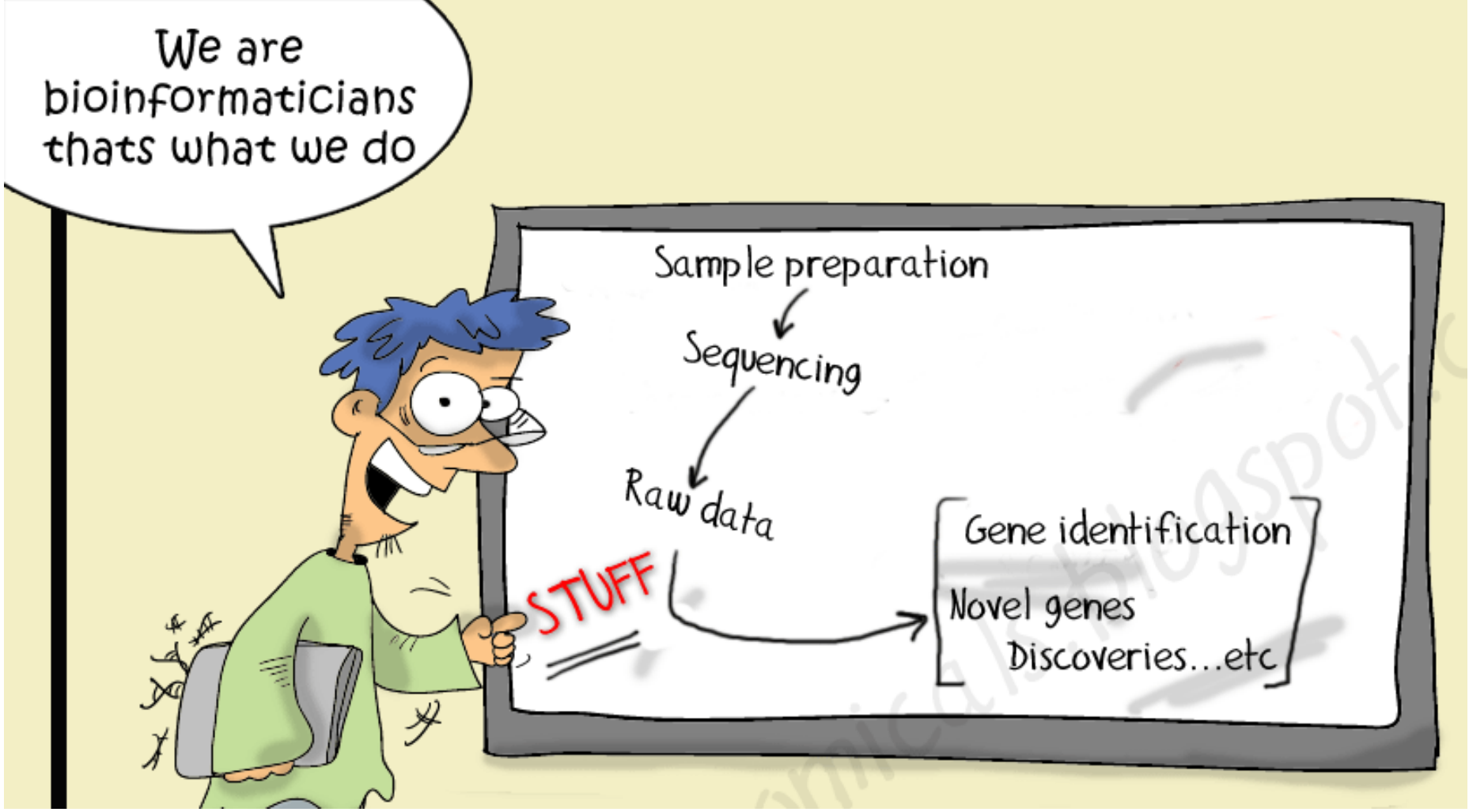
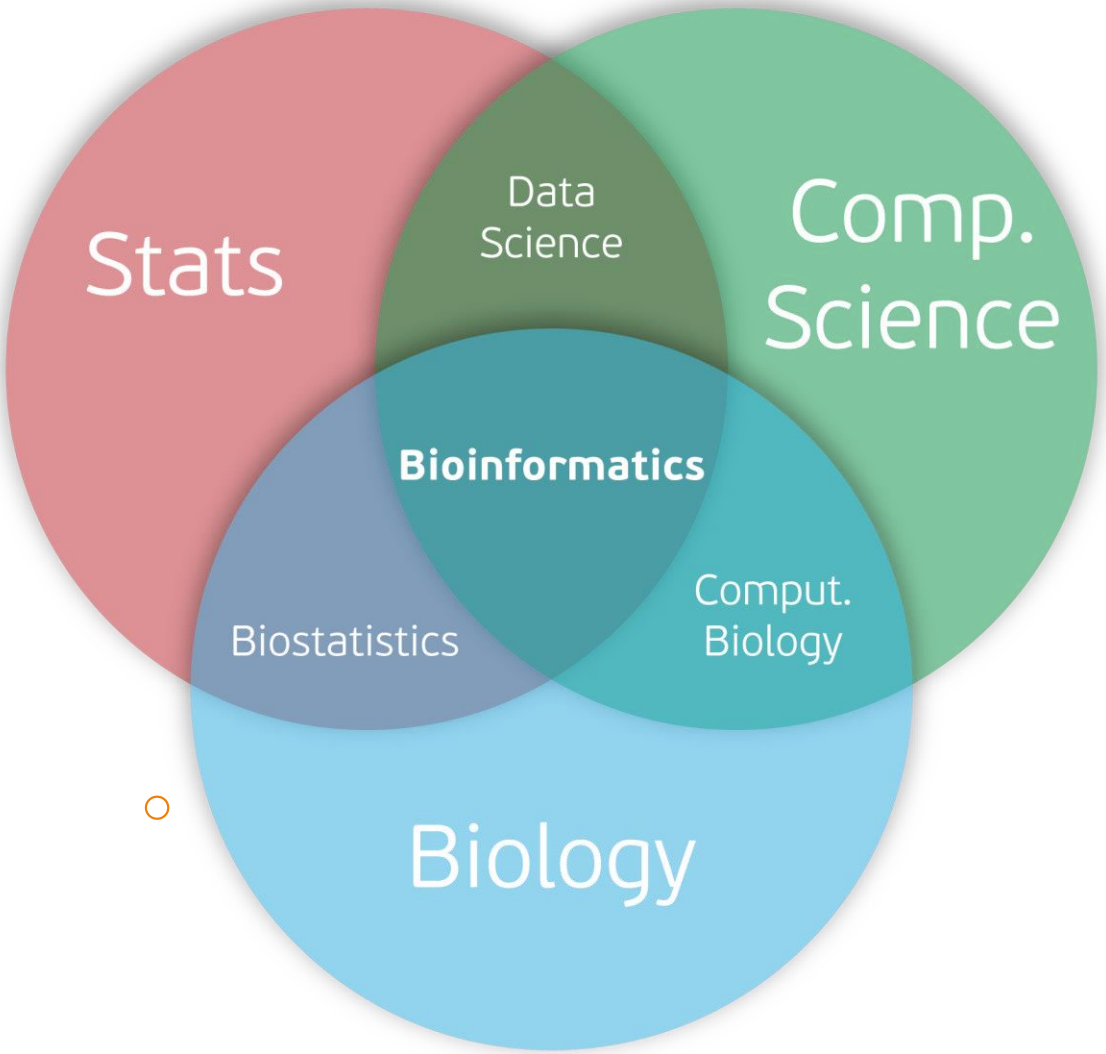


How does the “stuff “ happen?

Miglė Survilaitė

Šiek tiek apie mane

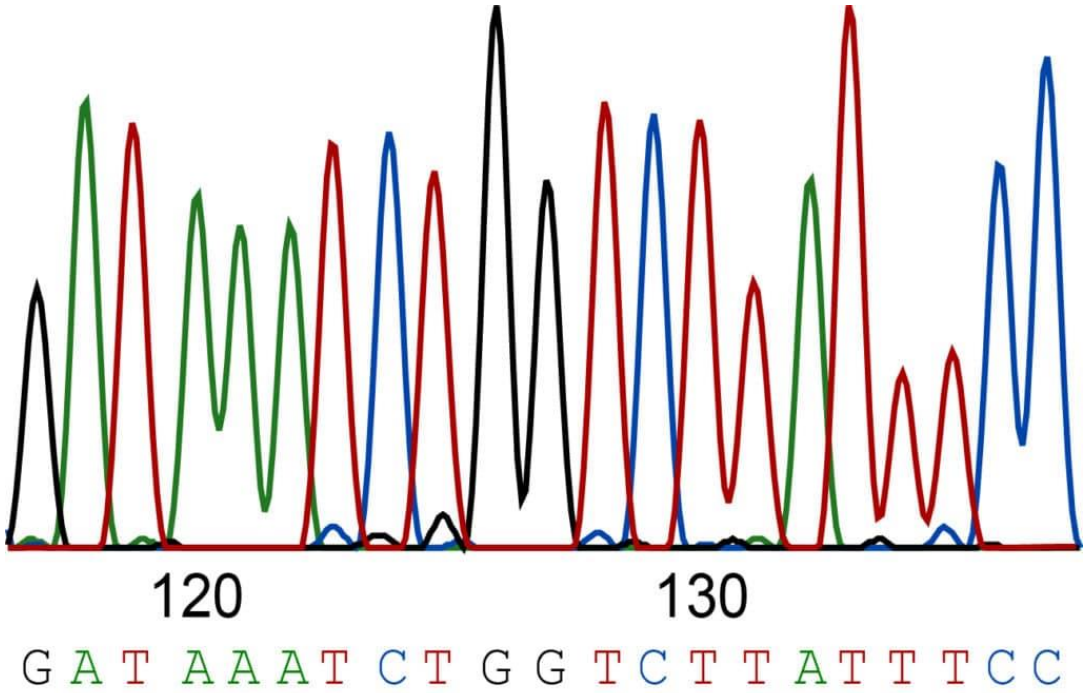
- 2012 – 2016 Bakalauro studijos Vilniaus Universitete, Biochemija
- 2016 – 2018 Magistro studijos Kopenhagos Universitete, Bioinformatika
- 2017 – ... bio.tools, bioinformatinių tools‘ų kuravimas
- 2017 – ... Genominės medicinos centras, Rigshospitalet

