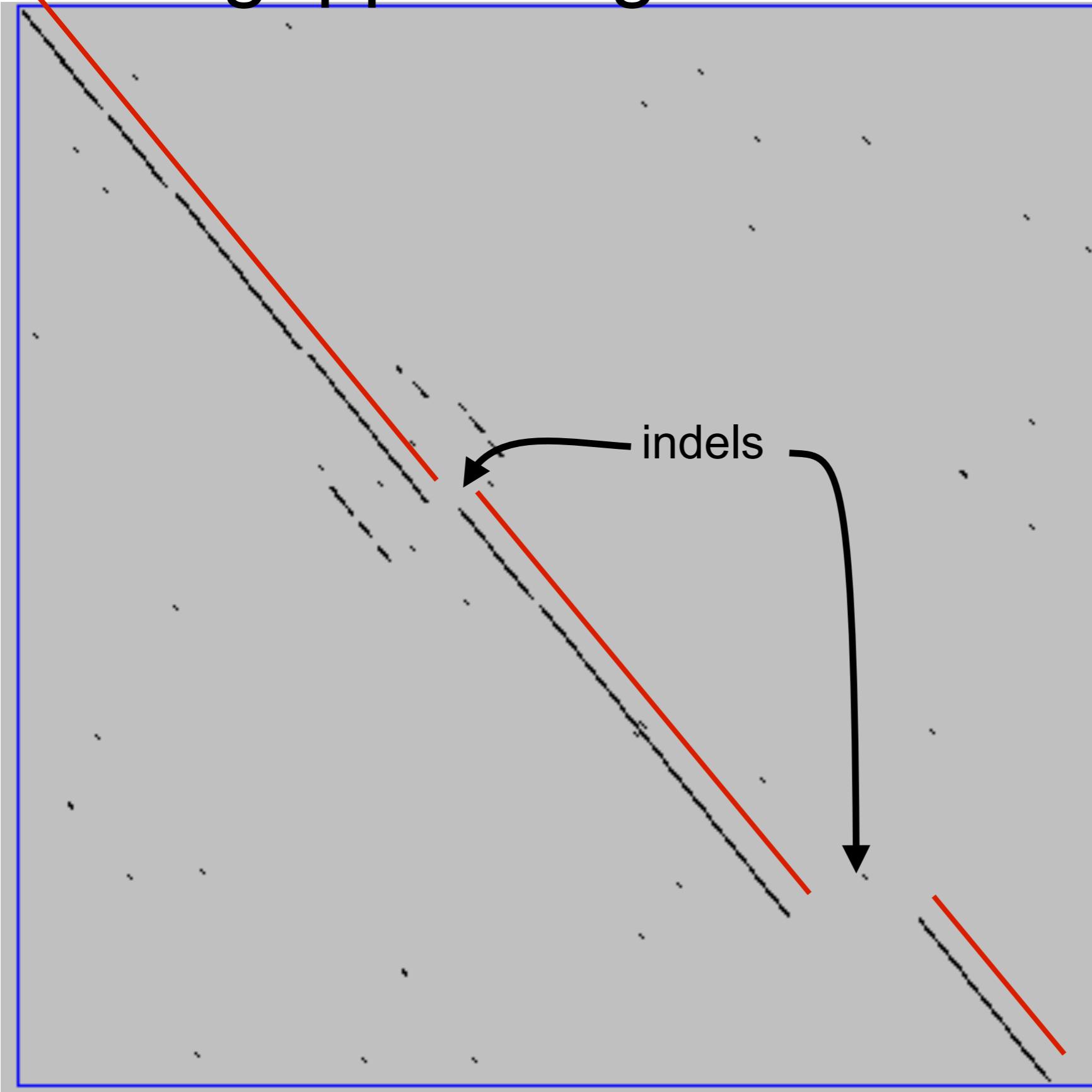


This is a dot plot of the same sequence pair. Now 7 bases in a row must match for a dot to be placed. Noise is reduced.

Using windows of a certain length is very similar to using words (kmers) of N characters in the heuristic alignment search tools

Bigger window (kmer)
fewer matches to consider

Ungapped alignments



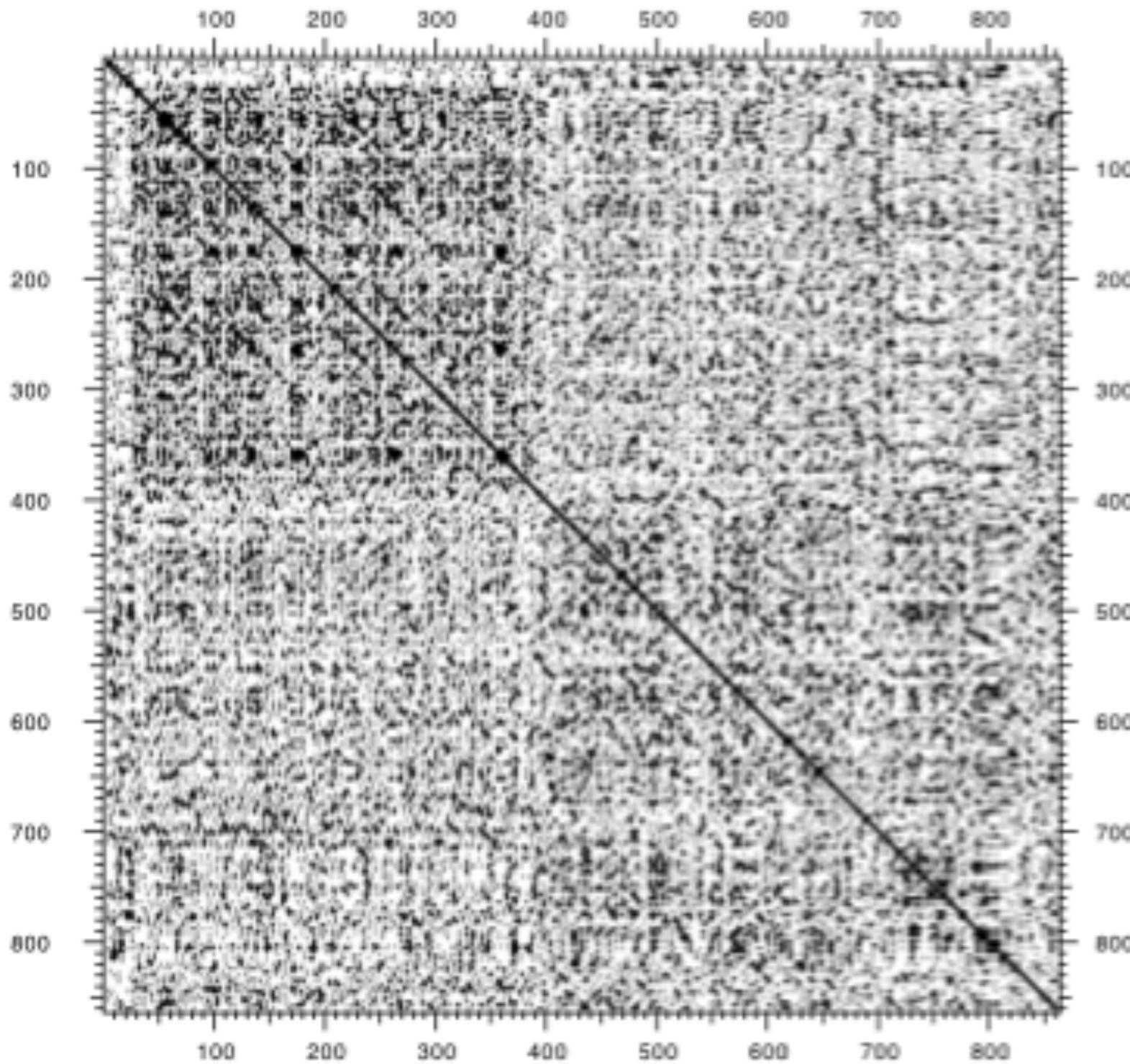
Only **diagonals** can be followed.

Downward or rightward paths represent **insertion** or **deletions** (gaps in one sequence or the other).

Uses for dot matrices

- Visually assessing the similarity of two protein or two nucleic acid sequences
- Finding local repeat sequences within a larger sequence by comparing a sequence to itself
 - Repeats appear as a set of diagonal runs stacked vertically and/or horizontally

Repeats

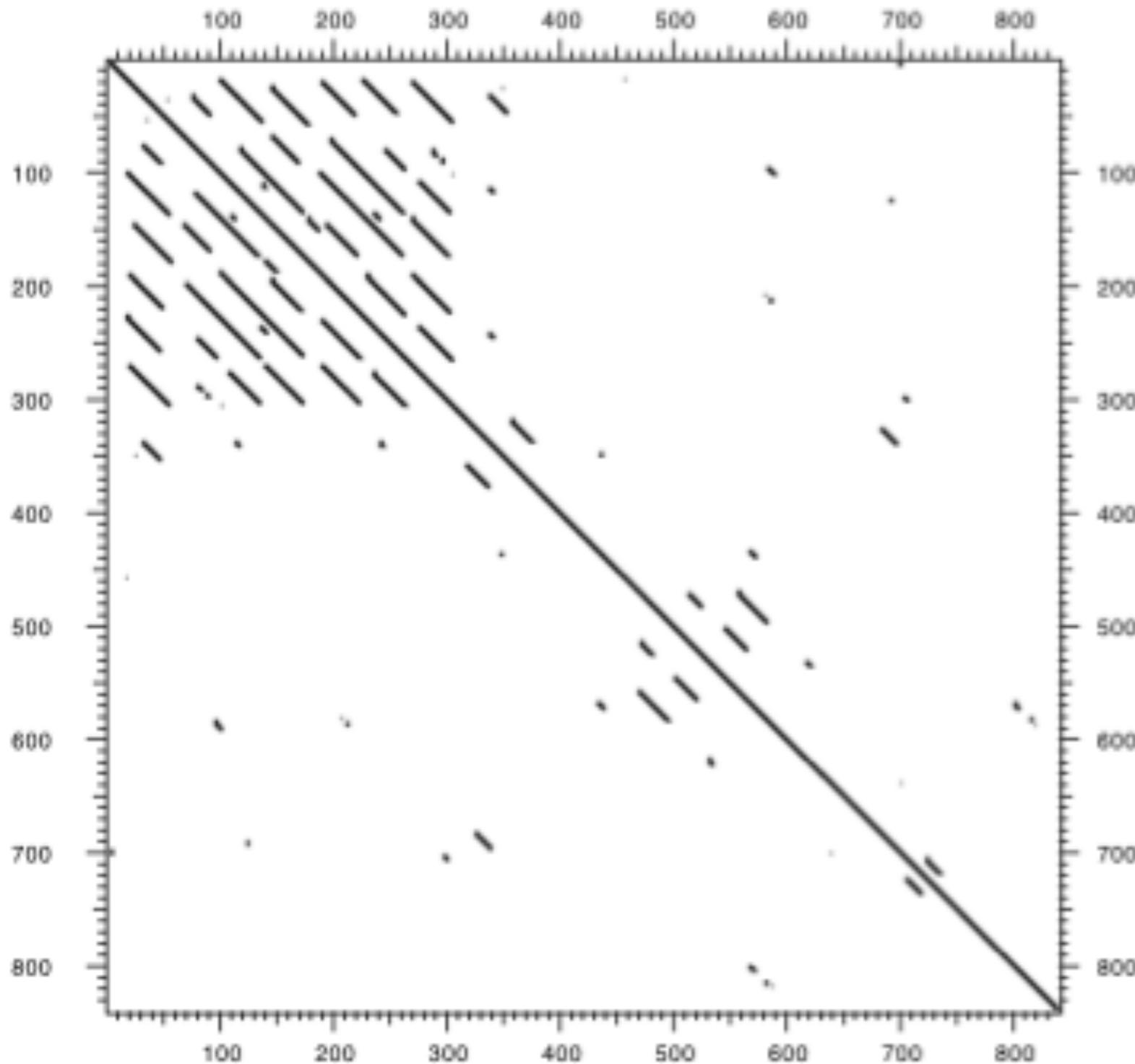


Human LDL receptor
protein sequence
(Genbank P01130)

$$\begin{aligned}W &= 1 \\S &= 1\end{aligned}$$

(Figure from Mount, "Bioinformatics sequence and genome analysis")

Repeats



Human LDL receptor
protein sequence
(Genbank P01130)

$$\begin{aligned} W &= 23 \\ S &= 7 \end{aligned}$$

(Figure from Mount, "Bioinformatics sequence and genome analysis")

Your Turn!

Exploration of dot plot parameters (hands-on worksheet **Section 1**)

<http://bio3d.ucsd.edu/dotplot/>

<https://bioboot.shinyapps.io/dotplot/>

BGGN-213: Dot Plot Comparison of Two Sequences

Dot plots are a simple graphical approach for the visual comparison of two sequences. They have a long history (see [Maizel and Lenk 1981](#) and references therein) and entail placing one sequence on the vertical axis of a 2D grid (or matrix) and the other on the horizontal. In its simplest form, a dot is placed where the horizontal and vertical sequence values match. That is a dot is produced at position (i,j) if character number i in the first sequence is the same as character number j in the second sequence. More elaborate forms use 'sliding windows' composed of multiple characters and a threshold value, or 'match stringency' for two windows to be considered as matched.

Dot Plot Parameters

Alter the parameters below to change the displayed protein and DNA dot plots. It is important to have a good feel for these parameters when we get to alignment heuristic approaches later.

Window Size:

Moving window step size:

Match stringency:

Match stringency specifies the number of match characters required per window. It should not be larger than your window size!

Protein Dot Plot
wsize = 3 wstep = 3 , nmatch = 2

DNA Dot Plot
wsize = 3 wstep = 3 , nmatch = 2

<https://bioboot.shinyapps.io/dotplot2/>

Questions for discussion:

- Why does the DNA sequence have more dots than the protein sequence plot?
- How can we increase the signal to noise ratio?
- What does a 'Match stringency' larger than 'Window size' yield and why?

ALIGNMENT FOUNDATIONS

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 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

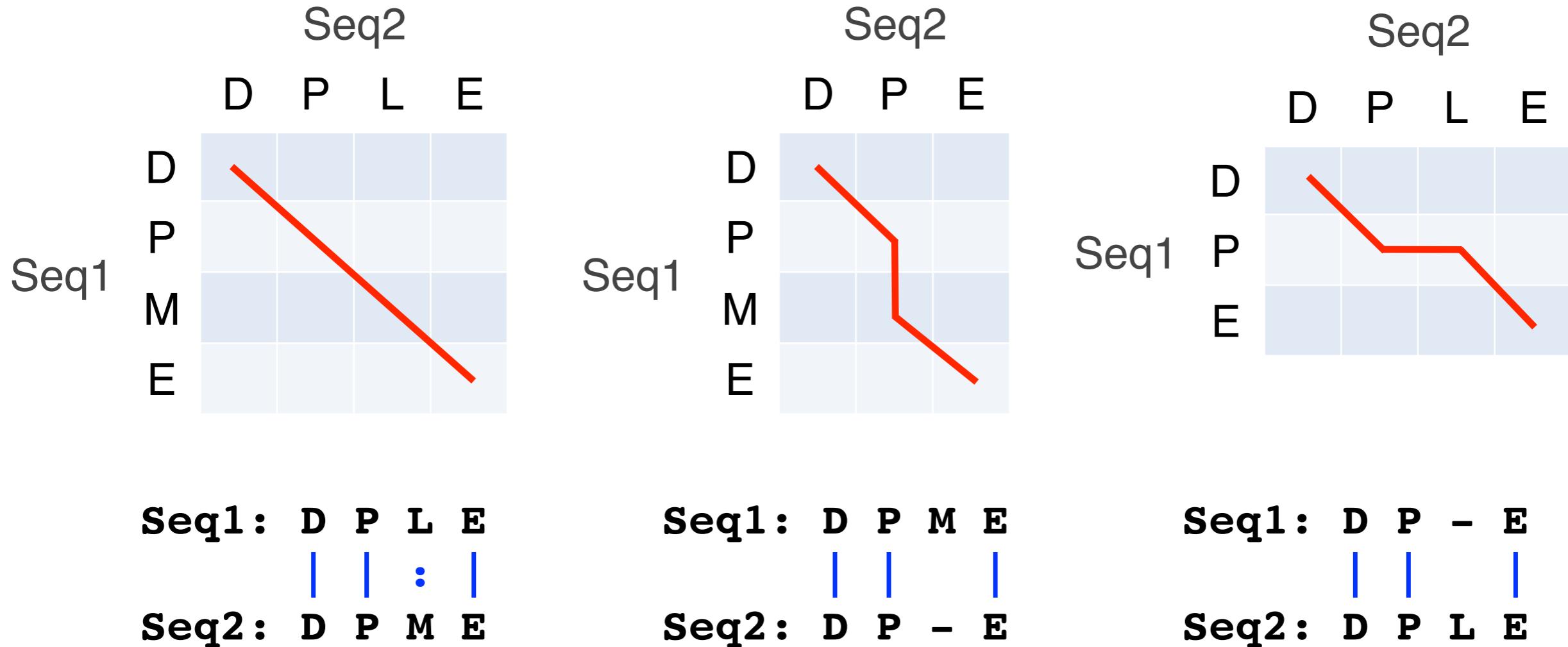
The Dynamic Programming Algorithm

- The dynamic programming algorithm can be thought of an extension to the dot plot approach
 - One sequence is placed down the side of a grid and another across the top
 - Instead of placing a dot in the grid, we compute a score for each position
 - Finding the optimal alignment corresponds to finding the path through the grid with the best possible score



Needleman, S.B. & Wunsch, C.D. (1970) “A general method applicable to the search for similarities in the amino acid sequences of two proteins.” J. Mol. Biol. 48:443-453.

Different paths represent different alignments



Matches are represented by diagonal paths &
indels with horizontal or vertical path segments

Algorithm of Needleman and Wunsch

- The Needleman–Wunsch approach to global sequence alignment has three basic steps:
 - (1) setting up a 2D-grid (or alignment matrix),
 - (2) scoring the matrix, and
 - (3) identifying the optimal path through the matrix



Needleman, S.B. & Wunsch, C.D. (1970) “A general method applicable to the search for similarities in the amino acid sequences of two proteins.” J. Mol. Biol. 48:443-453.