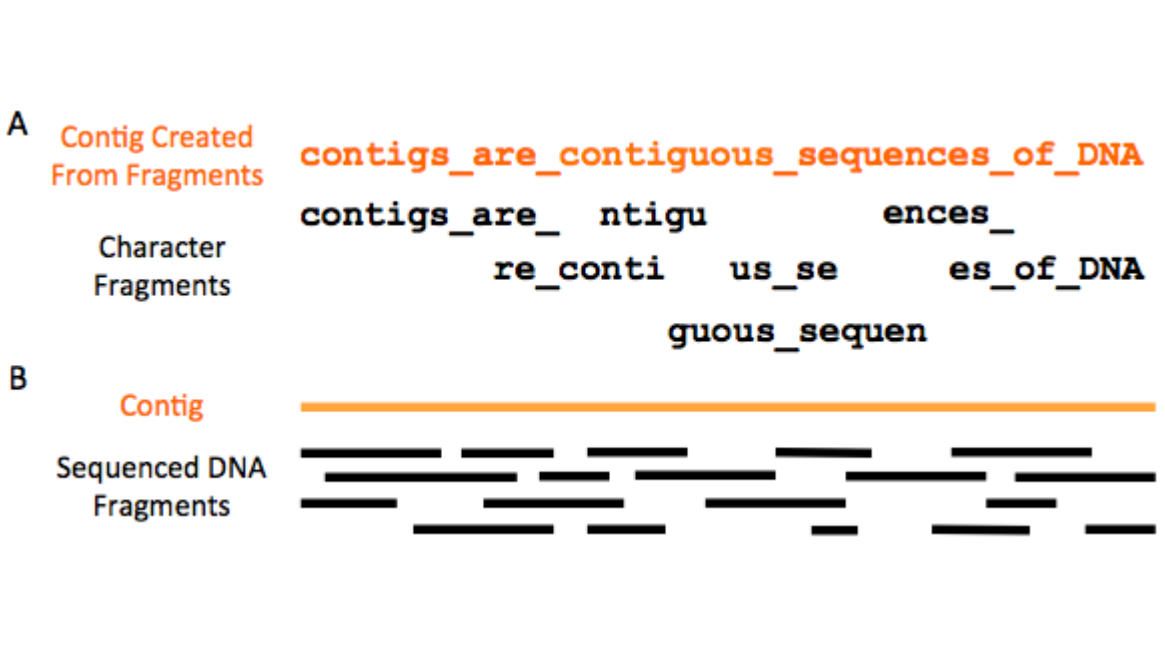


Kas ta bioinformatika?

- Wikipedia:
  - Bioinformatics is an interdisciplinary field that develops methods and software tools for understanding biological data.
- Even better:
  - Bioinformatics is an interdisciplinary field that develops and applies methods and software tools for understanding biological data.
- Pagrindiniai bioinformatikų tipai?

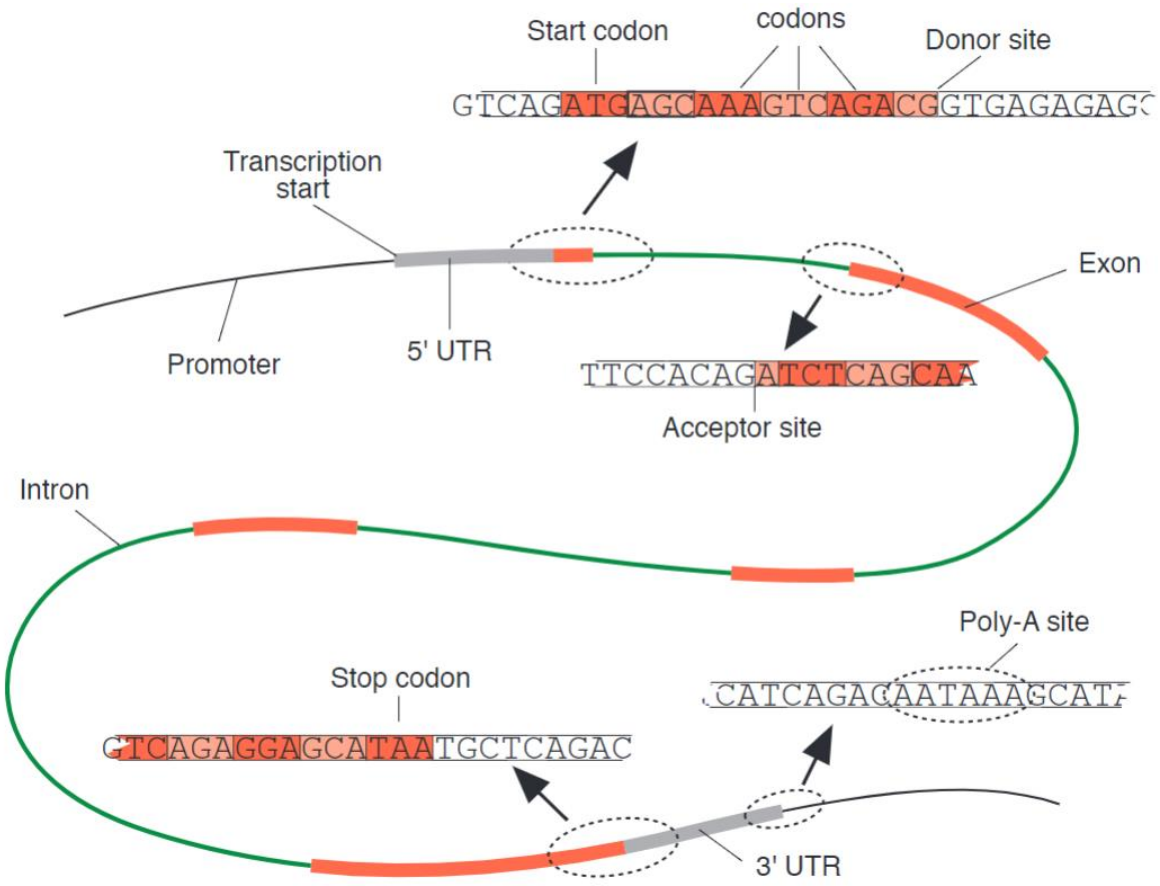
Kaip atpažinti genus iš sekoskaitos rezultatų?