Scoring the alignment matrix

- Start by filling in the first row and column – these are all indels (gaps).
 - Each step you take you will add the gap penalty to the score ($S_{i,j}$) accumulated in the previous cell

		j	Sequence 2					Scores: match = +1, mismatch = -1, gap = -2		
		-	D	P	L	E				
Sequence 1		-	0	-2	-4	-6	-8			
—	-									
	D	-2								
	P	-4								
	M	-6								
	E	-8								

Scoring the alignment matrix

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		-	D	P	L	E			
Sequence 1		-	0	-2	-4	-6	-8		
—	-		0	-2	-4	-6	-8		
	D		-2						
	P		-4						
	M		-6						
	E		-8						

$S_{i+4} = (-2) + (-2) + (-2) + (-2)$

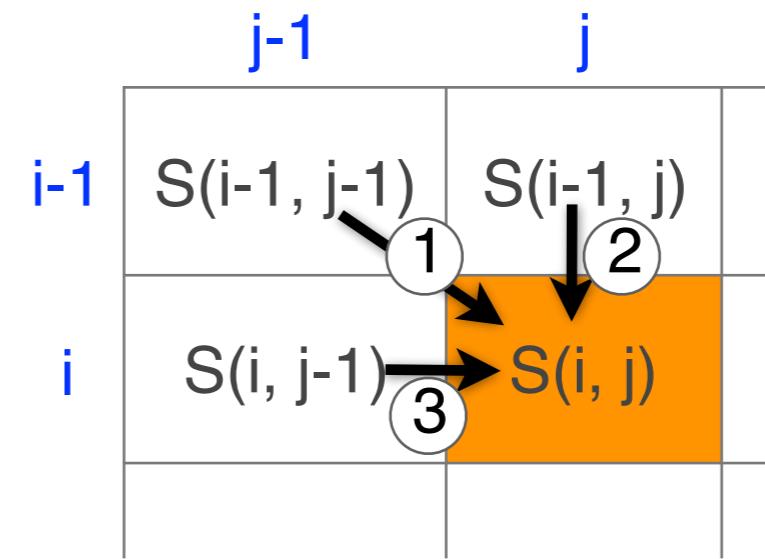
Seq1: **DPME**
Seq2: **-----**

Scoring the alignment matrix

- Then go to the empty corner cell (upper left). It has filled in values in up, left and diagonal directions
 - Now can ask which of the three directions gives the highest score?
 - keep track of this score and direction

		j			
		D	P	L	E
-		-2	-4	-6	-8
-	D	-2	?		
P		-4			
M		-6			
E		-8			

Scores: match = +1, mismatch = -1, gap = -2



Scoring the alignment matrix

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		j				
		D	P	L	E	
-		0	-2	-4	-6	-8
D	-2	?				
P	-4					
M	-6					
E	-8					

Scores: match = +1, mismatch = -1, gap = -2

$$S(i, j) = \text{Max} \begin{cases} S(i-1, j-1) + (\text{mis})\text{match} \\ S(i-1, j) + \text{gap penalty} \\ S(i, j-1) + \text{gap penalty} \end{cases}$$

1
2
3

Scoring the alignment matrix

- Then go to the empty corner cell (upper left). It has filled in values in up, left and diagonal directions
 - Now can ask which direction gives the highest score
 - keep track of direction and score

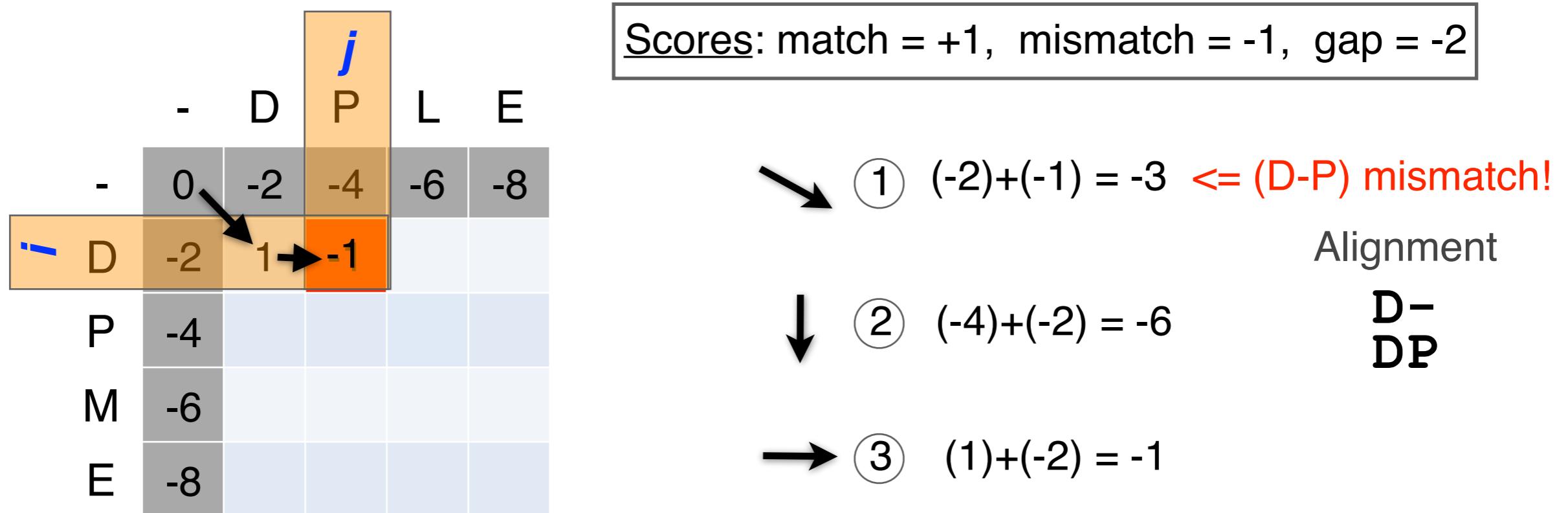
		j				
		D	P	L	E	
-		0	-2	-4	-6	-8
-	D	-2	1			
P	-4					
M	-6					
E	-8					

Scores: match = +1, mismatch = -1, gap = -2

- Alignment D
D
- ① $(0) + (+1) = +1 \leq (D-D) \text{ match!}$
- ② $(-2) + (-2) = -4$
- ③ $(-2) + (-2) = -4$

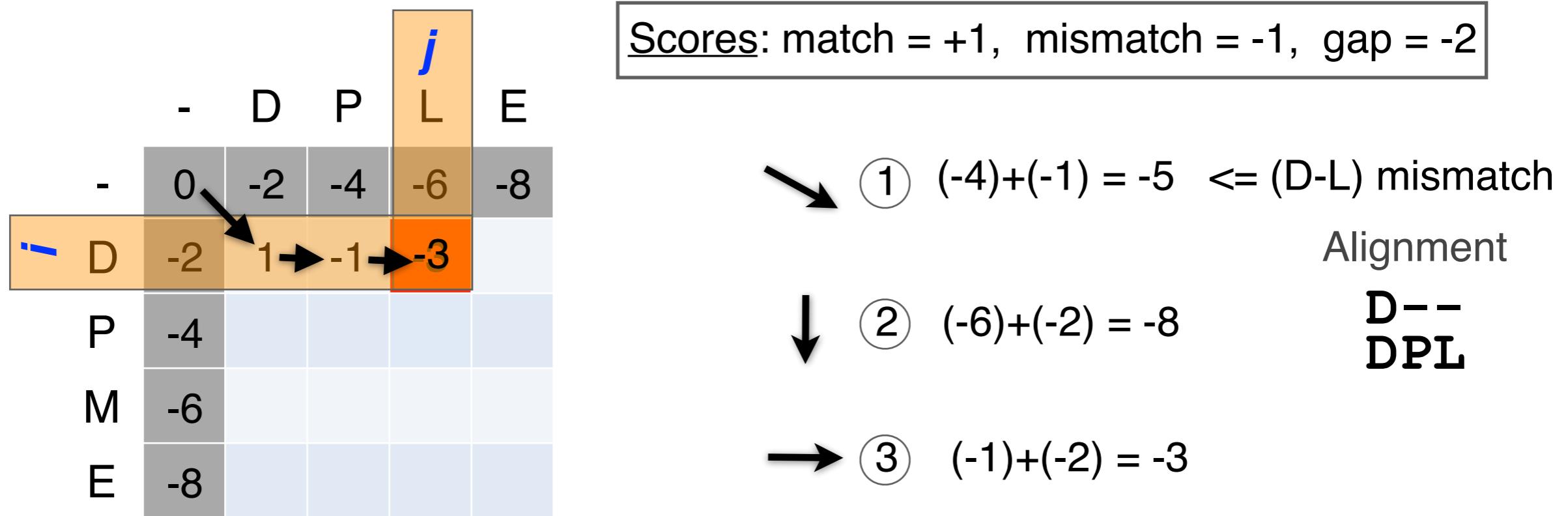
Scoring the alignment matrix

- At each step, the score in the current cell is determined by the scores in the neighboring cells
 - The maximal score and the direction that gave that score is stored (we will use these later to determine the optimal alignment)



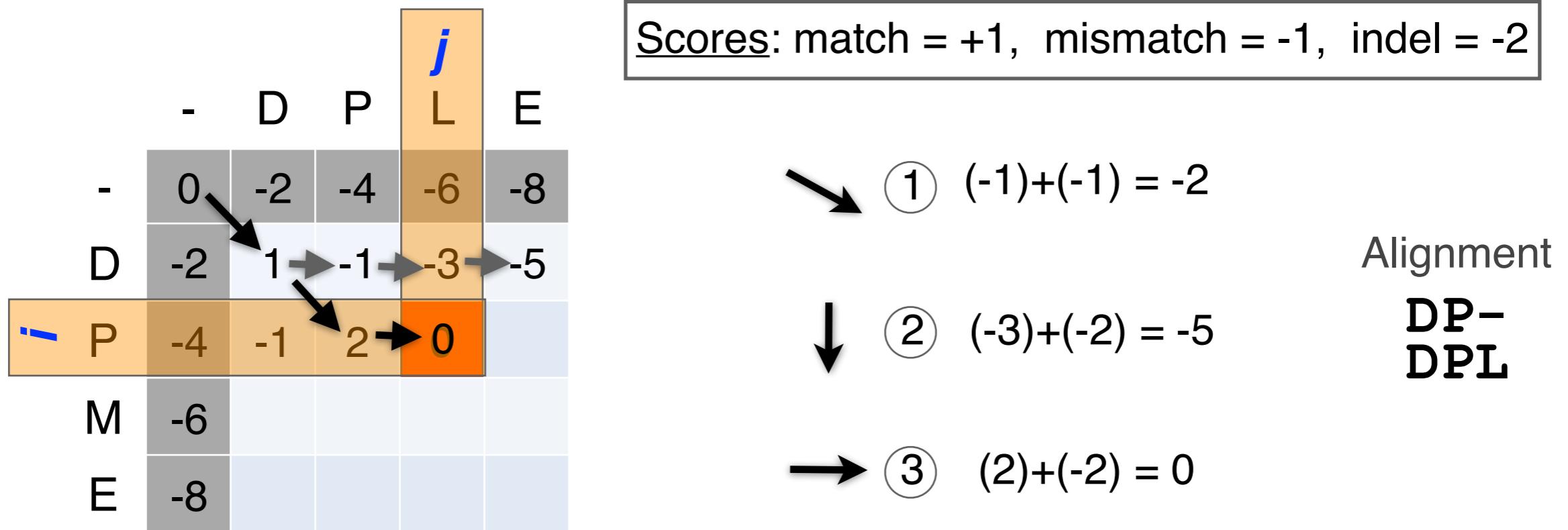
Scoring the alignment matrix

- We will continue to store the alignment score ($S_{i,j}$) for all possible alignments in the alignment matrix.



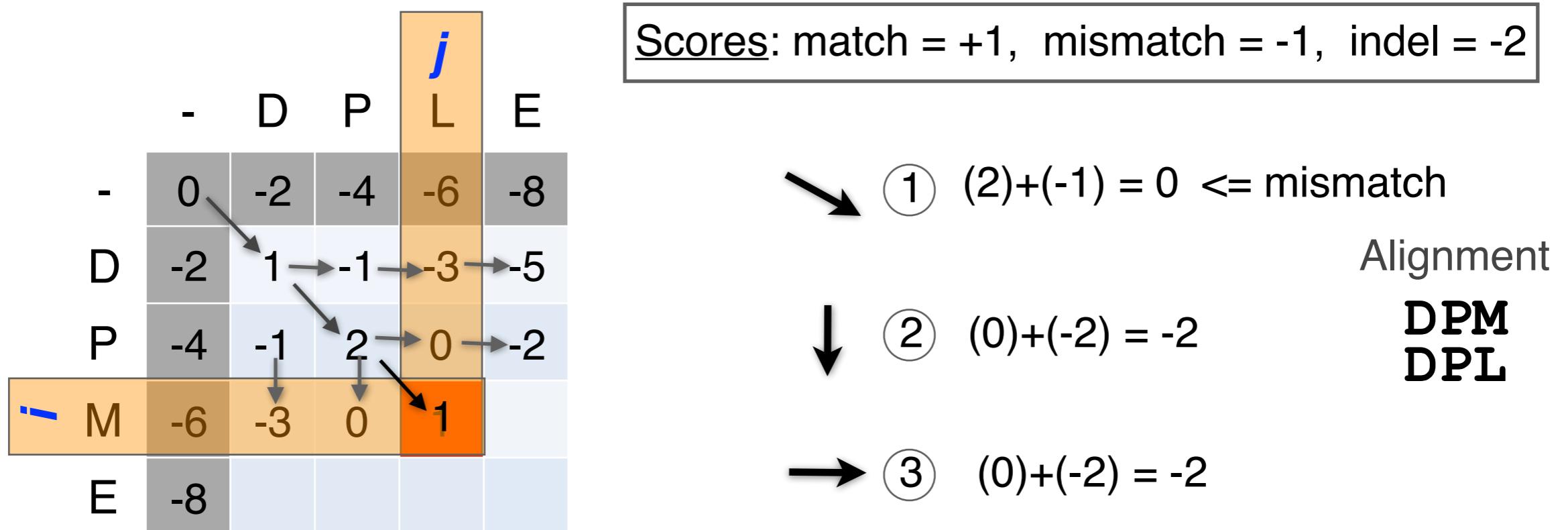
Scoring the alignment matrix

- For the highlighted cell, the corresponding score ($S_{i,j}$) refers to the score of the optimal alignment of the first i characters from sequence1, and the first j characters from sequence2.



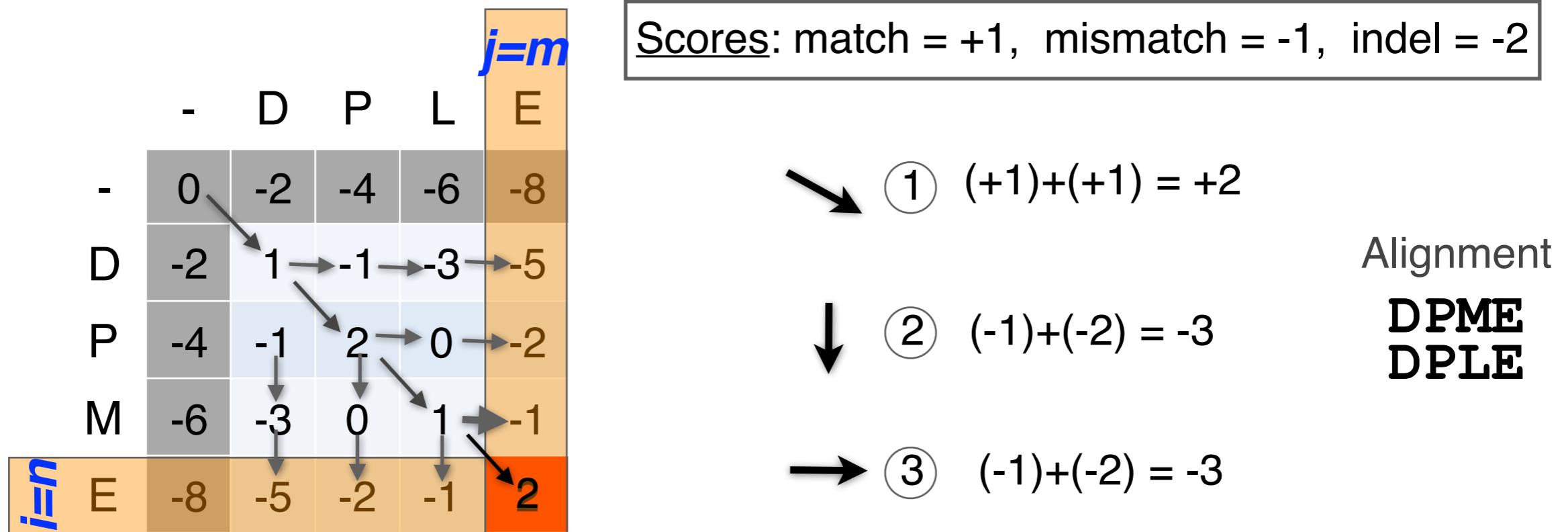
Scoring the alignment matrix

- At each step, the score in the current cell is determined by the scores in the neighboring cells
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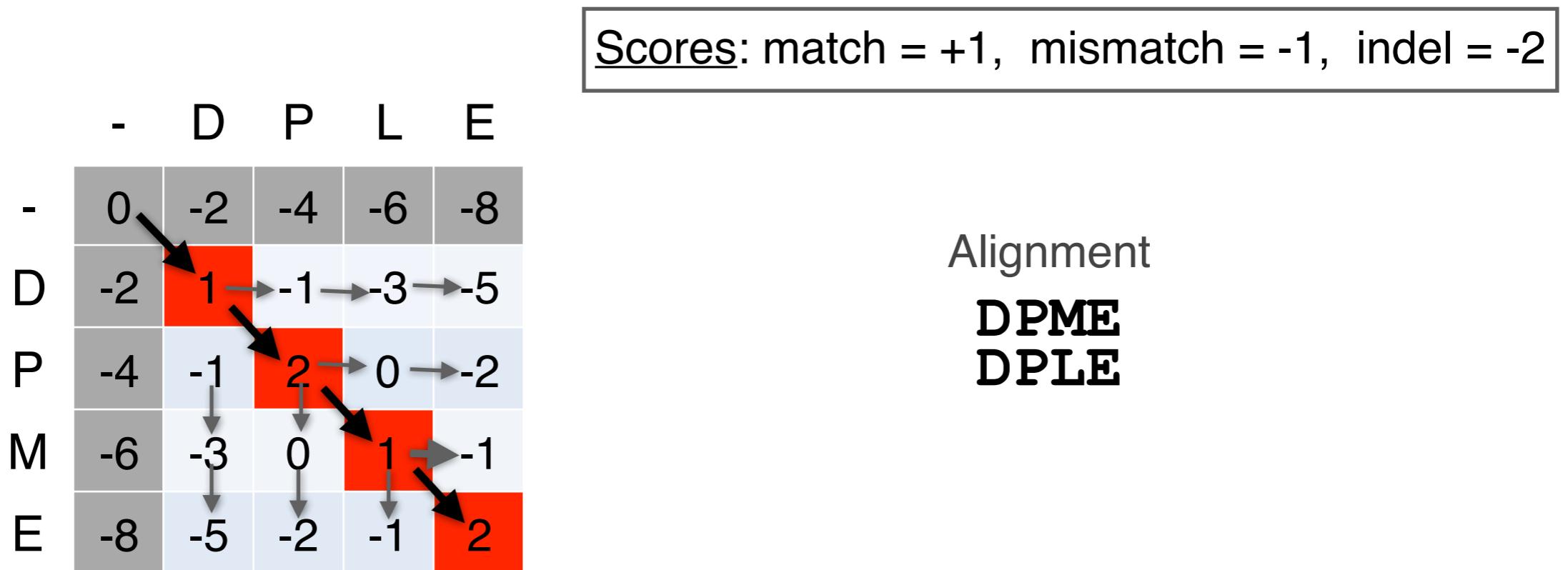
Scoring the alignment matrix

- The score of the best alignment of the entire sequences corresponds to $S_{n,m}$
 - (where n and m are the length of the sequences)



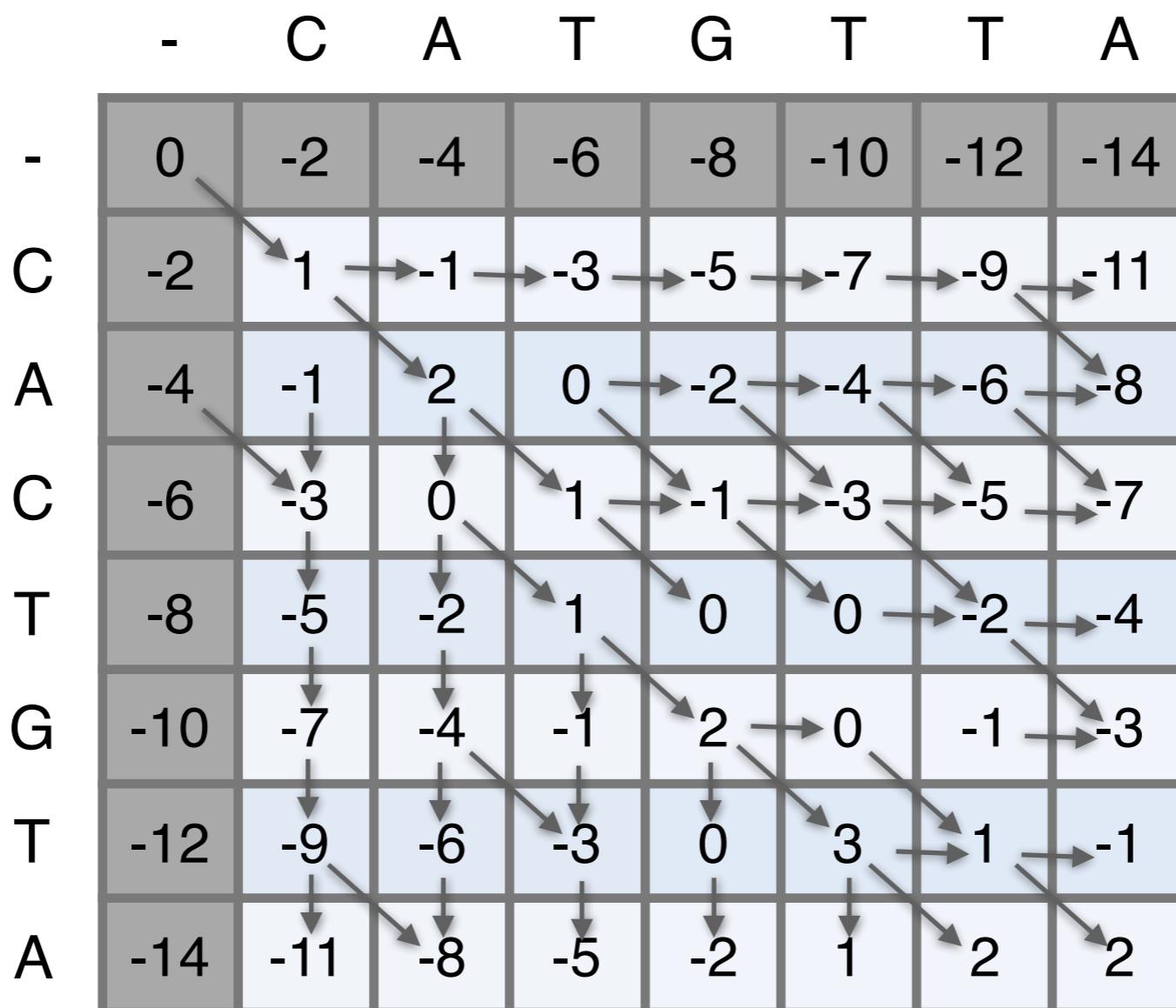
Scoring the alignment matrix

- To find the best alignment, we retrace the arrows starting from the bottom right cell
 - N.B. The optimal alignment score and alignment are dependent on the chosen scoring system



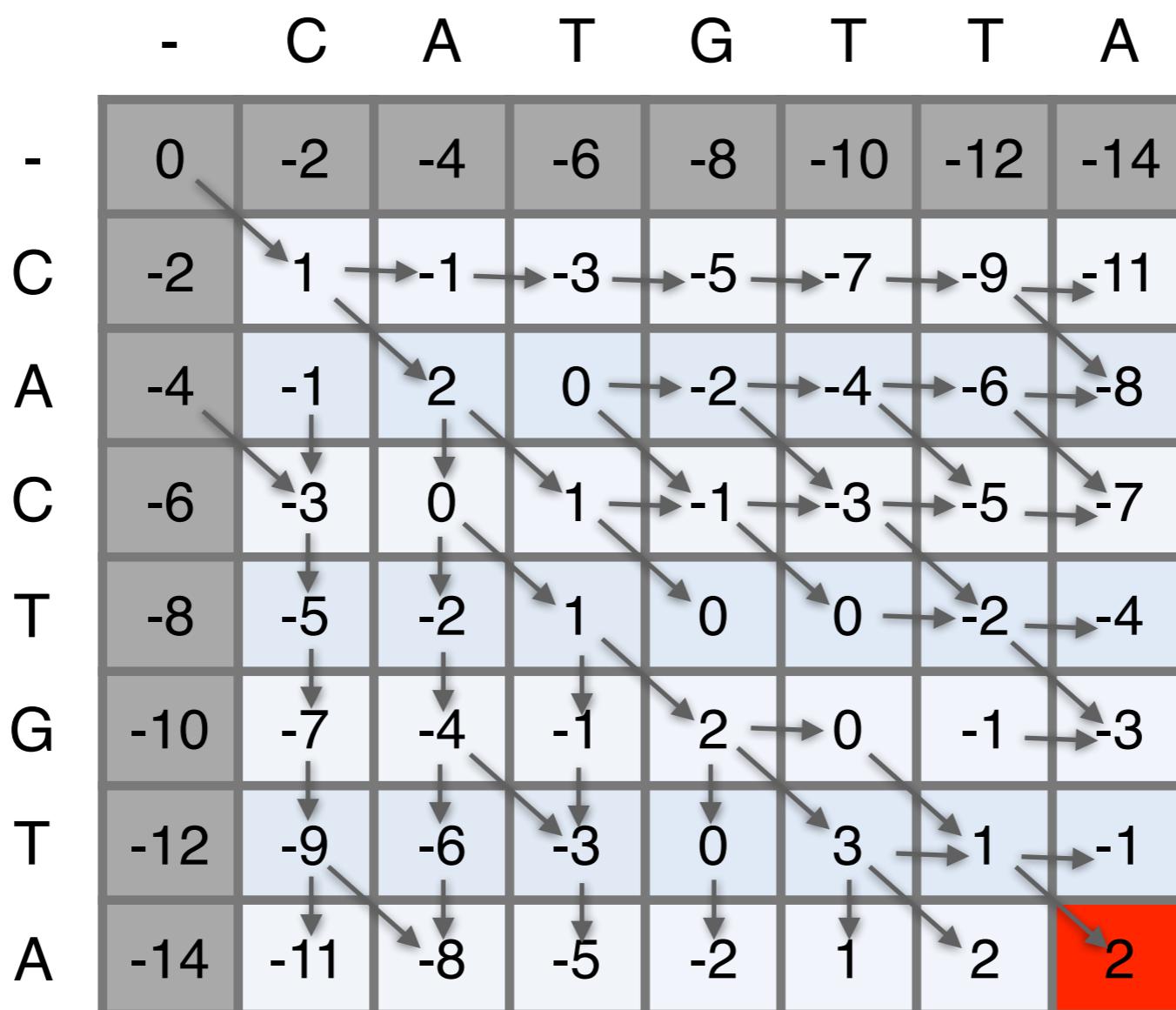
Questions:

- What is the optimal score for the alignment of these sequences and how do we find the optimal alignment?



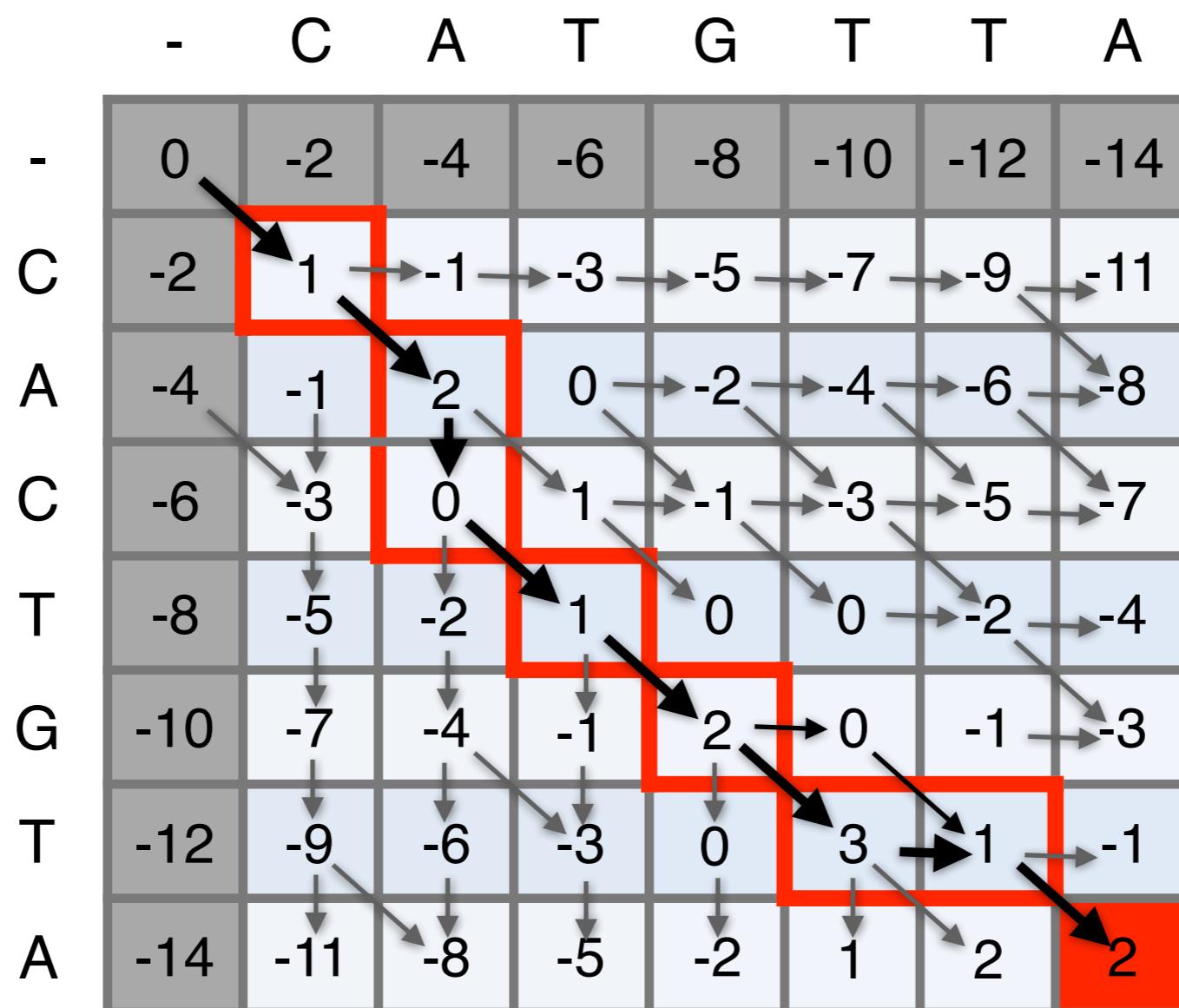
Questions:

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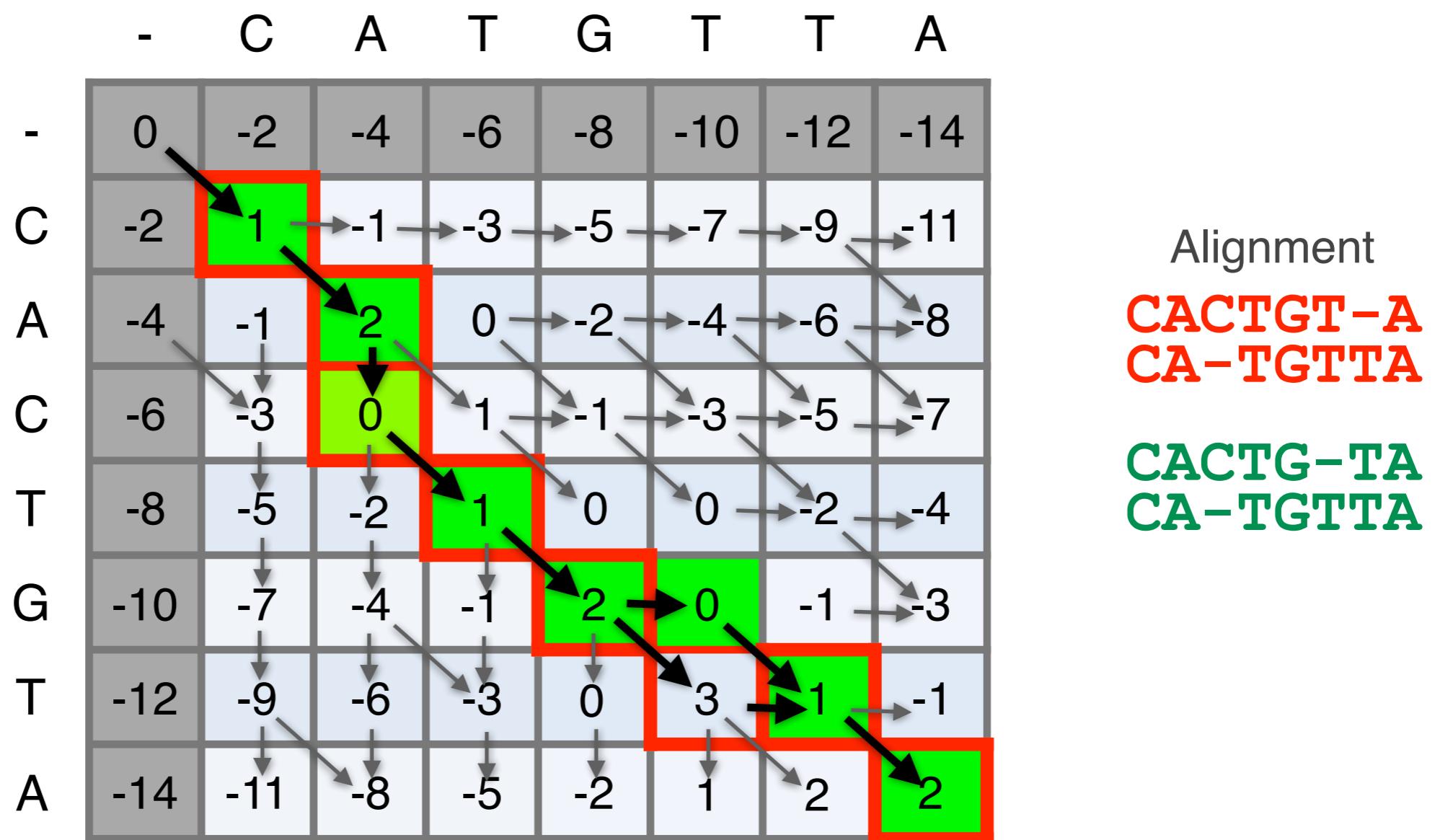
Questions:

- To find the best alignment we retrace the arrows starting from the bottom right cell