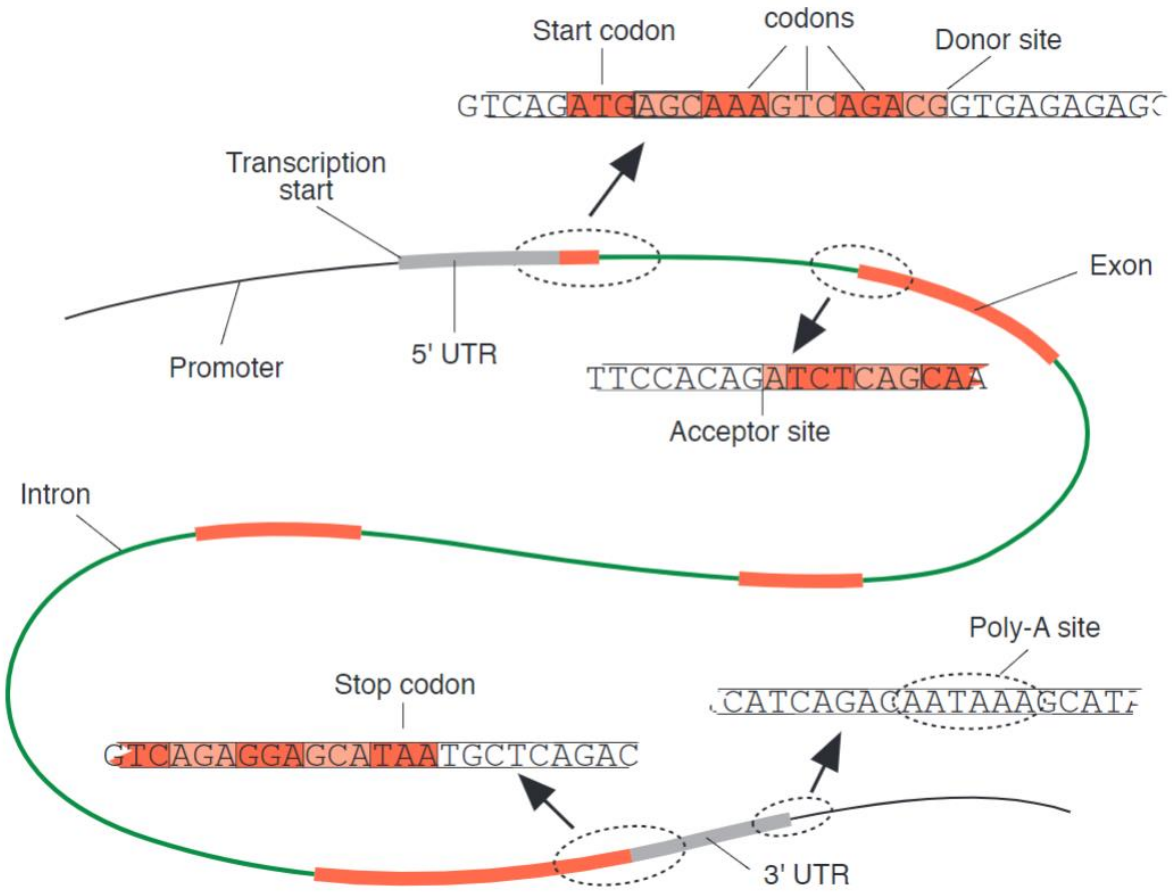


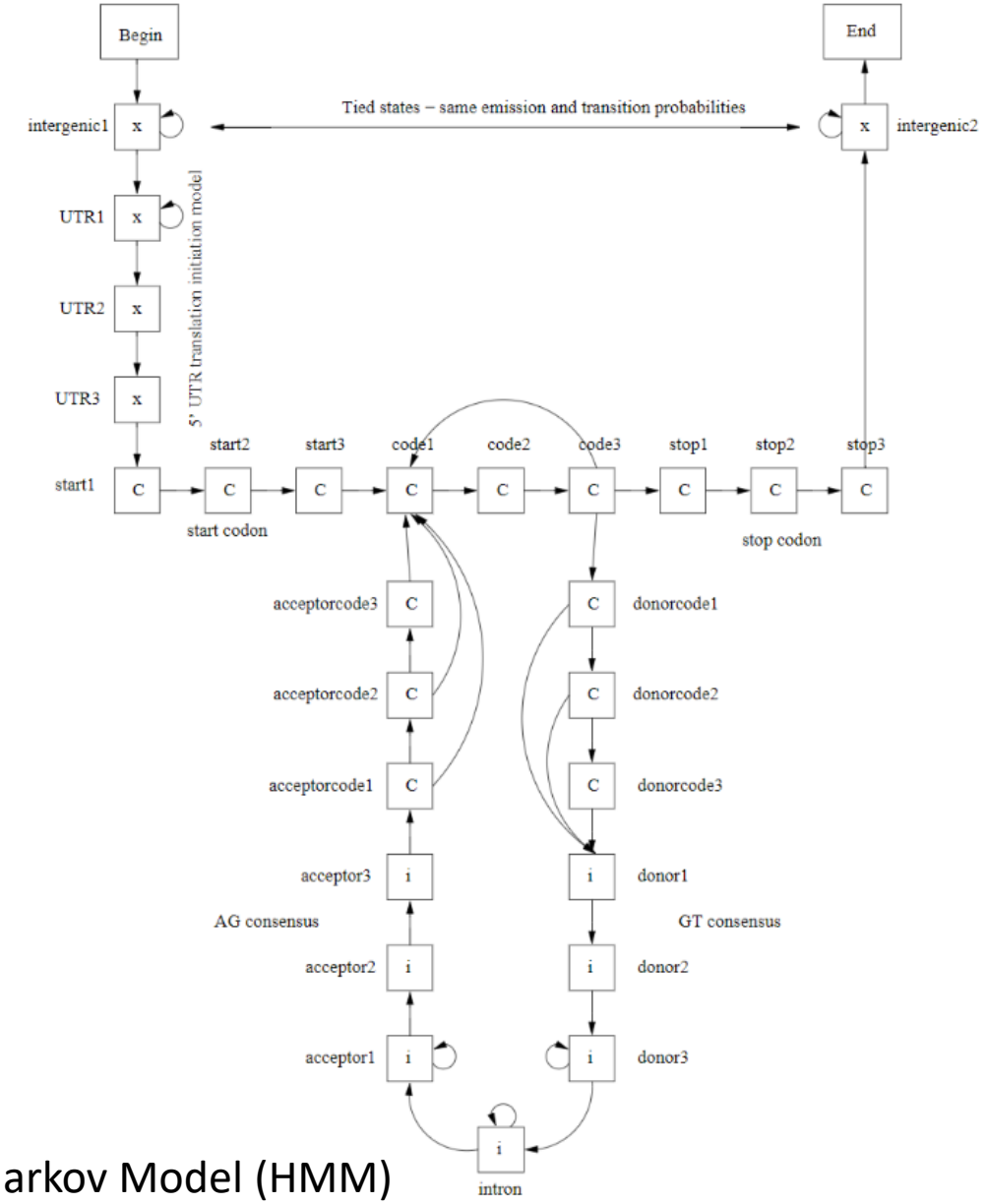
Kas yra sekoskaita?

Kaip atpažinti genus iš sekoskaitos rezultatų?



- 5‘UTR
- Start kodonas
- Kodonai
- Donorinė seka
- Intronas
- Akceptorinė seka
- Stop kodonas
- Poly-A seka





Hidden Markov Model (HMM)

Kaip atpažinti genus iš sekoskaitos rezultatų?

Realybėje viskas daug sudėtingiau ☺

Ką gali bioinformatika?

- Sequence analysis
- Structural bioinformatics
- Phylogenetic analysis/population genetics
- Bioinformatics of high-throughput analysis
- Statistics, visualizations

FASTA formatas

- Daugumos sequence analysis tools'ų input formatas yra FASTA.
- FASTA failai susideda iš sekos pavadinimo (1 eilutė prasidedanti > ženklu) ir nukleotidų/aminorūgščių sekos.
- Pavyzdys:

  > Some fancy name

  TACAANAAAATTAGCCAGGCATGATNGTGCATGNCTATGGTCCCANNTNCNNGGNAGGCTGAGGCAGGAGNATNGNTTGAACCTGN
  GANGNNNNGGNTNCAGTNNNNCANGNTNNCNCNNNNGCNNTCCCGNNNNNGNANNNGNGCNNNNC

- FASTQ failai susideda iš 4 eilučių (@ prasidedantis *sequence identifier*; nukleotidų/aminorūgšių seka; + (ir *optional sequence identifier*); nukleotidų/aminorūgščių *quality scores*)

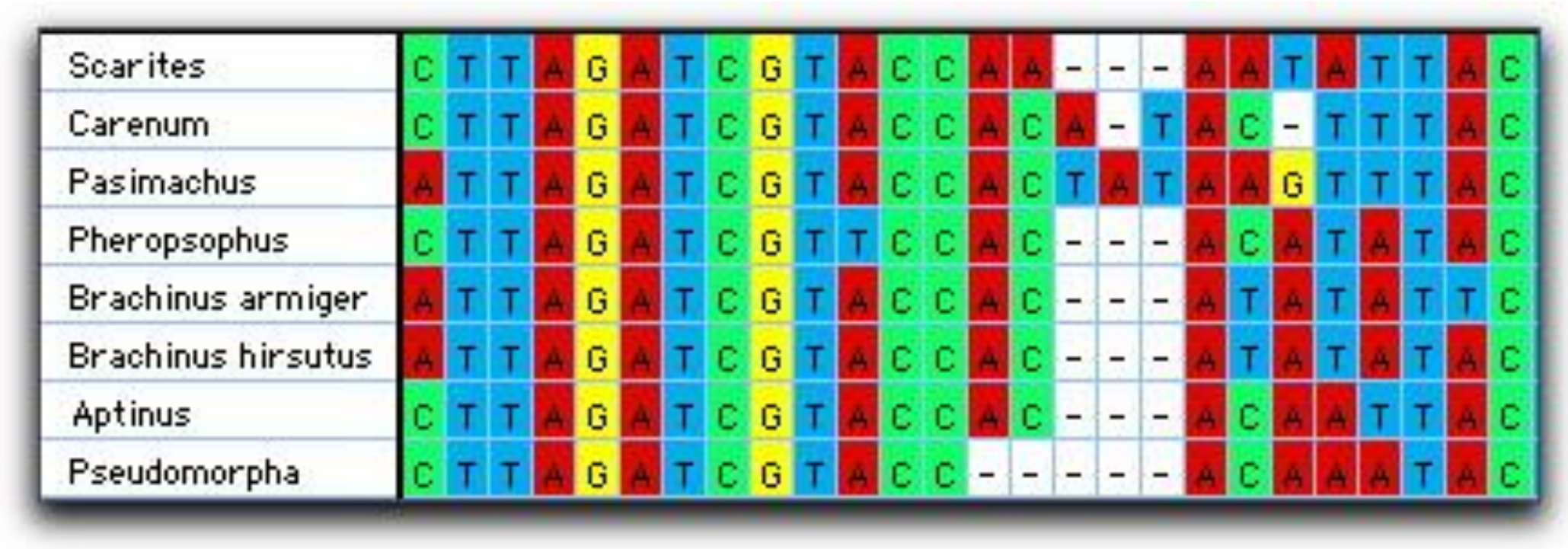
  @NS500314:279:HFT5JBGX5:1:11101:4769:1044 1:N:0:AGTCAA