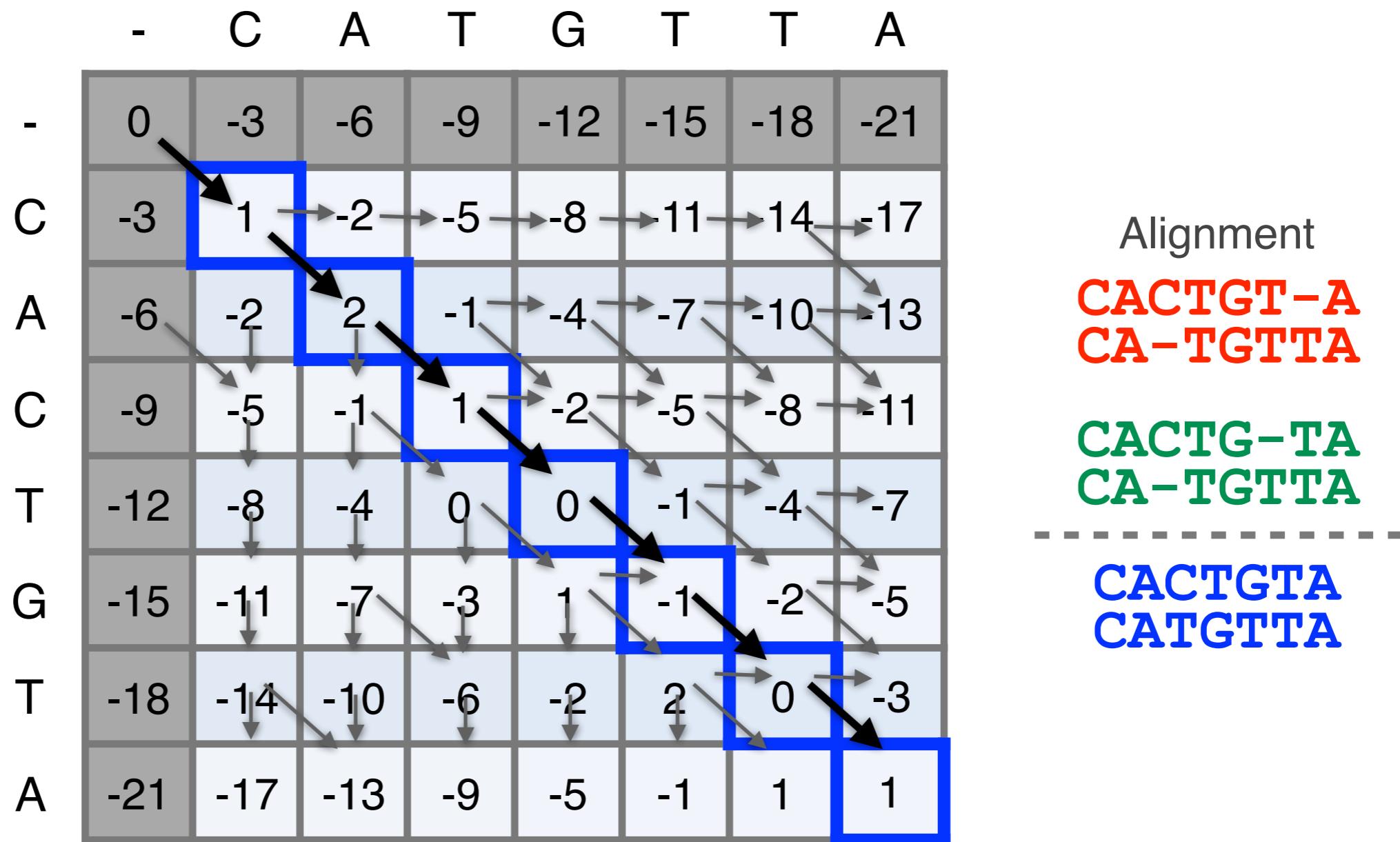
More than one alignment possible

- Sometimes more than one alignment can result in the same optimal score



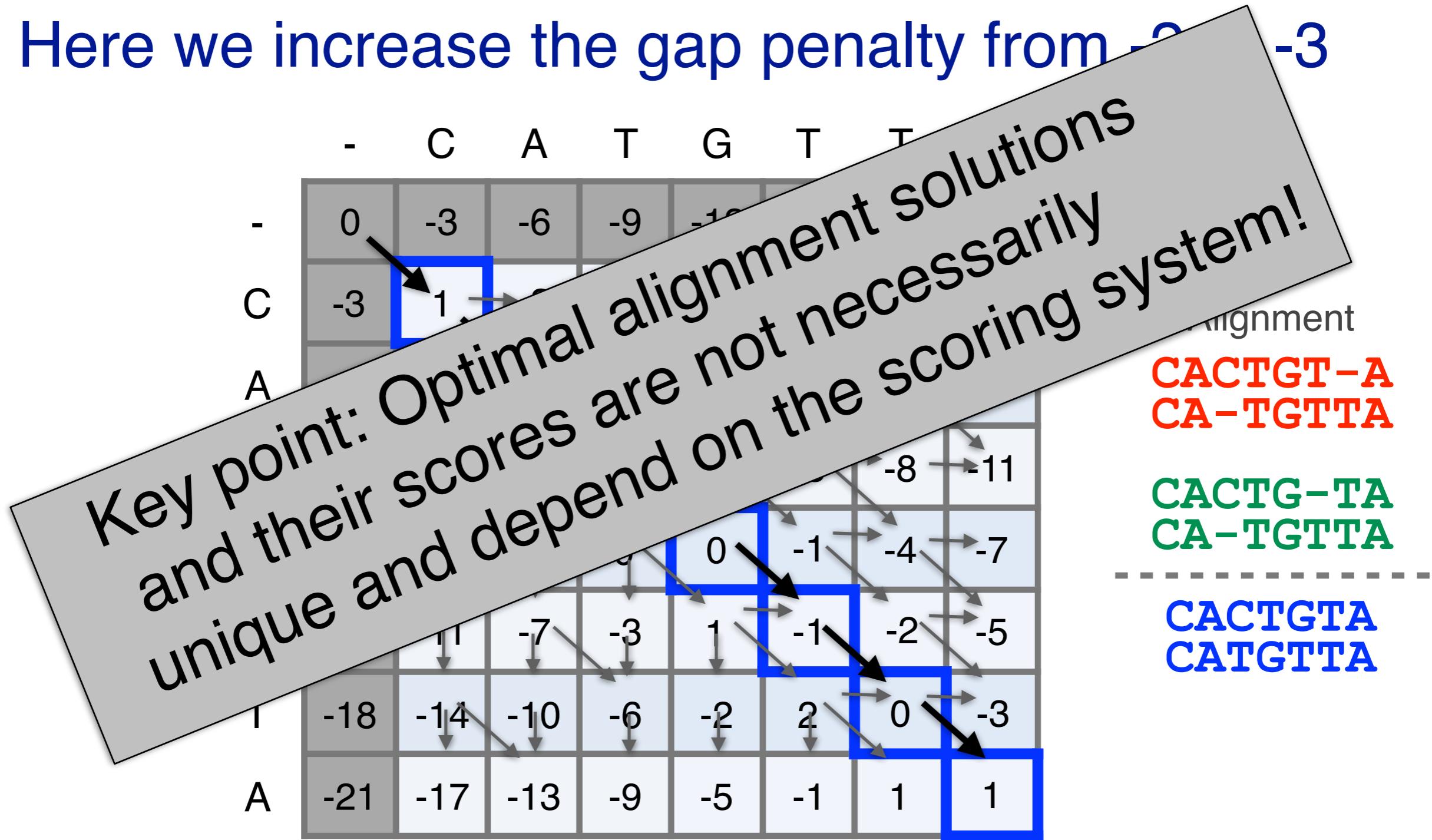
The alignment and score are dependent on the scoring system

- Here we increase the gap penalty from -2 to -3



The alignment and score are dependent on the scoring system

- Here we increase the gap penalty from -9 to -3



NW DYNAMIC PROGRAMMING

Match: +2

Mismatch: -1

Gap: -2

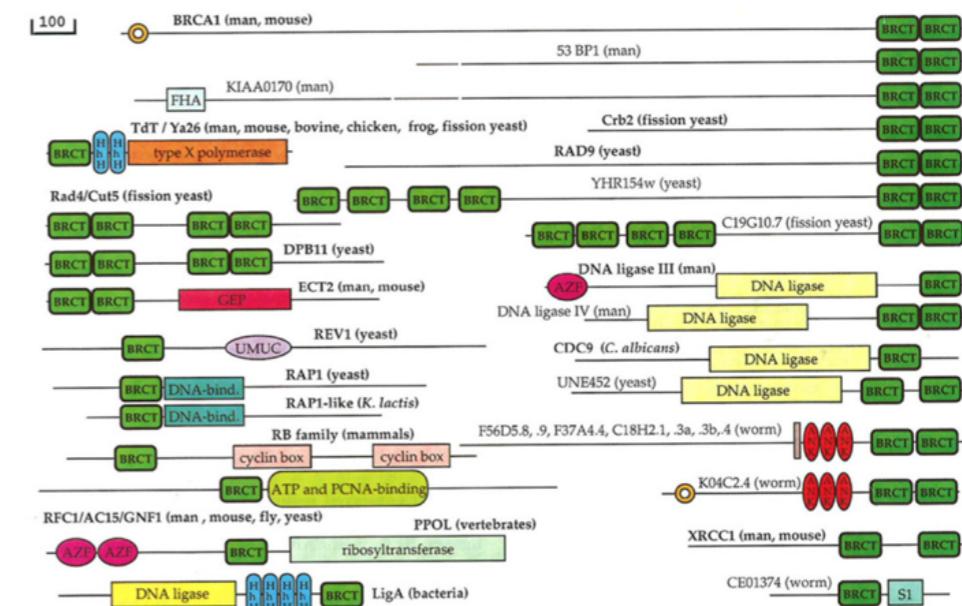
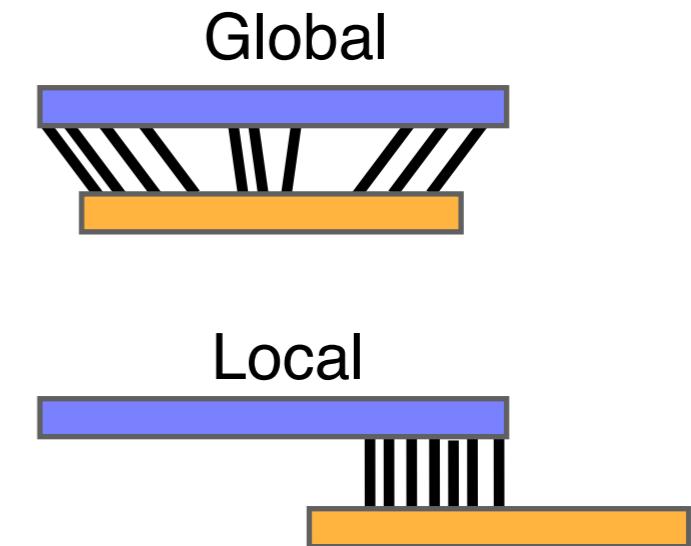
	A	G	T	T	C
A	0				
T					
T					
G					
C					

ALIGNMENT FOUNDATIONS

- **Why...**
 - Why compare biological sequences?
- **What...**
 - Alignment view of sequence changes during evolution
(matches, mismatches and gaps)
- **How...**
 - ▶ Dot matrices
 - ▶ Dynamic programming
 - Global alignment
 - Local alignment
 - ▶ BLAST heuristic approach

Global vs local alignments

- Needleman-Wunsch is a global alignment algorithm
 - Resulting alignment spans the complete sequences end to end
 - This is appropriate for closely related sequences that are similar in length
- For many practical applications we require local alignments
 - Local alignments highlight sub-regions (e.g. protein domains) in the two sequences that align well



Local alignment: Definition

- Smith & Waterman proposed simply that a local alignment of two sequences allow arbitrary-length segments of each sequence to be aligned, with no penalty for the unaligned portions of the sequences.
Otherwise, the score for a local alignment is calculated the same way as that for a global alignment

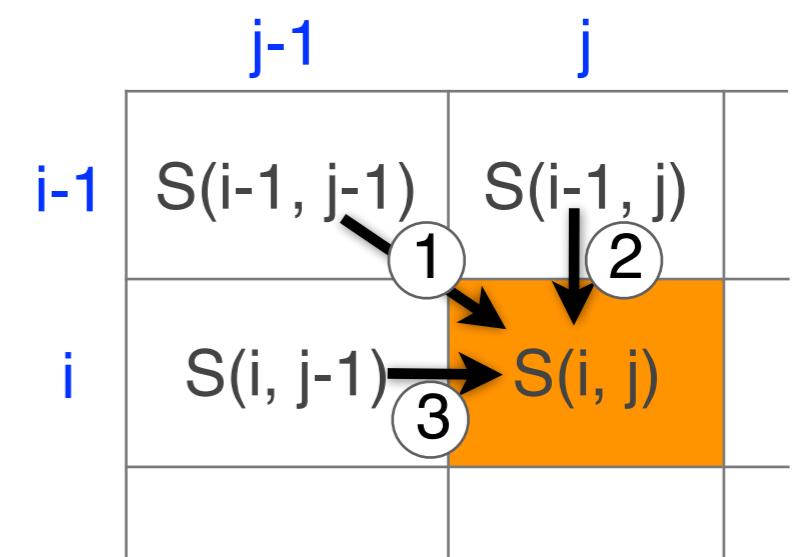
Smith, T.F. & Waterman, M.S. (1981) “Identification of common molecular subsequences.” J. Mol. Biol. 147:195-197.

The Smith-Waterman algorithm

- Three main modifications to Needleman-Wunsch:
 - Allow a node to start at 0
 - The score for a particular cell cannot be negative
 - if all other score options produce a negative value, then a zero must be inserted in the cell
 - Record the highest- scoring node, and trace back from there

$$S(i, j) = \text{Max} \left\{ \begin{array}{l} S(i-1, j-1) + (\text{mis})\text{match} \\ S(i-1, j) - \text{gap penalty} \\ S(i, j-1) - \text{gap penalty} \\ 0 \end{array} \right\}$$

(1)
(2)
(3)
(4)



Sequence 1

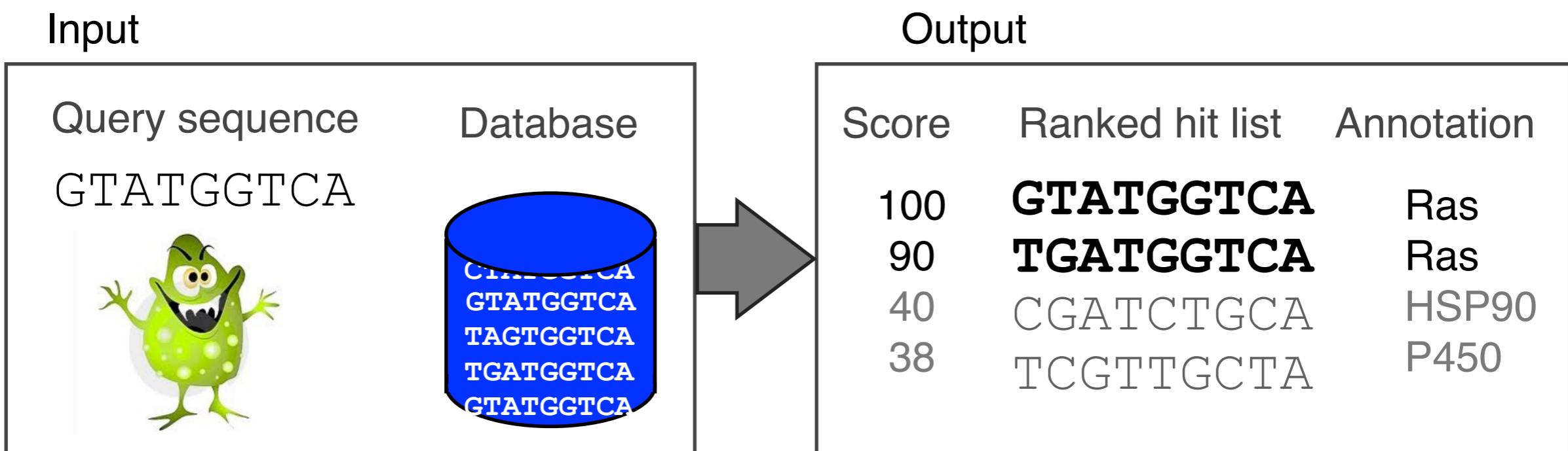
	-	C	A	G	C	C	U	C	G	C	U	U	A	G
-	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
A	0.0	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.0
A	0.0	0.0	1.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	1.0	0.7
U	0.0	0.0	0.0	0.7	0.3	0.0	1.0	0.0	0.0	0.0	1.0	1.0	0.0	0.7
G	0.0	0.0	0.0	1.0	0.3	0.0	0.0	0.7	1.0	0.0	0.0	0.7	0.7	1.0
C	0.0	1.0	0.0	0.0	2.0	1.3	0.3	1.0	0.3	2.0	0.7	0.3	0.3	0.3
C	0.0	1.0	0.7	0.0	1.0	3.0	1.7	1.3	1.0	1.3	1.7	0.3	0.0	0.0
A	0.0	0.0	2.0	0.7	0.3	1.7	2.7	1.3	1.0	0.7	1.0	1.3	1.3	0.0
U	0.0	0.0	0.7	1.7	0.3	1.3	2.7	2.3	1.0	0.7	1.7	2.0	1.0	1.0
U	0.0	0.0	0.3	0.3	1.3	1.0	2.3	2.3	2.0	0.7	1.7	2.7	1.7	1.0
G	0.0	0.0	0.0	1.3	0.0	1.0	1.0	2.0	3.3	2.0	1.7	1.3	2.3	2.7
A	0.0	0.0	1.0	0.0	1.0	0.3	0.7	0.7	2.0	3.0	1.7	1.3	2.3	2.0
C	0.0	1.0	0.0	0.7	1.0	2.0	0.7	1.7	1.7	3.0	2.7	1.3	1.0	2.0
G	0.0	0.0	0.7	1.0	0.3	0.7	1.7	0.3	2.7	1.7	2.7	2.3	1.0	2.0
G	0.0	0.0	0.0	1.7	0.7	0.3	0.3	1.3	1.3	2.3	1.3	2.3	2.0	2.0

Local alignment

GCC–UCG**GCCAUUG**

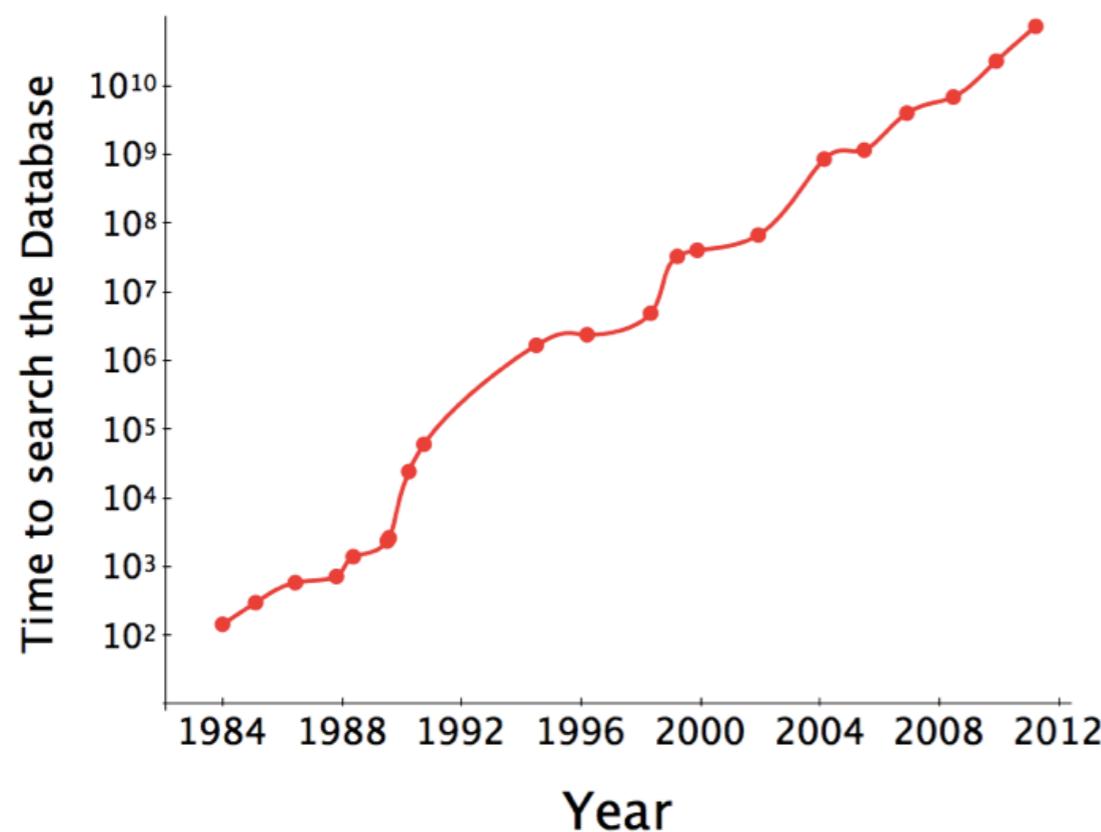
Local alignments can be used for database searching

- Goal: Given a query sequence (Q) and a sequence database (D), find a list of sequences from D that are most similar to Q
 - Input: Q, D and scoring scheme
 - Output: Ranked list of hits



The database search problem

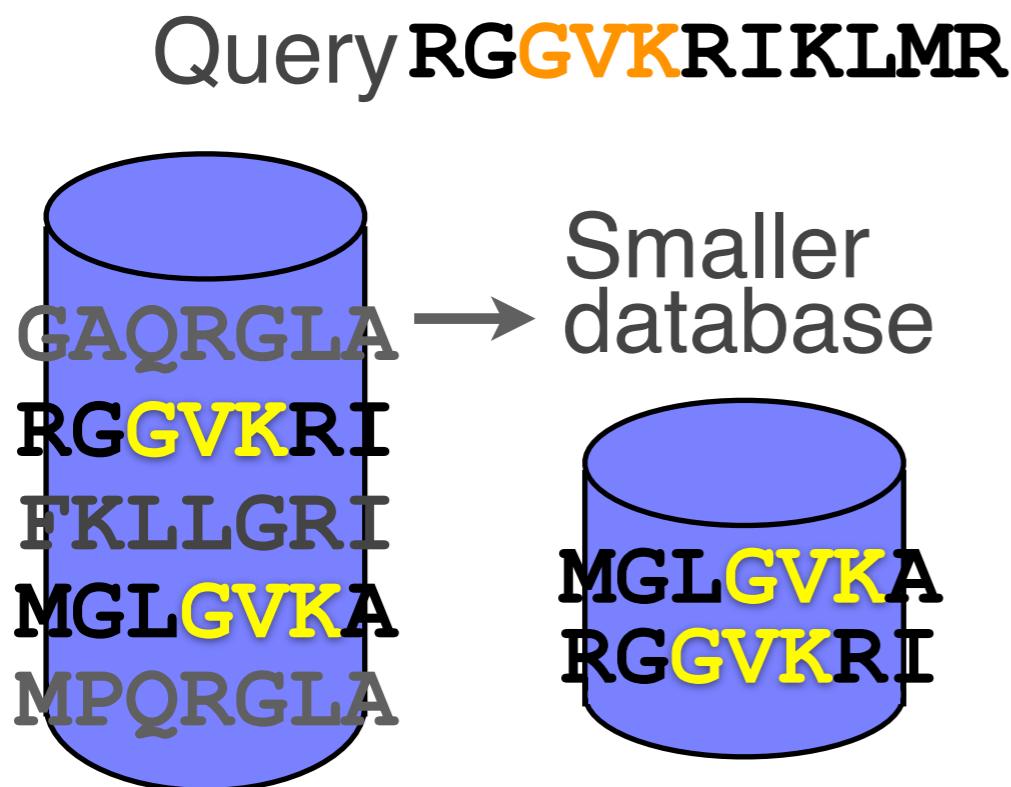
- Due to the rapid growth of sequence databases, search algorithms have to be both efficient and sensitive
 - Time to search with SW is proportional to $m \times n$ (m is length of query, n is length of database), too slow for large databases!