  AGGAANTAAAATTAAATATGTCTTCNTCCACCTNAGCCAGGGATGNNANCNNCTNCTGTGAGCCCTGGACNCTNANCATGCAGCCNG
  CNCNNNNNANGNTCGNNNNNGCNCNCNNCNGNNNNCCNNTCACANNNNNCNANNNCNTANNN

  +

  6AAAA#EEEEEEEEEEEEEEEEEE#EEEAEEE#EEEEEEEEEEE##E#E##/E#EEEEEAEEA/EEEEE#AE#/#/EEE</EEE#EE#E######E#/#E
  EE#####A/#E#A##/#/####6E##EE//A#####E#E###/#E/###

Sequence alignment – sekų palyginimas



Pairwise alignment – dynamic programming

	C	T	A	A	G
C					
A					
G					

Pairwise alignment – dynamic programming

		C	T	A	A	G
	-	-	-	-	-	-
C	-	1	1	1	1	1
A	-	1	1	2	2	2
G	-	1	1	2	2	3

Match (+1)

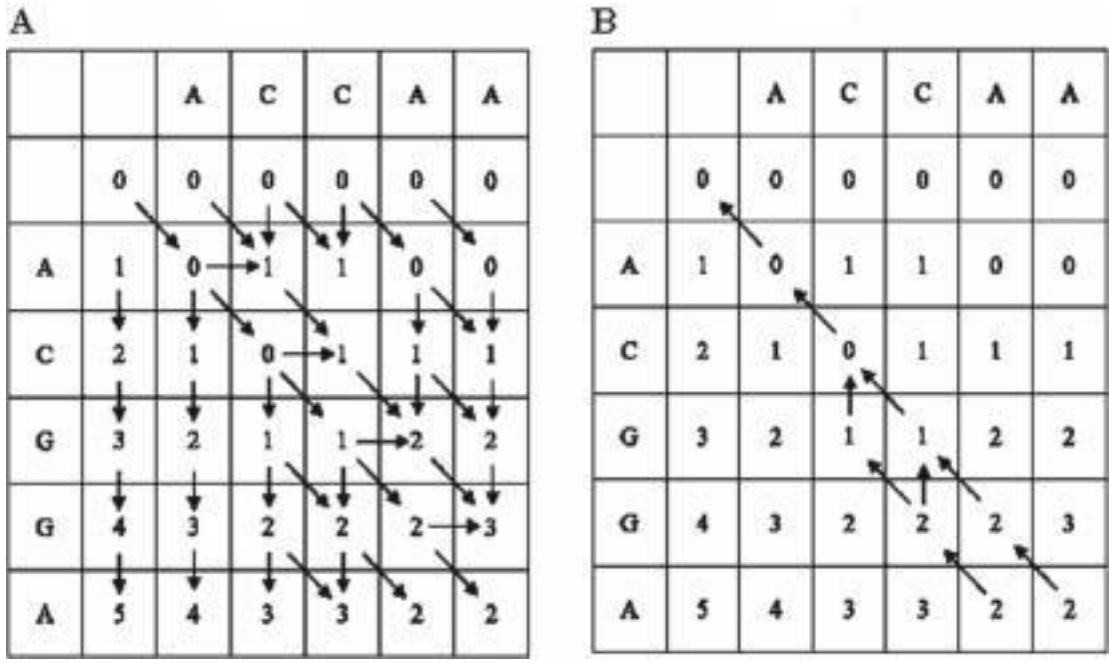
Pairwise alignment – dynamic programming

		C	T	A	A	G
	-	-	-	-	-	-
C	-	1	0	-1	-2	-3
A	-	0	0	-1	0	-1
G	-	-1	-1	-1	-2	1

Gap (-1)

Match (+1)/Mismatch (-1)

Pairwise alignment – dynamic programming



Pairwise alignment – dynamic programming

		C	T	A	A	G
	-	-	-	-	-	-
C	-	1	0	-1	-2	-3
A	-	0	0	-1	0	-1
G	-	-1	-1	-1	-1	1

Gap (-1)

Match (+1)/Mismatch(-1)

Pairwise alignment – dynamic programming

	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
A	**5**	-1	-2	-1	-3	0	-2	-1	-1	-2	-1	-1	-1	-1	-2	1	0	0	-3	-2
C	-1	**13**	-4	-3	-2	-3	-3	-2	-3	-2	-2	-2	-4	-3	-4	-1	-1	-1	-5	-3
D	-2	-4	**8**	2	-5	-1	-1	-4	-1	-4	-4	2	-1	0	-2	0	-1	-4	-5	-3
E	-1	-3	2	**6**	-3	-3	0	-4	1	-3	-2	0	-1	2	0	-1	-1	-3	-3	-2
F	-3	-2	-5	-3	**8**	-4	-1	0	-4	1	0	-4	-4	-4	-3	-3	-2	-1	1	4
G	0	-3	-1	-3	-4	**8**	-2	-4	-2	-4	-3	0	-2	-2	-3	0	-2	-4	-3	-3
H	-2	-3	-1	0	-1	-2	**10**	-4	0	-3	-1	1	-2	1	0	-1	-2	-4	-3	2
I	-1	-2	-4	-4	0	-4	-4	**5**	-3	2	2	-3	-3	-3	-4	-3	-1	4	-3	-1
K	-1	-3	-1	1	-4	-2	0	-3	**6**	-3	-2	0	-1	2	3	0	-1	-3	-3	-2
L	-2	-2	-4	-3	1	-4	-3	2	-3	**5**	3	-4	-4	-2	-3	-3	-1	1	-2	-1
M	-1	-2	-4	-2	0	-3	-1	2	-2	3	**7**	-2	-3	0	-2	-2	-1	1	-1	0
N	-1	-2	2	0	-4	0	1	-3	0	-4	-2	**7**	-2	0	-1	1	0	-3	-4	-2
P	-1	-4	-1	-1	-4	-2	-2	-3	-1	-4	-3	-2	**10**	-1	-3	-1	-1	-3	-4	-3
Q	-1	-3	0	2	-4	-2	1	-3	2	-2	0	0	-1	**7**	1	0	-1	-3	-1	-1
R	-2	-4	-2	0	-3	-3	0	-4	3	-3	-2	-1	-3	1	**7**	-1	-1	-3	-3	-1
S	1	-1	0	-1	-3	0	-1	-3	0	-3	-2	1	-1	0	-1	**5**	2	-2	-4	-2
T	0	-1	-1	-1	-2	-2	-2	-1	-1	-1	-1	0	-1	-1	-1	2	**5**	0	-3	-2
V	0	-1	-4	-3	-1	-4	-4	4	-3	1	1	-3	-3	-3	-3	-2	0	**5**	-3	-1
W	-3	-5	-5	-3	1	-3	-3	-3	-3	-2	-1	-4	-4	-1	-3	-4	-3	-3	**15**	2
Y	-2	-3	-3	-2	4	-3	2	-1	-2	-1	0	-2	-3	-1	-1	-2	-2	-1	2	**8**

		H	E	A	G	A	W	G	H	E	E
P		-2	-2	-2	-2	-2	-2	-2	-2	-2	-2
A		-2	-2	1	-2	1	-2	-2	-2	-2	-2
W		-2	-2	-2	-2	-2	1	-2	-2	-2	-2
H		1	-2	-2	-2	-2	-2	-2	1	-2	-2
E		-2	1	-2	-2	-2	-2	-2	-2	1	1
A		-2	-2	1	-2	1	-2	-2	-2	-2	-2
E		-2	1	-2	-2	-2	-2	-2	-2	1	1

Gap penalty -2

Pairwise alignment – dynamic programming

	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
A	**5**	-1	-2	-1	-3	0	-2	-1	-1	-2	-1	-1	-1	-1	-2	1	0	0	-3	-2
C	-1	**13**	-4	-3	-2	-3	-3	-2	-3	-2	-2	-2	-4	-3	-4	-1	-1	-1	-5	-3
D	-2	-4	**8**	2	-5	-1	-1	-4	-1	-4	-4	2	-1	0	-2	0	-1	-4	-5	-3
E	-1	-3	2	**6**	-3	-3	0	-4	1	-3	-2	0	-1	2	0	-1	-1	-3	-3	-2
F	-3	-2	-5	-3	**8**	-4	-1	0	-4	1	0	-4	-4	-4	-3	-3	-2	-1	1	4
G	0	-3	-1	-3	-4	**8**	-2	-4	-2	-4	-3	0	-2	-2	-3	0	-2	-4	-3	-3
H	-2	-3	-1	0	-1	-2	**10**	-4	0	-3	-1	1	-2	1	0	-1	-2	-4	-3	2
I	-1	-2	-4	-4	0	-4	-4	**5**	-3	2	2	-3	-3	-3	-4	-3	-1	4	-3	-1
K	-1	-3	-1	1	-4	-2	0	-3	**6**	-3	-2	0	-1	2	3	0	-1	-3	-3	-2
L	-2	-2	-4	-3	1	-4	-3	2	-3	**5**	3	-4	-4	-2	-3	-3	-1	1	-2	-1
M	-1	-2	-4	-2	0	-3	-1	2	-2	3	**7**	-2	-3	0	-2	-2	-1	1	-1	0
N	-1	-2	2	0	-4	0	1	-3	0	-4	-2	**7**	-2	0	-1	1	0	-3	-4	-2
P	-1	-4	-1	-1	-4	-2	-2	-3	-1	-4	-3	-2	**10**	-1	-3	-1	-1	-3	-4	-3
Q	-1	-3	0	2	-4	-2	1	-3	2	-2	0	0	-1	**7**	1	0	-1	-3	-1	-1
R	-2	-4	-2	0	-3	-3	0	-4	3	-3	-2	-1	-3	1	**7**	-1	-1	-3	-3	-1
S	1	-1	0	-1	-3	0	-1	-3	0	-3	-2	1	-1	0	-1	**5**	2	-2	-4	-2
T	0	-1	-1	-1	-2	-2	-2	-1	-1	-1	-1	0	-1	-1	-1	2	**5**	0	-3	-2
V	0	-1	-4	-3	-1	-4	-4	4	-3	1	1	-3	-3	-3	-3	-2	0	**5**	-3	-1
W	-3	-5	-5	-3	1	-3	-3	-3	-3	-2	-1	-4	-4	-1	-3	-4	-3	-3	**15**	2
Y	-2	-3	-3	-2	4	-3	2	-1	-2	-1	0	-2	-3	-1	-1	-2	-2	-1	2	**8**

		H	E	A	G	A	W	G	H	E	E
	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20
P	-2	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20
A	-4	-4	-4	-3	-5	-7	-9	-11	-13	-15	-17
W	-6	-6	-6	-5	-5	-7	-6	-8	-10	-12	-14
H	-8	-5	-7	-7	-7	-7	-8	-8	-7	-9	-11
E	-10	-7	-4	-6	-8	-9	-9	-10	-9	-6	-8
A	-12	-9	-6	-3	-5	-7	-9	-11	-11	-8	-8
E	-14	-11	-8	-5	-5	-7	-9	-11	-13	-10	-7

Gap penalty -2

Pairwise alignment – gap penalty

- Scoring matrix:
  - PAM
  - BLOSUM
- Linear – netenkamas vienodas kiekis taškų už kiekvieną *gap‘ą*
  - $\gamma(g) = -gd$
    - *g – gap length*
    - *d – gap penalty*
- Affine – netenkama daugiau taškų už *gap‘o* iniciavimą ir mažiau už *gap‘o extendinim‘ą*
  - $\gamma(g) = -d – (g-1)e$
    - *g – gap length*
    - *d – gap-open penalty*
    - *e – gap extention penalty*

Local vs global alignment

Pairwise alignment with linear gap score

GLOBAL (NEEDLEMAN-WUNCSH)

$$F_{(i,j)} = \max \begin{cases} F_{(i-1,j-1)} + s(x_i, y_i) \\ F_{(i,j-1)} - d \\ F_{(i-1,j)} - d \end{cases}$$

$$F_{(i,0)} = -id$$

$$F_{(0,j)} = -jd$$

$F_{(i,j)}$ - matricos pozicija

d - gap penalty

s - score

LOCAL (SMITH-WATERMAN)

$$F_{(i,j)} = \max \begin{cases} F_{(i-1,j-1)} + s(x_i, y_i) \\ F_{(i,j-1)} - d \\ F_{(i-1,j)} - d \\ 0 \end{cases}$$

BLAST – Basic Local Alignment Search Tool

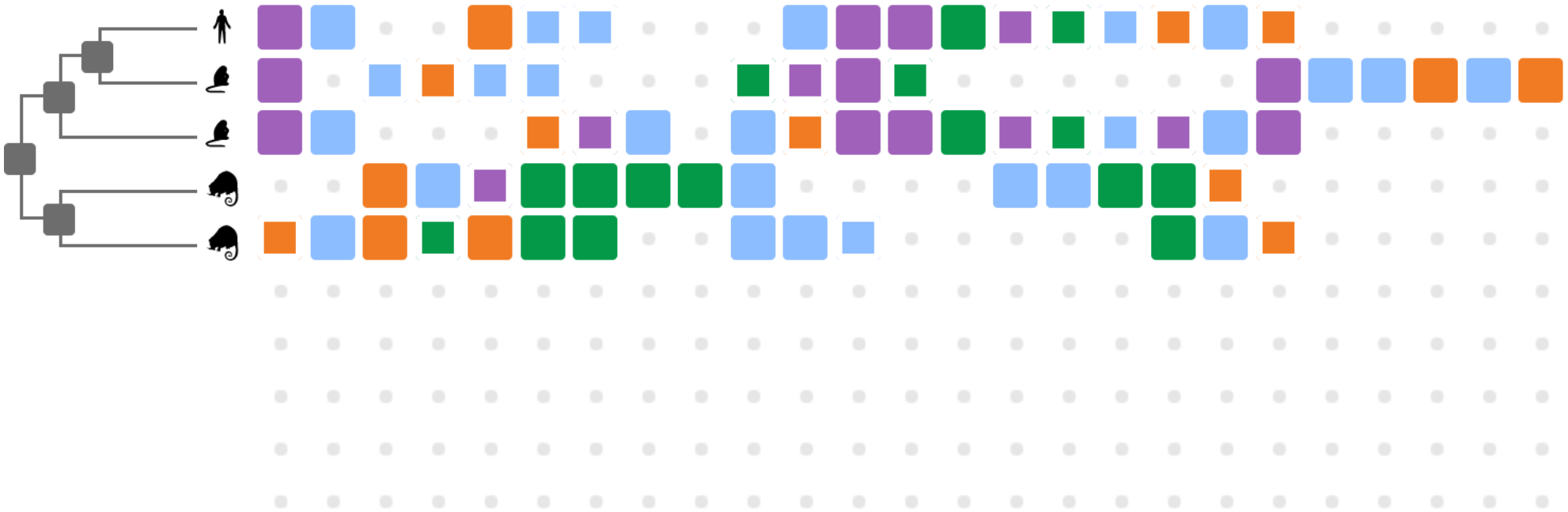
- Heuristinis metodas – mažesnis jautrumas/tikslumas, sutaupoma laiko ir vietos (*storage*)
- Identifikuojami trumpi sutampantys regionai (žodžiai)
- Jei žodžio *score* yra didesnis nei riba (*threshold*), žodis yra plečiamas (*extended*) į abi puses be *gap‘ų*
- Algoritmas sustoja plėsti *alignment‘ą,* kai žodis pasiekia maksimalią taškų sumą
- Naujos BLAST versijos bando sujungti kelis *alignment‘us* tarp kurių yra *gap‘as*

BLAST – praktinė užduotis

- Nueikite į UNIPROT duomenų bazę (http://www.uniprot.org/) ir raskite P38398 baltymą.
- Kairėje pasirinkite *Sequences* ir atsidarykite *Isoform1* FASTA formatu
- Nukopijuokite seką į BLAST webserver‘į (http://blast.ncbi.nlm.nih.gov/Blast.cgi), pasirinkite blastp (baltymų sekoms) ir paleiskite su *default* parametrais
- Kokių organizmų sekas gaunate? Ar tai tik žmogaus genomo sekos? Kokias išvadas galima daryti iš pateiktų BLAST rezultatų?

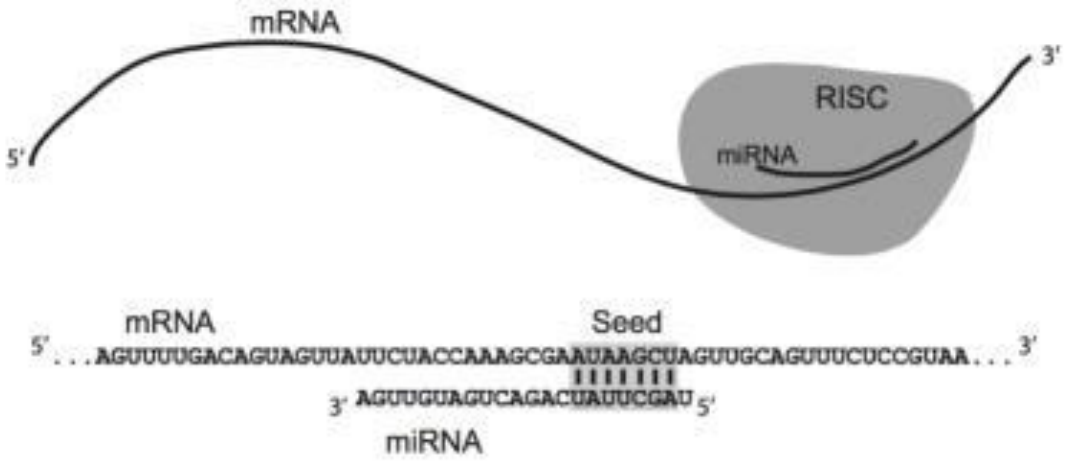
Multiple sequence alignment – 5 minutės žaidimo

http://phylo.cs.mcgill.ca/tutorial/index.html#EN



Motif discovery - užduoties įvadas

A microRNA (miRNA) is a small RNA molecule, around 22 bases long, which regulates gene expression by inhibiting the translation of mRNAs. A miRNA is incorporated into the RNA-induced silencing complex (RISC), which facilitates the base-pairing of the miRNA with the target single stranded mRNA. This yields a partially double stranded mRNA which cannot be translated by the ribosome. Most often the mRNA target site is complementary to the sequence going from positions 2-7 or 2-8 of the miRNA. The complementary region in the mRNA is called a **seed site**. Normally the seed sites are located in the 3' untranslated part of the mRNA (the 3'UTR)
An example for the human miRNA 21 (hsa-mir-21) is in the right.