To reduce search time heuristic algorithms, such as BLAST, first remove database sequences without a strong local similarity to the query sequence in a quick initial scan.

The database search problem

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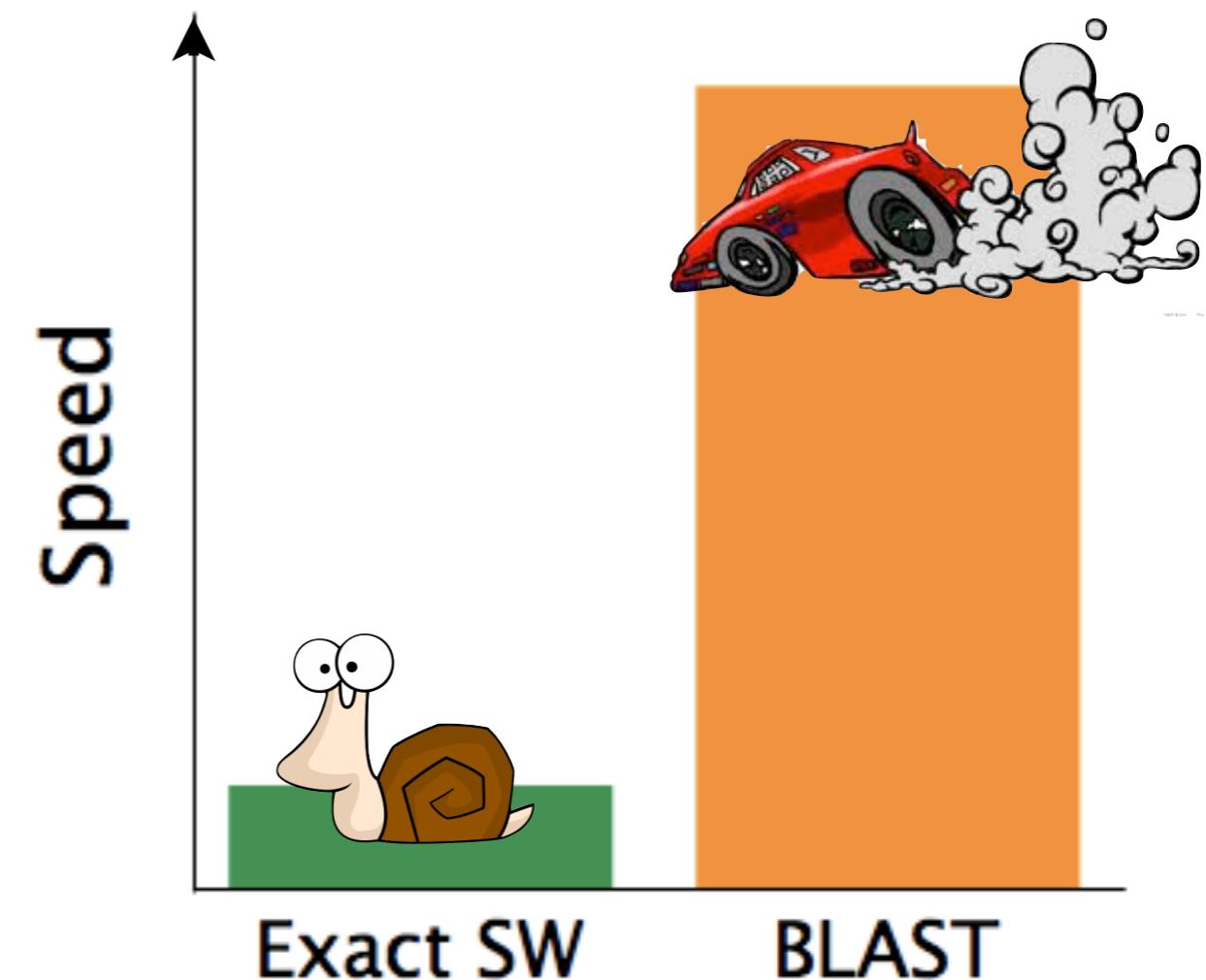
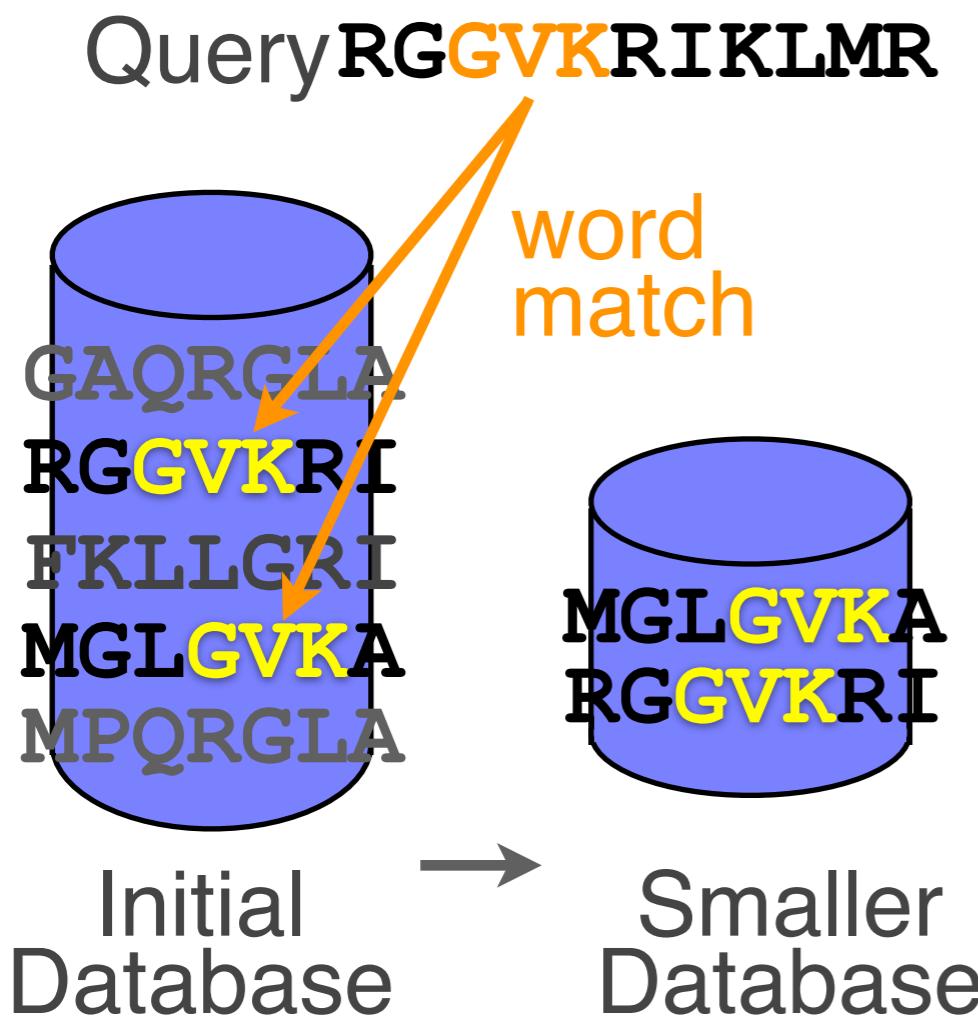
Rapid, heuristic versions of Smith–Waterman: BLAST

- BLAST (Basic Local Alignment Search Tool) is a simplified form of Smith-Waterman (SW) alignment that is popular because it is fast and easily accessible
 - BLAST is a heuristic approximation to SW - It examines only part of the search space
 - BLAST saves time by restricting the search by scanning database sequences for likely matches before performing more rigorous alignments
 - Sacrifices some sensitivity in exchange for speed
 - In contrast to SW, BLAST is not guaranteed to find optimal alignments

Rapid, heuristic versions of Smith–Waterman: BLAST

- BLAST (Basic Local Alignment Search T)
simplified form of Smith-Waterman
that is popular because it is fast
 - BLAST finds regions of similarity between two sequences
 - BLAST uses a “seed” approach to sequence pairs that contain an initial word pair match
- “The central idea of the BLAST algorithm is to confine attention to sequence pairs that contain an initial word pair match”
Altschul et al. (1990)
- The search by scanning for local matches before performing alignments
- Some sensitivity in exchange for speed
- In contrast to SW, BLAST is not guaranteed to find optimal alignments

- BLAST uses this pre-screening heuristic approximation resulting in an approach that is about 50 times faster than the Smith-Waterman



How BLAST works

- Four basic phases
 - Phase 1: compile a list of query word pairs ($w=3$)

generate list
of $w=3$ words
for query

RGGVKRI Query sequence

RGG

GGV

GVK

VKR

KRI

Blast

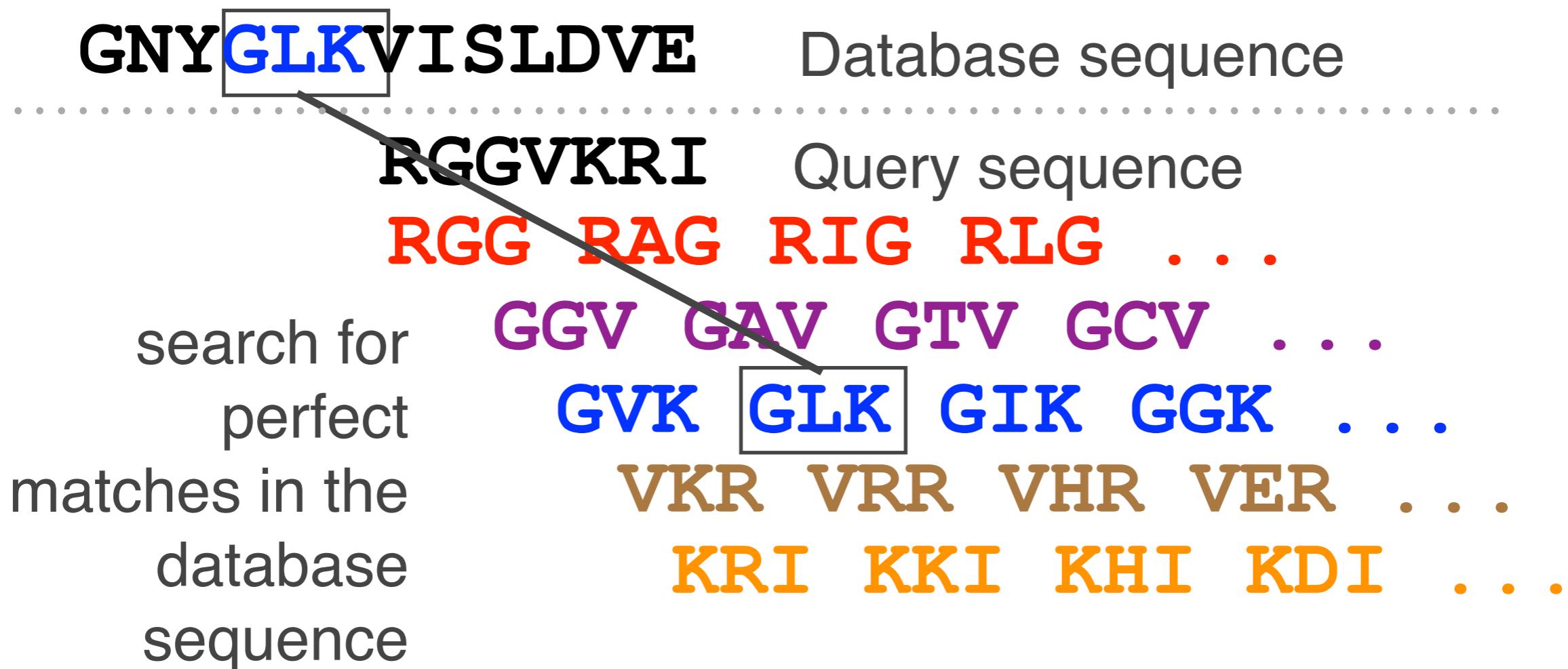
- Phase 2: expand word pairs to include those similar to query (defined as those above a similarity threshold to original word, i.e. match scores in substitution matrix)

extend list of
words similar
to query

RGGVKRI Query sequence
RGG RAG RIG RLG . . .
GGV GAV GTV GCV . . .
GVK GAK GIK GGK . . .
VKR VRR VHR VER . . .
KRI KKI KHI KDI . . .

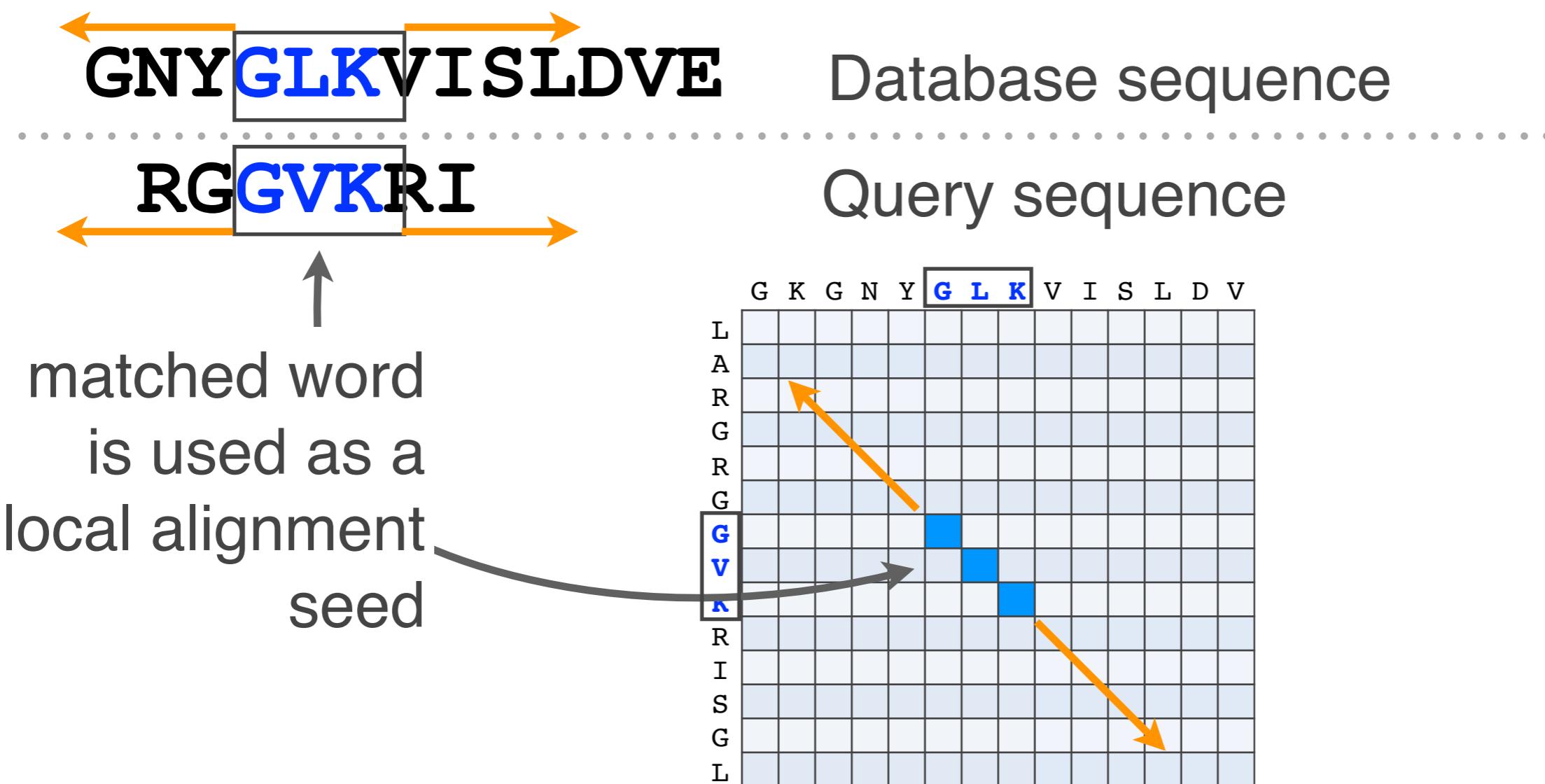
Blast

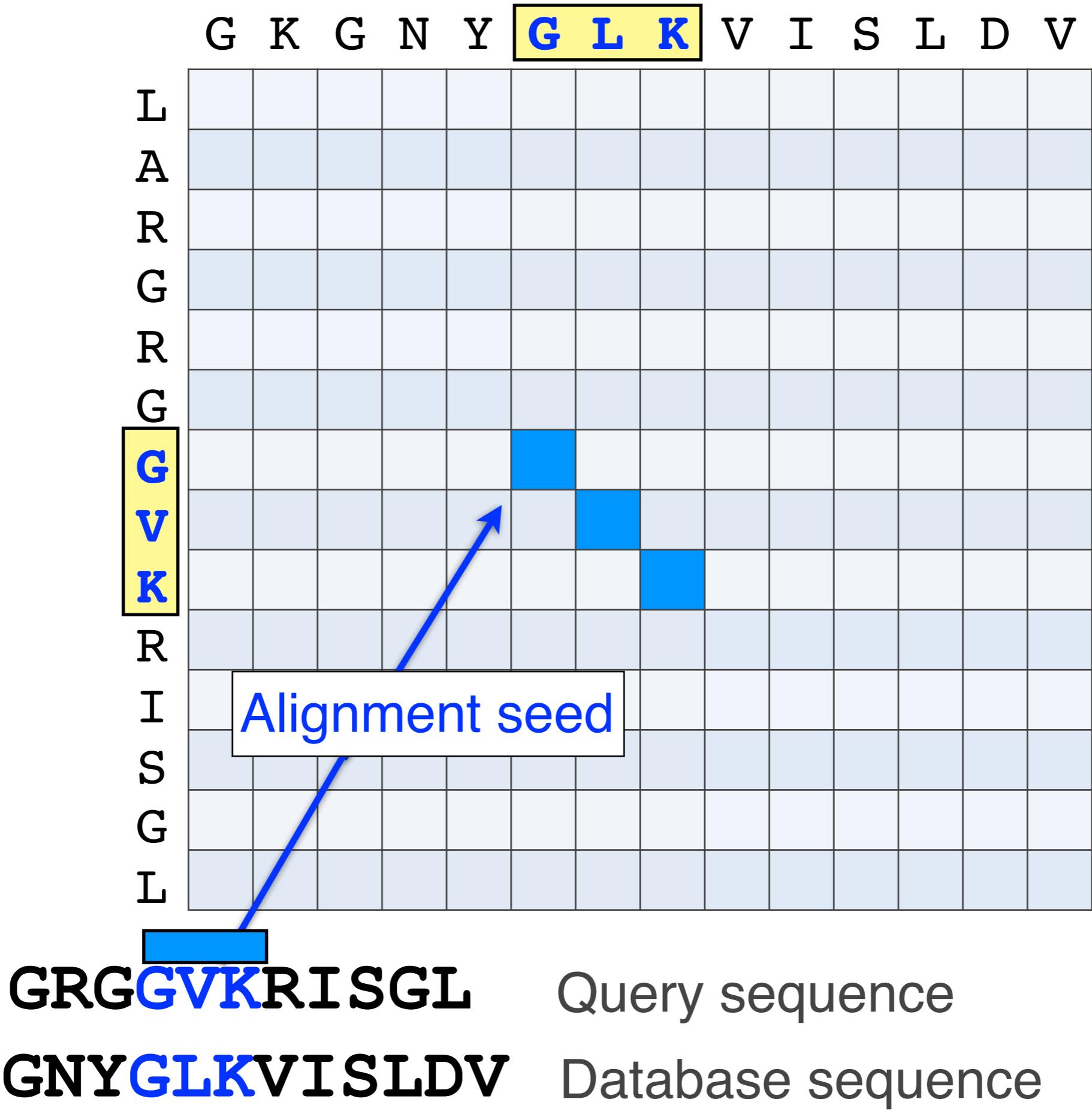
- Phase 3: a database is scanned to find sequence entries that match the compiled word list