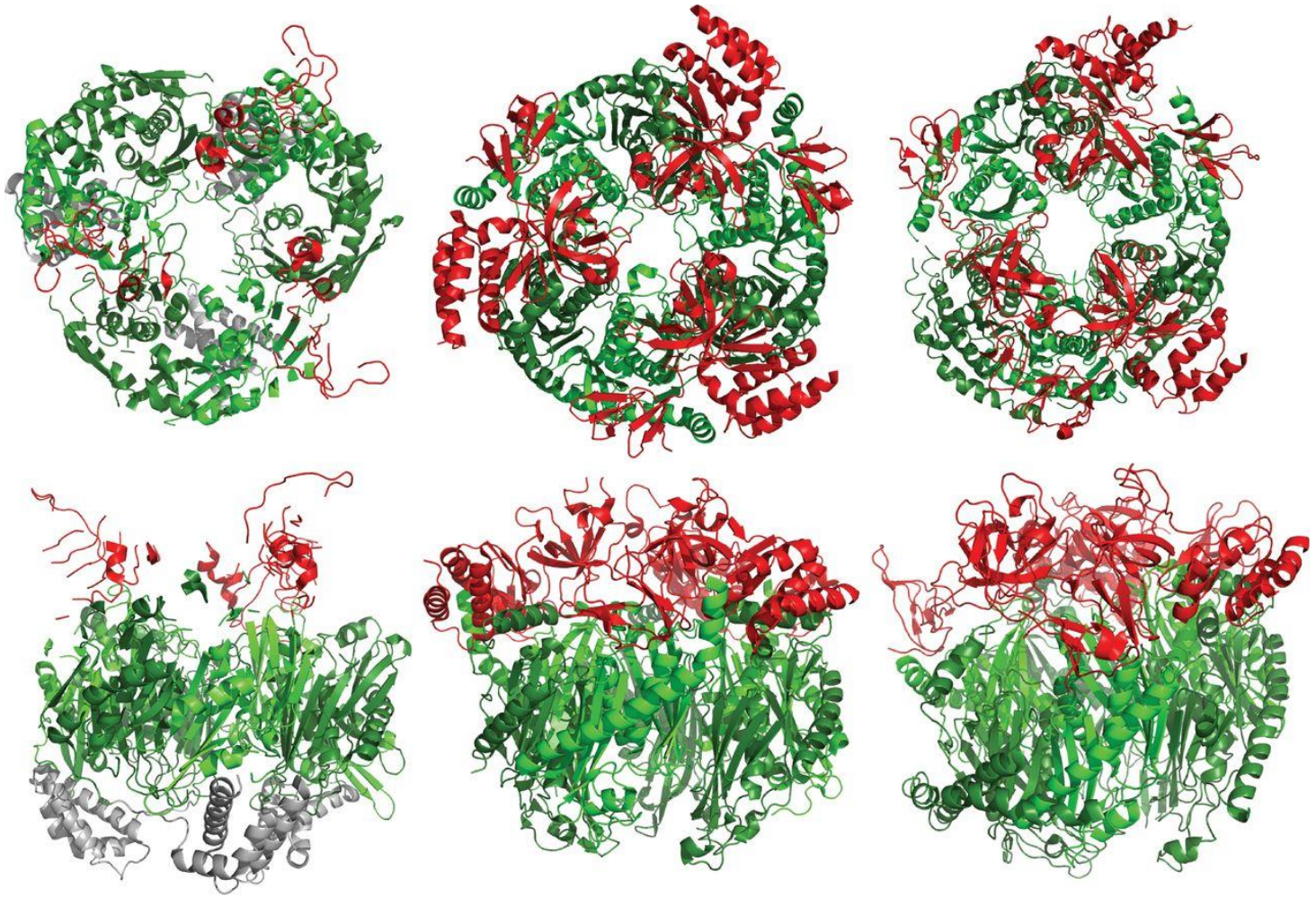
How can one identify the target sites of a particular miRNA? The idea is simply to perturb the expression levels of the miRNA and then do a **motif finding analysis** on the set of up or down regulated genes. The perturbation is most commonly done in two ways. In the first one you transfect into the cell multiple copies of the miRNA of interest, thereby increasing the cellular levels of the corresponding miRNA, which in turn enhances the repression of the miRNA target genes. In the second one you introduce in the cell a sequence which is complementary to the miRNA, which will bind the miRNA and thus it will block its binding to the seed site. Thus, in contrast to the first approach, in this case the function of the miRNA will be inhibited.

Motif discovery - užduotis

- Eksperimento metu žmogaus ląstelių linija buvo transfekuota miR-16, 500 labiausiai *up-regulated* genų buvo naudojami tolimesnėje analizėje
- Nueikite į MEME webserver‘į (http://meme-suite.org/tools/meme)
- Įkelkite pateiktą FASTA failą (PUM2.top500.fa) į MEME webserver‘į ir paleiskite su *default* parametrais
- Pasirinkite HTML output‘ą, naudodamiesi pateiktais LOGO atsakykite į pateiktus klausimus
- Ar visi identifikuoti motyvai yra vienodai tikėtini būti *true positives*?
- Ar galite pasakyti kokį motyvą didžiausia tikimybė rasti pagal MEME? Jei motyvas nėra visiškai konservatyvus, kokia yra labiausiai specifinė seka?
- Kokią išvadą apie miR-16 *seed site* galima daryti iš gautų rezultatų?