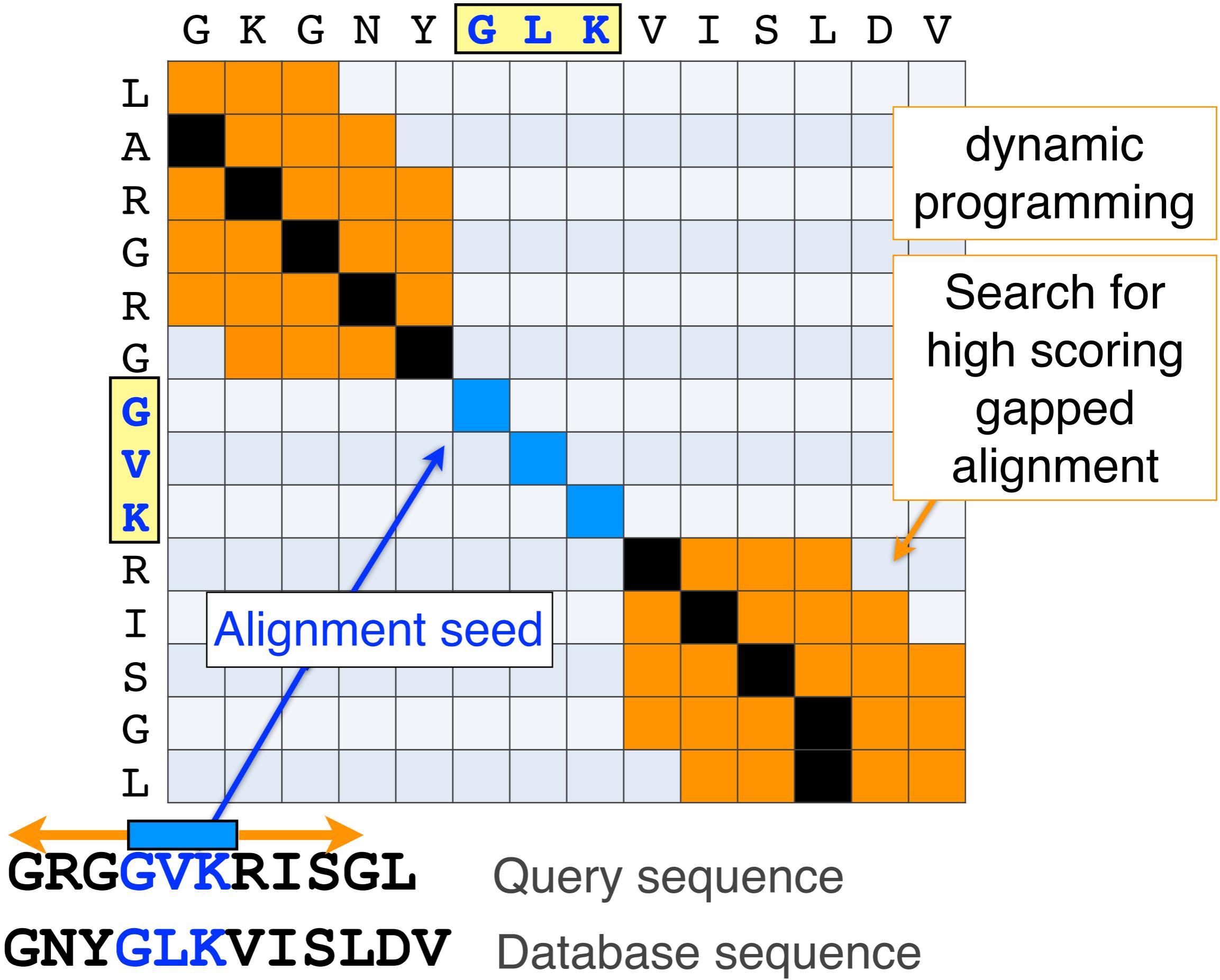


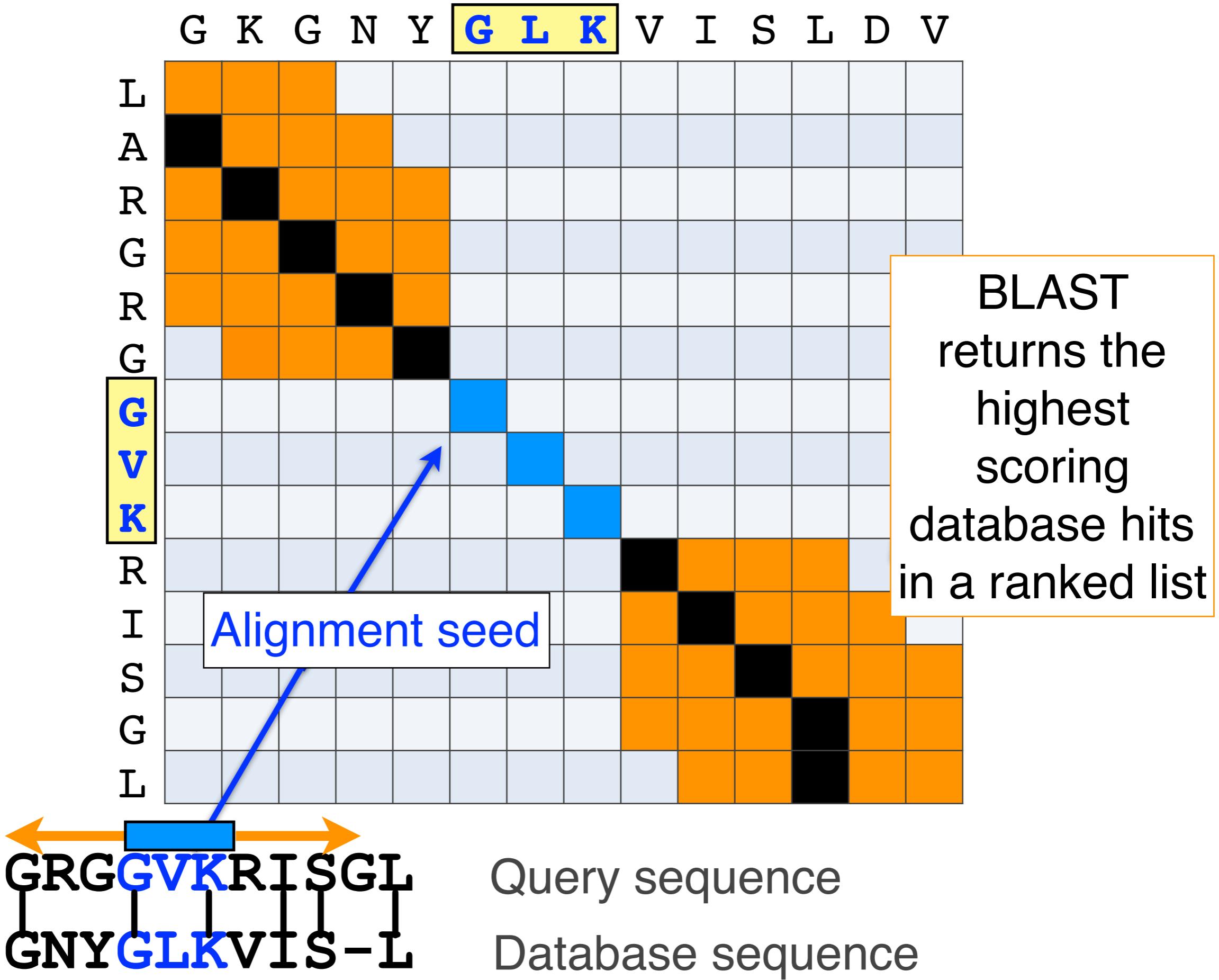
Blast

- Phase 4: the initial database hits are extended in both directions using dynamic programming









BLAST output

- BLAST returns the highest scoring database hits in a ranked list along with details about the target sequence and alignment statistics

Description	Max score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	100%	0	98%	AAA20133.1
Kinesin-14 heavy chain [Danio rerio]	595	88%	0	78%	XP_00320703
hypothetical protein EGK_18589	48.2	40%	0.03	32%	ELK35081.1
mKIAA4102 protein [Mus musculus]	42.7	38%	3.02	24%	EHH28205.1

Statistical significance of results

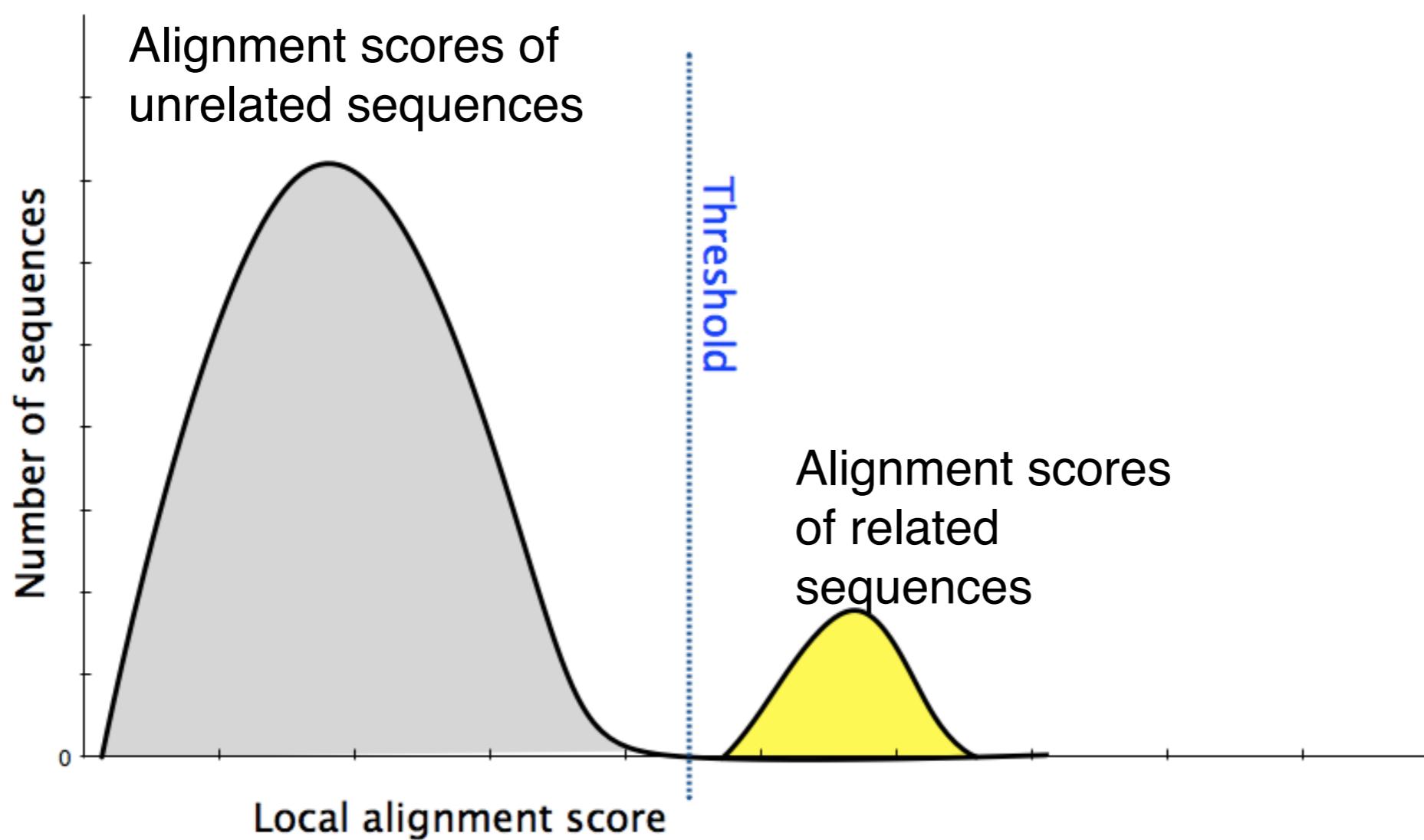
- An important feature of BLAST is the computation of statistical significance for each hit. This is described by the E value (expect value)

Description	Max score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	100%	0	98%	AAA20133.1
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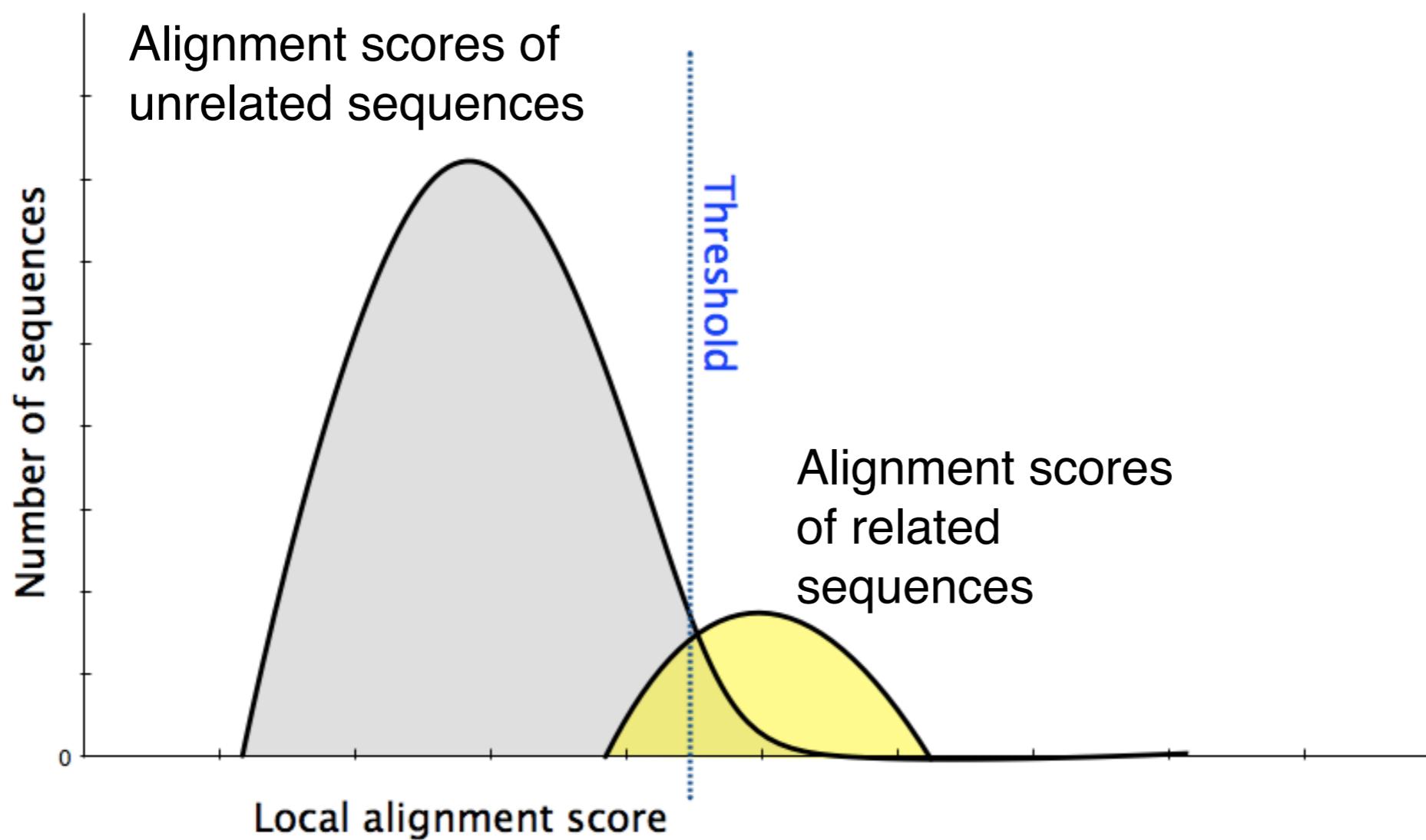
BLAST scores and E-values

- The E value is the expected number of hits that are as good or better than the observed local alignment score (with this score or better) if the query and database are random with respect to each other
 - i.e. the number of alignments expected to occur by chance with equivalent or better scores
- Typically, only hits with E value below a significance threshold are reported
 - This is equivalent to selecting alignments with score above a certain score threshold

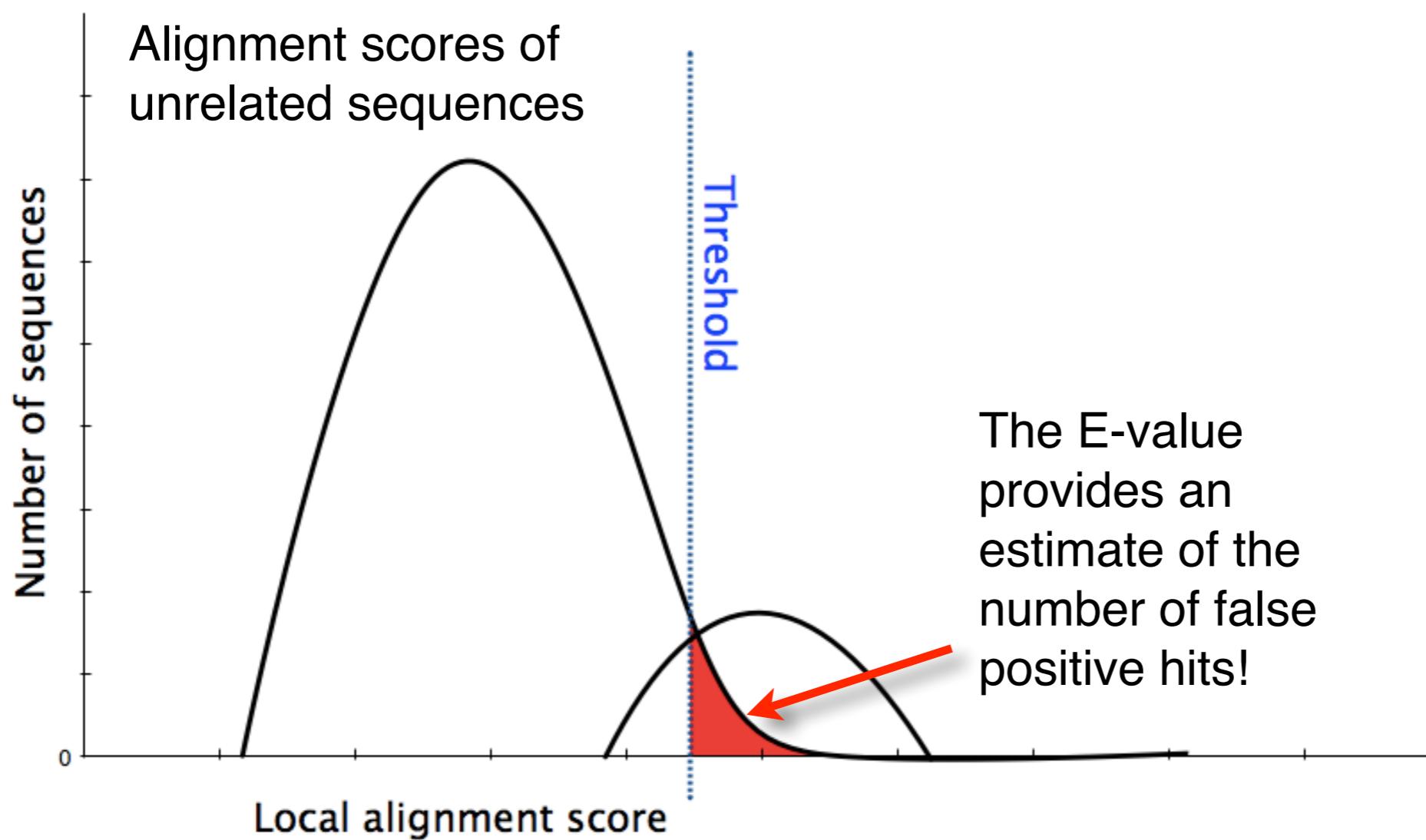
- Ideally, a threshold separates all query related sequences (yellow) from all unrelated sequences (gray)