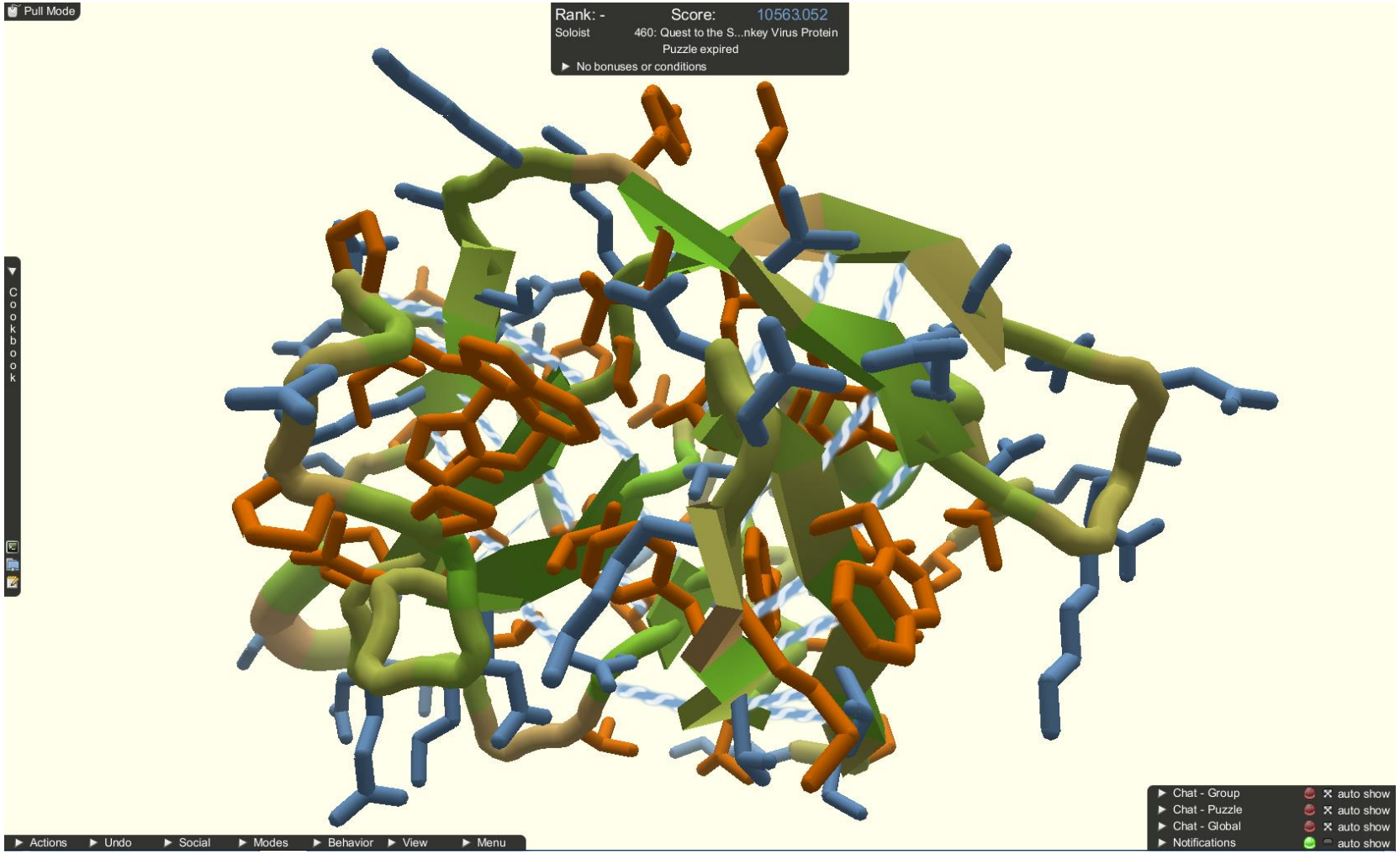
Tools‘ai sekų analizei

- Pairwise alignment:
  - BLAST - https://blast.ncbi.nlm.nih.gov/Blast.cgi
  - Needle (global) PROTEIN - https://www.ebi.ac.uk/Tools/psa/emboss_needle/
  - Needle (global) NUCLEOTIDE - https://www.ebi.ac.uk/Tools/psa/emboss_needle/nucleotide.html
  - Water (local) PROTEIN – https://www.ebi.ac.uk/Tools/psa/emboss_water/
  - Water (local) NUCLEOTIDE - https://www.ebi.ac.uk/Tools/psa/emboss_water/nucleotide.html
- Multiple sequence alignment:
  - Clustal W/Clustal Ω - https://www.ebi.ac.uk/Tools/msa/clustalo/
  - MUSCLE (protein) - https://www.ebi.ac.uk/Tools/msa/muscle/
  - T-Coffee - https://www.ebi.ac.uk/Tools/msa/tcoffee/
  - Visualization Jalview - http://www.jalview.org/
- Motif discovery:
  - MEME – http://meme-suite.org/tools/meme



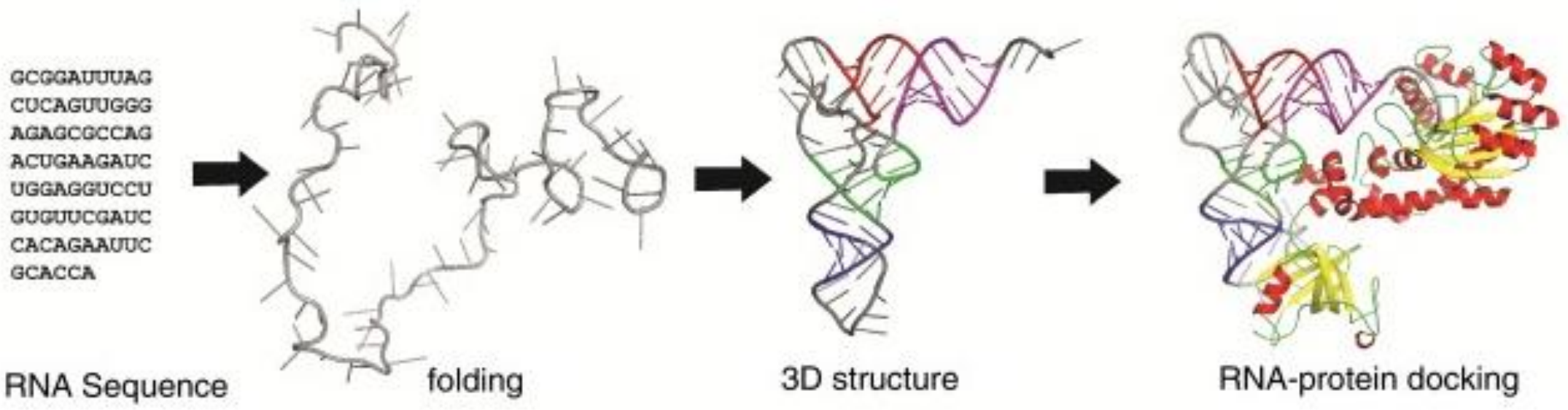
Struktūrinė bioinformatika

- Baltymų struktūrų analizė
- RNR struktūrų analizė


Pull Mode
Rank: -
Score: 10563.052
Soloist
460: Quest to the S...nkey Virus Protein
Puzzle expired
No bonuses or conditions
Cookbook
Chat - Group
Chat - Puzzle
Chat - Global
Notifications
auto show
Actions
Undo
Social
Modes
Behavior
View
Menu

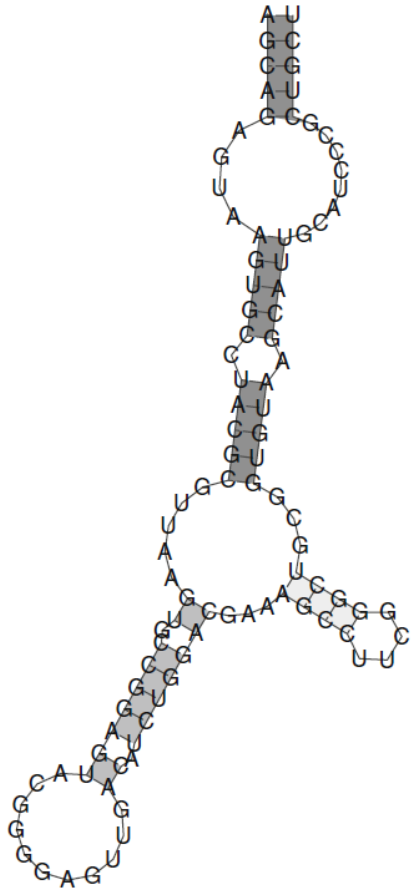
Fold.it

RNR erdvinės struktūros

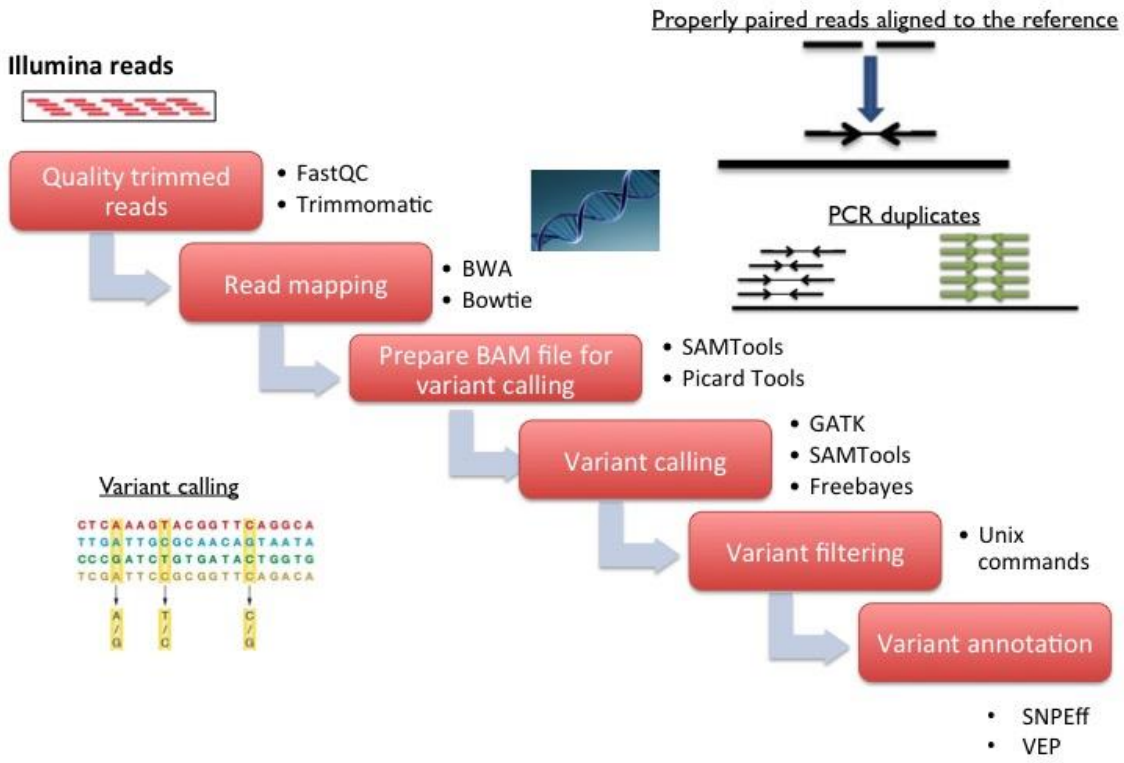


RNR struktūrų analizės užduotis

- Nukopijuokite RNR seką į RNAfold webserver‘į ir paleiskite su default parametrais (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAfold.cgi)
  - AGCAGAGUAAGUGCCUACGCGUUAAGUGCCGGAGUACGGGGAGUUGACAUCUGGA CGAAAGCCUUCGGGCUGCGGUGUAAGCAUUGCAUCCCGCUGCU
- Palyginkite gautą struktūrą (MFE) su struktūra, pavaizduota skaidrės dešinėje
- Nueikite į RNR anotacijų duomenų bazę Rfam (http://rfam.xfam.org/) ir raskite **RF01831** RNR šeimą (*Jump to*), pasirinkite pirmas 10 sekų multiple alignmen‘us (Eikite į *Alignment*, tuomet *download/view* (pasirinkite *View*) *FASTA alignment in gapped format)*
- Paleiskite rastas 10 sekų su RNAalifold naudojant default parametrus (http://rna.tbi.univie.ac.at/cgi-bin/RNAWebSuite/RNAalifold.cgi)
- Palyginkite gautą struktūrą su struktūra, pavaizduota skaidrės dešinėje, ir struktūra iš RNAfold webserver‘io? Kodėl matote jų skirtumus? (Hint: konservatyvios sekos)