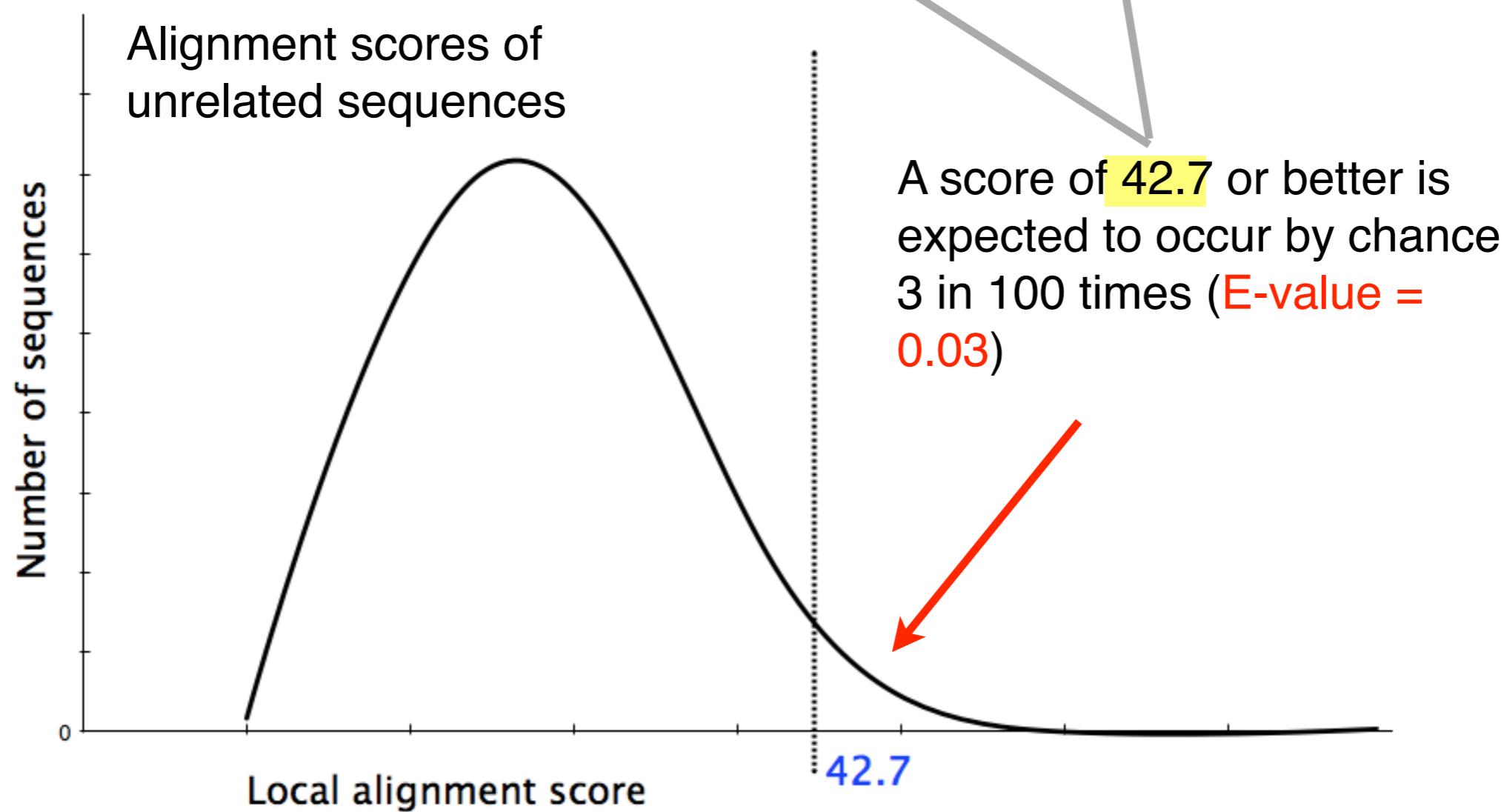
- Unfortunately, often both score distributions overlap
 - The E value describes the expected number of hits with a score above the threshold if the query and database are unrelated



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 - The E value describes the expected number of hits with a score above the threshold if the query and database are unrelated



Description	Max score	Query cover	E value	Max ident	Accession
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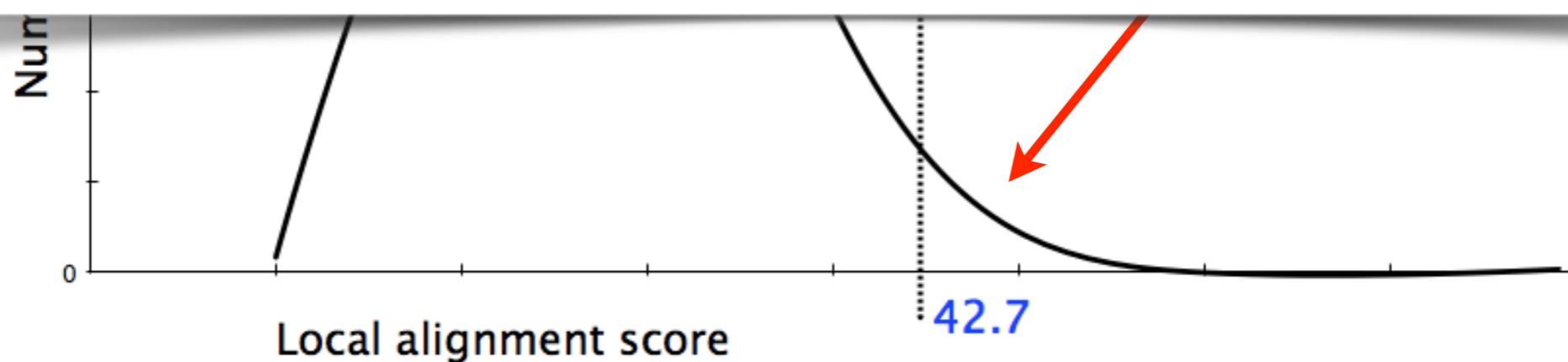


Description	Max score	Total score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo sapiens]	677	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	676	100%	0	98%	AAA20133.1

In general E values < 0.005 are usually significant.

To find out more about E values see: “*The Statistics of Sequence Similarity Scores*” available in the help section of the NCBI BLAST site:

<http://www.ncbi.nlm.nih.gov/blast/tutorial/Altschul-1.html>



Your Turn!

Hands-on worksheet **Sections 6**

- ▶ Please do answer the last lab review question (**Q19**).
- ▶ We encourage discussion and exploration!

Summary

- Sequence alignment is a fundamental operation underlying much of bioinformatics.
- Even when optimal solutions can be obtained they are not necessarily unique or reflective of the biologically correct alignment.
- Dynamic programming is a classic approach for solving the pairwise alignment problem.
- Reviewed global and local alignment approaches and their major application areas.
- Heuristic approaches are often necessary for large database searches and many genomic applications.

FOR NEXT CLASS...

Check out the online:

- Reading**: Sean Eddy's "What is dynamic programming?"
- Homework**: (1) **Quiz**, (2) **Alignment Exercise**.

Homework Grading

Both (1) quiz questions and (2) alignment exercise carry equal weights (i.e. 50% each).

(Homework 2) Assessment Criteria	Points
Setup labeled alignment matrix	1
Include initial column and row for GAPs	1
All alignment matrix elements scored (i.e. filled in)	1
Evidence for correct use of scoring scheme	1
Direction arrows drawn between all cells	1
Evidence of multiple arrows to a given cell if appropriate	1
Correct optimal score position in matrix used	1
Correct optimal score obtained for given scoring scheme	1
Traceback path(s) clearly highlighted	1
Correct alignment(s) yielding optimal score listed	1
	A+

REFERENCE SLIDES...

Additional reference slides for the motivated student

Practical database searching with BLAST

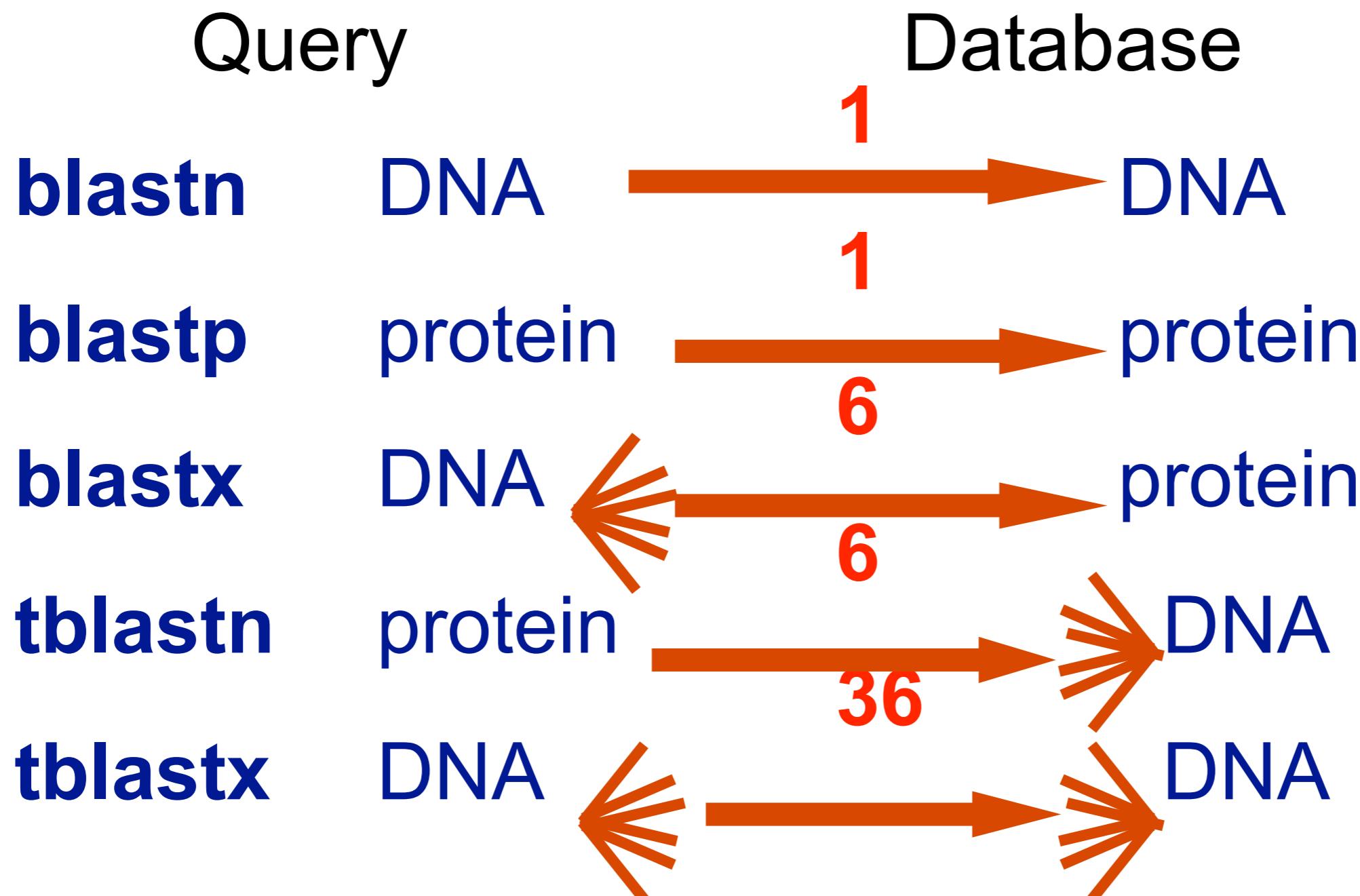
- There are four basic components to a traditional BLAST search
 - (1) Choose the sequence (query)
 - (2) Select the BLAST program
 - (3) Choose the database to search
 - (4) Choose optional parameters
- Then click “BLAST”

Step 1: Choose your sequence

- Sequence can be input in FASTA format or as accession number

The screenshot shows the NCBI Protein search results for "hemoglobin subunit beta [Homo sapiens]". At the top, there's a navigation bar with links for NCBI, Resources, How To, and My N. Below it is a search bar with "Search: Protein" and a dropdown menu. To the right are links for Limits, Advanced search, and Help. A main search field contains the query, followed by a "Search" button and a "Clear" button. On the left, under "Display Settings", the "FASTA" option is selected (indicated by a red oval). Below the search results, the protein name "hemoglobin subunit beta [Homo sapiens]" is displayed. Underneath, the "NCBI Reference Sequence" is listed as "NP_000509.1" (also circled in red). There are links for "GenPept" and "Graphics". The protein sequence itself is shown in a multi-line text area. On the right side, there's a sidebar with options like "Change region shown", "Analyze this sequence" (in brown), "Run BLAST", "Identify Conserved Domains", and "Find in this Sequence".

Step 2: Choose the BLAST program



DNA potentially encodes six proteins

5' CAT CAA

5' ATC AAC

5' TCA ACT



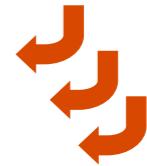
5' CATCAACTACAACCTCAAAGACACCCCTTACACATCAACAAACCTACCCAC 3'

3' GTAGTTGATGTTGAGGTTCTGTGGGAATGTGTAGTTGTTGGATGGGTG 5'

5' GTG GGT

5' TGG GTA

5' GGG TAG



Protein BLAST: search protein databases using a protein query

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PAGE_TYPE=BlastSearch

Reader

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#)

```
>gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVYPWTQRFESFGDLSTPDAVMGNPKVKAHCK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLGNVLVCVLAHHFGKEFTPPVQAAYQK
VVAGVANALAHKYH
```

Query subrange [?](#)

From To

Or, upload file [Choose File](#) no file selected [?](#)

Job Title
Enter a descriptive title for your BLAST search [?](#)

Align two or more sequences [?](#)

Choose Search Set

Database [Non-redundant protein sequences \(nr\)](#) [?](#)

Organism [Optional](#) Exclude [+](#)
Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown. [?](#)

Exclude [Optional](#) Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query [Optional](#)
Enter an Entrez query to limit search [?](#)

Program Selection

Algorithm blastp (protein-protein BLAST)
 PSI-BLAST (Position-Specific Iterated BLAST)
 PHI-BLAST (Pattern Hit Initiated BLAST)
 DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)
Choose a BLAST algorithm [?](#)

BLAST Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)
 Show results in a new window

[Algorithm parameters](#)



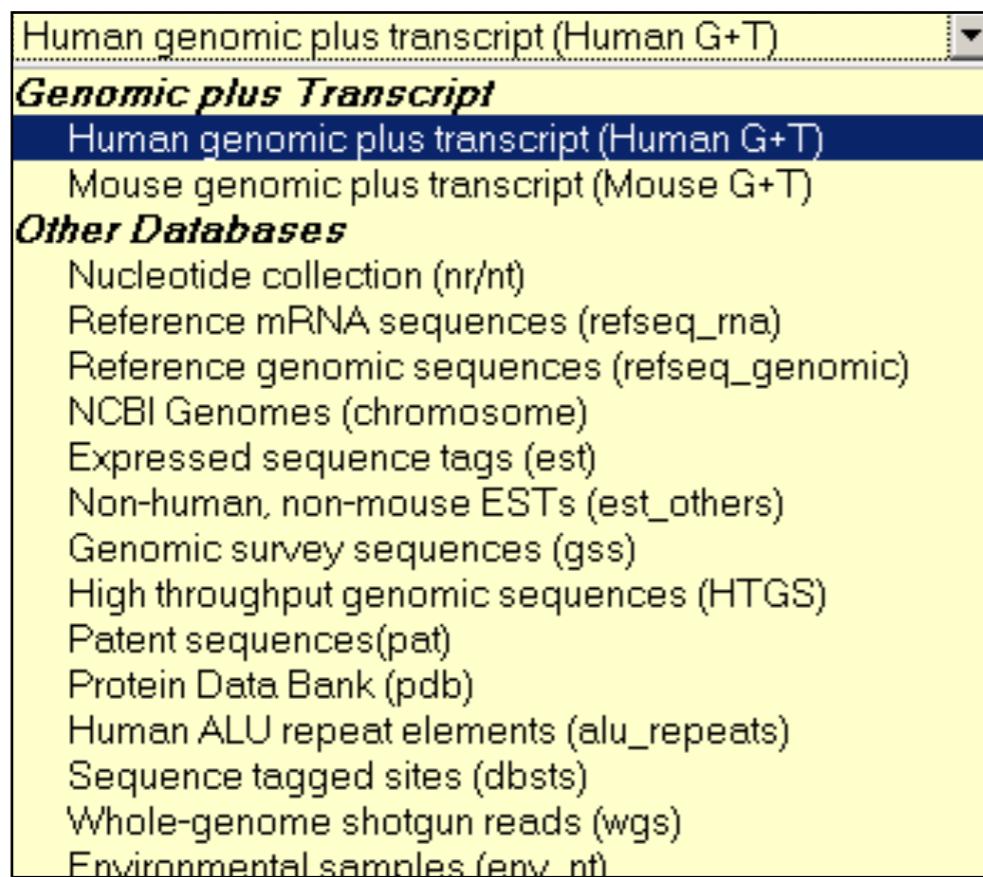
Step 3: Choose the database

nr = non-redundant (most general database)

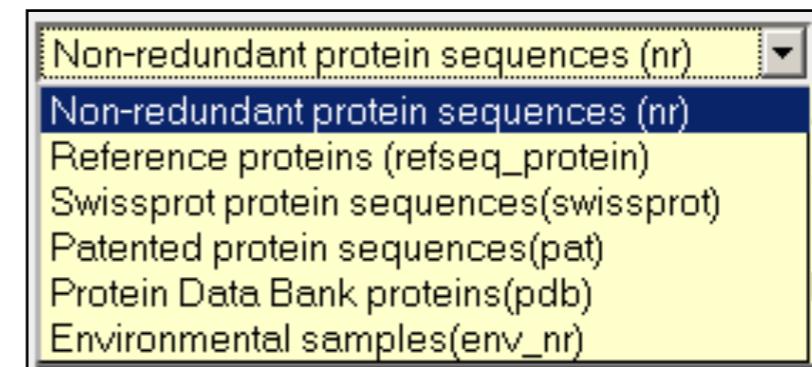
dbest = database of expressed sequence tags

dbsts = database of sequence tag sites

gss = genomic survey sequences



nucleotide databases



protein databases

Protein BLAST: search protein databases using a protein query

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PAGE_TYPE=Blast+Search

Reader

Query subrange

From [] To []

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

>gi|4504349|ref|NP_000509.1| hemoglobin subunit beta [Homo sapiens]
MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGK
KVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLGNVLVCVLAHHFGKEFTPPVQAAYQK
VVAGVANALAHKYH

Or, upload file no file selected

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database: Non-redundant protein sequences (nr)

Organism: Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Exclude: Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query:

Enter an Entrez query to limit search

Program Selection

Algorithm:

blastp (protein-protein BLAST)
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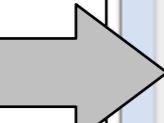
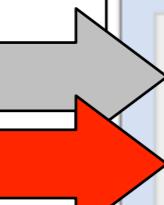
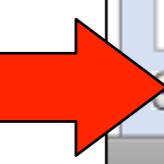
Choose a BLAST algorithm

BLAST

Search database Non-redundant protein sequences (nr) using Blastp (protein-protein BLAST)

Show results in a new window

Algorithm parameters

Organism 
Entrez 
Settings! 

Step 4a: Select optional search parameters

Algorithm parameters

General Parameters

Max target sequences: 100
Select the maximum number of aligned sequences to display

Short queries: Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 3

Max matches in a query range: 0

Scoring Parameters

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjustment

Filters and Masking

Filter: Low complexity regions

Mask: Mask for lookup table only
 Mask lower case letters

BLAST: Search **database Non-redundant protein sequences (nr)** using **Blastp**
 Show results in a new window

Annotations highlight specific parameters:

- A blue double-headed arrow spans from the "Expect threshold" field to the "Word size" field, labeled "Expect" above and "Word size" below.
- An orange double-headed arrow spans from the "Matrix" dropdown to the "Gap Costs" dropdown, labeled "Scoring matrix" below.

Step 4: Optional parameters

- You can...
 - choose the organism to search
 - change the substitution matrix
 - change the expect (E) value
 - change the word size
 - change the output format

Results page

NCBI Blast:gi|4504349|ref|NP_000509.1| hemoglobin

blast.ncbi.nlm.nih.gov/Blast.cgi Reader

BLAST® Basic Local Alignment Search Tool My NCBI [Sign In] [Register]

Home Recent Results Saved Strategies Help

NCBI/BLAST/blastp suite/ Formatting Results - FVGUTMRZ013

Edit and Resubmit Save Search Strategies ► Formatting options ► Download Change the result display back to traditional format

You Tube Learn about the enhanced report Blast report description

gi|4504349|ref|NP_000509.1| hemoglobin

Query ID: Icl|84677 Database Name: nr
Description: gi|4504349|ref|NP_000509.1| hemoglobin subunit Description: All non-redundant GenBank CDS
beta [Homo sapiens] translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type: amino acid Program: BLASTP 2.2.27+ ► Citation
Query Length: 147

Other reports: ► Search Summary [Taxonomy reports] [Distance tree of results] [Related Structures] [Multiple alignment]

New DELTA-BLAST, a more sensitive protein-protein search Go

Graphic Summary

Show Conserved Domains

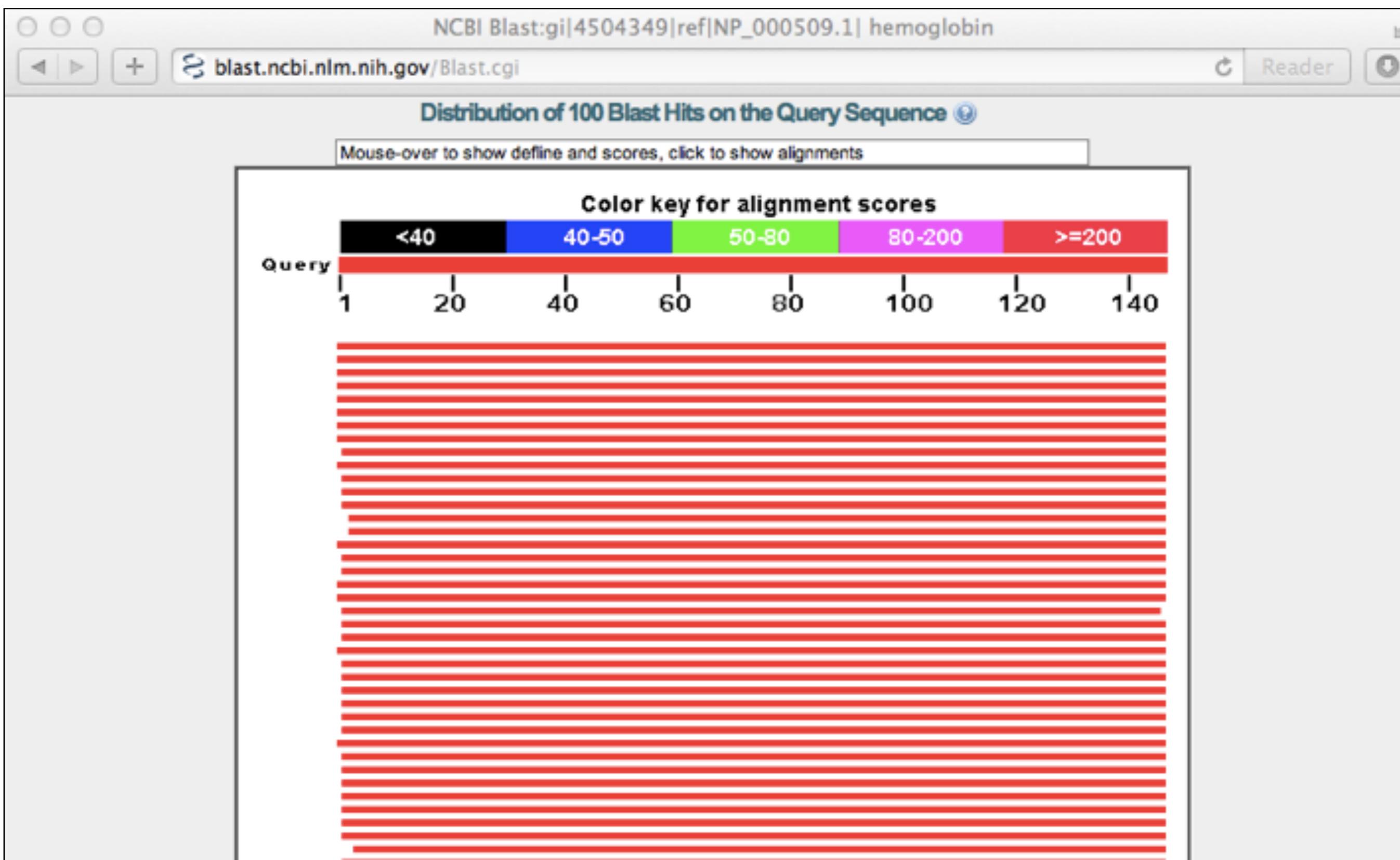
Putative conserved domains have been detected, click on the image below for detailed results.

Query seq. 1 25 50 75 100 125 147
Specific hits: hem-binding site globin
Superfamilies: globin_like superfamily

Distribution of 100 Blast Hits on the Query Sequence ⓘ

Mouse over to show details and scores, click to show alignments

Further down the results page...



Further down the results page...

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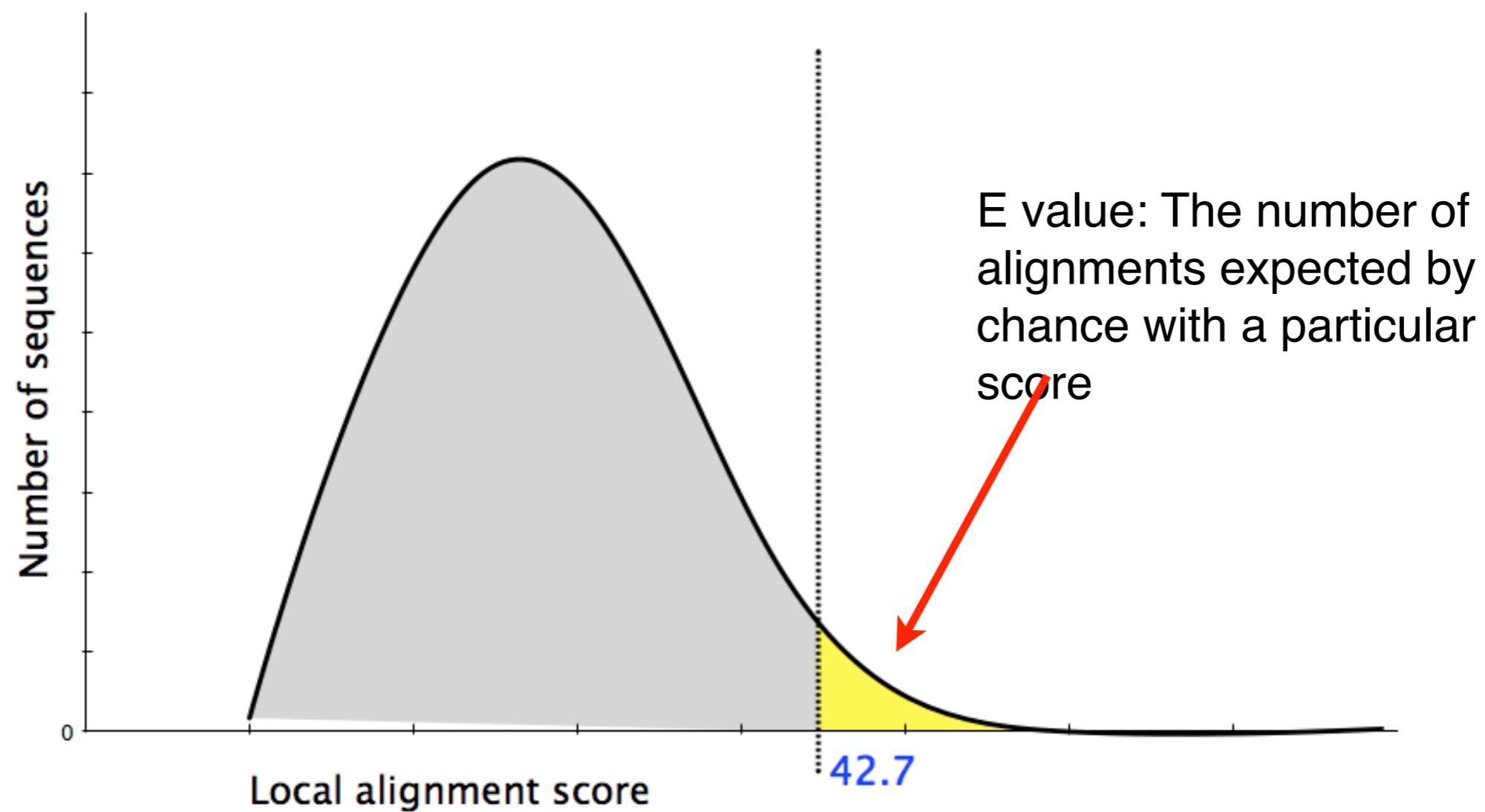
Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenPept Graphics Distance tree of results Multiple alignment

	Description	Max score	Total score	Query cover	E value	Max ident	Accession
<input type="checkbox"/>	hemoglobin beta [synthetic construct]	301	301	100%	9e-103	100%	AAX37051.1
<input type="checkbox"/>	hemoglobin beta [synthetic construct]	301	301	100%	1e-102	100%	AAX29557.1
<input type="checkbox"/>	hemoglobin subunit beta [Homo sapiens] >ref XP_508242.1 PREDICTED: hemoglobin s	301	301	100%	1e-102	100%	NP_000509.1
<input type="checkbox"/>	RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta	300	300	100%	4e-102	99%	P02024.2
<input type="checkbox"/>	beta globin chain variant [Homo sapiens]	299	299	100%	5e-102	99%	AAN84548.1
<input type="checkbox"/>	beta globin [Homo sapiens] >gb AAZ39781.1 beta globin [Homo sapiens] >gb AAZ39782.1 beta globin [Homo sapiens]	299	299	100%	5e-102	99%	AAZ39780.1
<input type="checkbox"/>	beta-globin [Homo sapiens]	299	299	100%	5e-102	99%	ACU56984.1
<input type="checkbox"/>	hemoglobin beta chain [Homo sapiens]	299	299	100%	6e-102	99%	AAD19696.1
<input type="checkbox"/>	Chain B, Structure Of Haemoglobin In The Deoxy Quaternary State With Ligand Bound At The Beta Subunit	298	298	99%	9e-102	100%	1COH_B
<input type="checkbox"/>	hemoglobin beta subunit variant [Homo sapiens] >gb AAA88054.1 beta-globin [Homo sapiens]	298	298	100%	1e-101	99%	AAF00489.1
<input type="checkbox"/>	Chain B, Human Hemoglobin D Los Angeles: Crystal Structure >pdb 2YRS D Chain D, H	298	298	99%	2e-101	99%	2YRS_B
<input type="checkbox"/>	Chain B, High-Resolution X-Ray Study Of Deoxy Recombinant Human Hemoglobins Synthesized In Escherichia Coli	297	297	99%	3e-101	99%	1DXU_B
<input type="checkbox"/>	Chain B, Analysis Of The Crystal Structure, Molecular Modeling And Infrared Spectroscopic Characterization Of Human Hemoglobin D Los Angeles	297	297	99%	3e-101	99%	1HDB_B

Description	Max score	Total score	Query cover	E value	Max ident	Accession
kinesin-1 heavy chain [Homo]	677	677	100%	0	100%	NP_004512.1
Kif5b protein [Mus musculus]	676	676	100%	0	98%	AAA20133.1
Kinesin-14 heavy chain [Danio rerio]	595	595	88%	0	78%	XP_00320703
hypothetical protein EGK_18589	48.2	52	40%	0.03	32%	ELK35081.1
mKIAA4102 protein [Mus musculus]	42.7	42.7	38%	3.02	24%	EHH28205.1



E values in BLAST

- Each alignment gets a score determined from the alignment and doesn't take into account the full length of the query, target or database
- The E value is what you want to look at
- **E value = Expect**
 - How often do I expect an alignment with this score given the length of my query and the size of the database
 - $E = Kmne^{-\lambda s}$
 - K and λ are scaling factors
 - S is the score
 - m – length of query, n – length of database
 - E corrects for multiple comparisons, i.e., query compared to many sequences – proportional to length of database and query for a given S (score)

Further down the results page...

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hemoglobin subunit beta [Homo sapiens]
Sequence ID: ref|NP_000509.1| Length: 147 Number of Matches: 1
► See 84 more title(s)

Range 1: 1 to 147 GenPept Graphics ▾ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
301 bits(770)	1e-102	Compositional matrix adjust.	147/147(100%)	147/147(100%)	0/147(0%)

Query 1 MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK 60
Sbjct 1 MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK 60

Query 61 VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG 120
Sbjct 61 VKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFG 120

Query 121 KEFTPQAAVYQKVVAGVANALAHKYH 147
Sbjct 121 KEFTPQAAVYQKVVAGVANALAHKYH 147

Related Information

[Gene](#) - associated gene detail
[UniGene](#) - clustered expressed sequence tags
[Map Viewer](#) - aligned genomic context
[Structure](#) - 3D structure displays
[PubChem Bio](#)
[Assay](#) - bioactivity screening

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RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain
Sequence ID: sp|P02024.2|HBB_GORGO Length: 147 Number of Matches: 1

Range 1: 1 to 147 GenPept Graphics ▾ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
300 bits(767)	4e-102	Compositional matrix adjust.	146/147(99%)	147/147(100%)	0/147(0%)

Related Information

Different output formats are available

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NCBI BLAST/blastp suite/ Formatting Results - FVGUTMRZ013

Edit and Resubmit Save Search Strategies ▾ Formatting options Download Change the result display back YouTube Learn about the enhanced report Blast

Formatting options

Show Alignment as HTML Old View Reset form to defaults

Alignment View Query-anchored with letters for identities

Display Graphical Overview Sequence Retrieval NCBI-gi

Masking Character: Lower Case Color: Grey

Limit results Descriptions: 50 Graphical overview: 50 Alignments: 50

Organism Type common name, binomial, taxid, or group name. Only 20 top taxa will be shown.
Enter organism name or id--completions will be suggested Exclude +

Entrez query:

Expect Min: Expect Max:

Percent Identity Min: Percent Identity Max:

Format for PSI-BLAST with inclusion threshold:

gi|4504349|ref|NP_000509.1| hemoglobin

E.g. Query anchored alignments

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Query	Score	Sequence	Length
AAX37051	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
AAX29557	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
NP_000509	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
P02024	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
AAN84548	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
AAZ39780	1	MVHLTPKEKS A VTALWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	60
ACU56984	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
AAD19696	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFLESFGDLSTPDAVMGNPK	60
1COH_B	1	VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	59
AAF00489	1	MVHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
2YRS_B	1	VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	59
1DXU_B	1	MHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	59
1HDB_B	1	VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	59
1DXV_B	2	HLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
3KMF_C	2	HLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
AAL68978	1	MVHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	60
1NQP_B	1	VHLTPEEKSAVTALWGKVNDEVGG KALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1K1K_B	1	VHLTPKEKS A VTALWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
AAN11320	1	MVHLTPVEKS A VTALWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	60
XP_002822173	1	MVHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	60
1Y85_B	1	VHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1YE0_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLAV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1O1O_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
CAA23759	1	MVHLTPVEKS A VTAXWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	60
1YE2_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVVFPWTQRFFESFGDLSTPDAVMGNPK	59
1Y5F_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1A00_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PYTQRFFESFGDLSTPDAVMGNPK	59
1HBS_B	1	VHLTPVEKS A VTALWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1ABY_B	1	MHLTPEEKSAVTALWGKVNDEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59
1CMY_B	1	VHLTPKEKS A VTALWGKVN DEVGG E ALGR LLVV Y PWTQRFFESFGDLSTPDAVMGNPK	59

... and alignments with dots for identities

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Reader

Query	Length	Sequence	Score
AAX37051	1	MVHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPK	60
AAX29557	1	60
NP_000509	1	60
P02024	1	60
AAN84548	1	60
AAZ39780	1K.....	60
ACU56984	1	60
AAD19696	1	60
1COH_B	1	59
AAF00489	1	60
2YRS_B	1	59
1DXU_B	1	M.....	59
1HDB_B	1	59
1DXV_B	2	59
3KMF_C	2	59
AAL68978	1	60
1NQP_B	1K.....	59
1K1K_B	1K.....	59
AAN11320	1V.....	60
XP_002822173	1	60
1Y85_B	1	59
1YE0_B	1	M.....A.....	59
1O1Q_B	1	M.....	59
CAA23759	1V.....X.....	60
1YE2_B	1	M.....F.....	59
1Y5F_B	1	M.....	59
1A00_B	1	M.....Y.....	59

Common problems

- Selecting the wrong version of BLAST
- Selecting the wrong database
- Too many hits returned
- Too few hits returned
- Unclear about the significance of a particular result - are these sequences homologous?

How to handle too many results

- Focus on the question you are trying to answer
 - select “refseq” database to eliminate redundant matches from “nr”
 - Limit hits by organism
 - Use just a portion of the query sequence, when appropriate
 - Adjust the expect value; lowering E will reduce the number of matches returned

How to handle too few results

- Many genes and proteins have no significant database matches
 - remove Entrez limits
 - raise E-value threshold
 - search different databases
 - try scoring matrices with lower BLOSUM values
(or higher PAM values)
 - use a search algorithm that is more sensitive than BLAST (e.g. PSI-BLAST or HMMer)