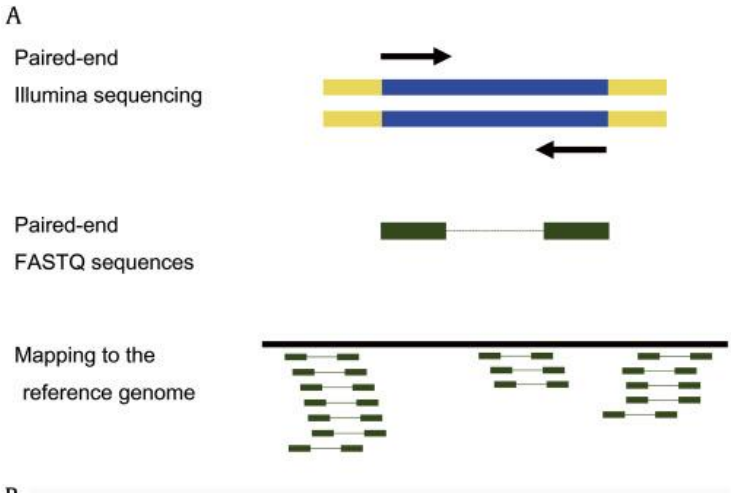


Bioinformatikos panaudojimas medicinoje

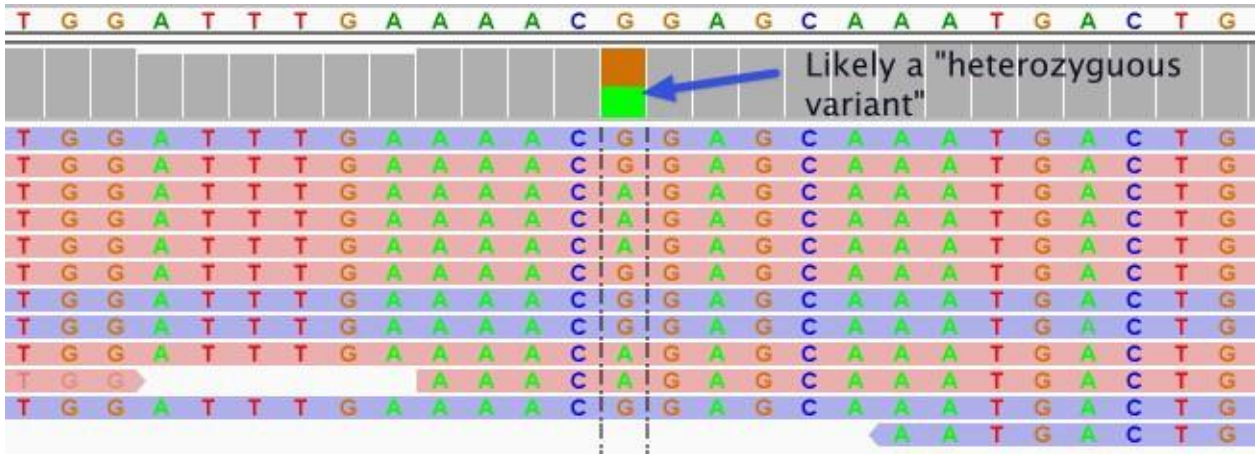


Bioinformatikos panaudojimas medicinoje

READ MAPPING



VARIANT CALLING



Bioinformatikos panaudojimas medicinoje

VARIANT IDENTIFICATION

Secure | https://variants.ingenuity.com/va/hgmd.jsp?id=CM002750

HGMD Professional subscriber? Click here to view this report in HGMD Professional

HGMD accession	Reported disease/phenotype	Variant class	Gene symbol	Codon change	Amino acid change	Codon number
CM002750	Breast cancer, association with	DFP	BRCA2	AAT-CAT	Asn-His	372

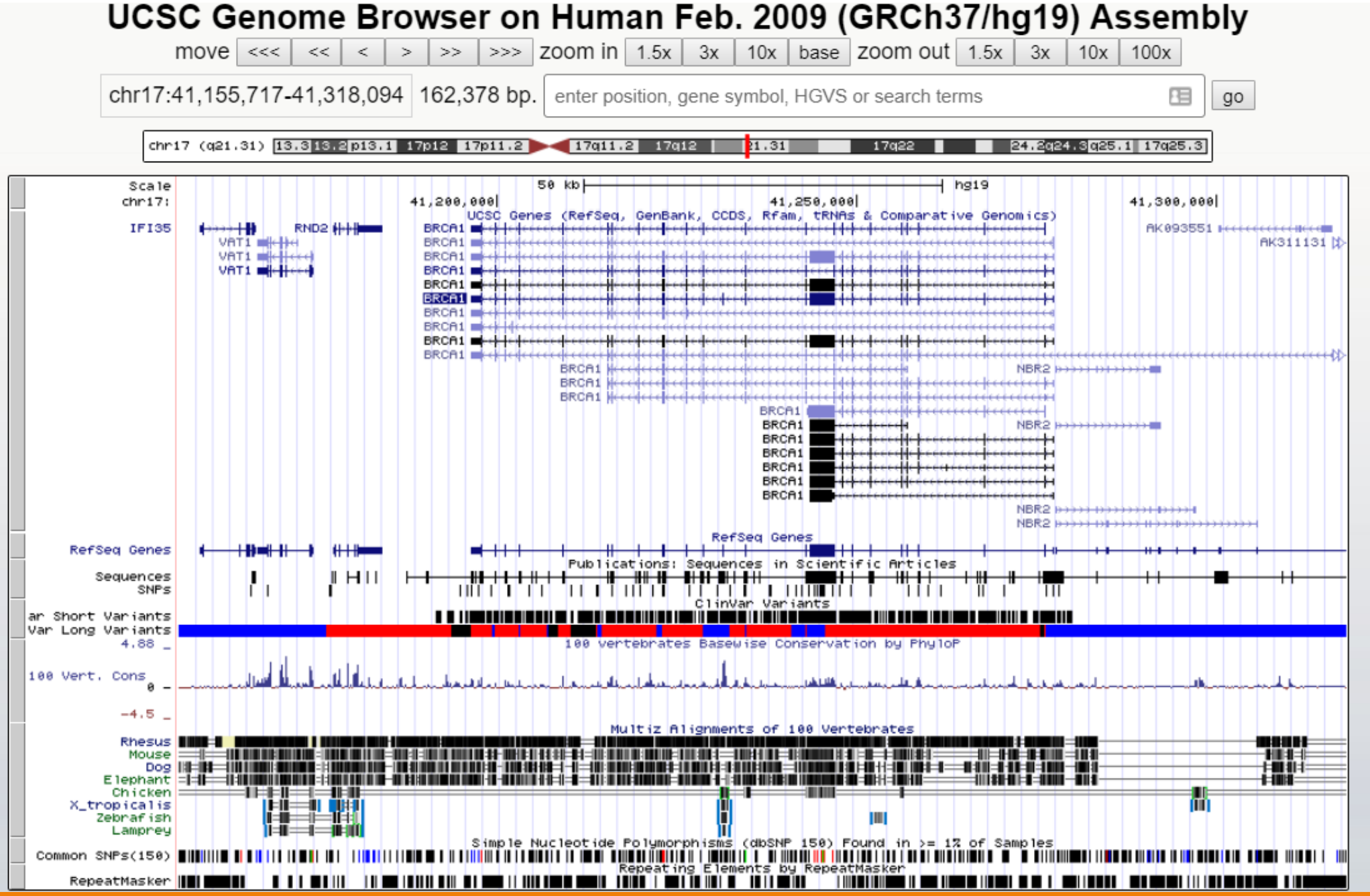
The N372H substitution exhibits a shift in polarity from polar to positively charged and displays an increase in Kyte-Doolittle hydrophobicity from -3.5 to -3.2. Approximately 0.21% of missense mutations in HGMD are Asn-His. The mutation occurs 3047 amino acids from the end of the protein.

Literature citation	Citation type	Support BETA	Comments/notes
1. Healey (2000) *Nat Genet* **26:** 362 PubMed: 11062481	Primary literature report	✓	No comments
2. Bayrakli (2011) *J Neurosurg Pediatr* **8:** 476 PubMed: 22044372	Additional phenotype	✓	Medulloblastoma; in homozygous form.
3. Bodian (2014) *PLoS One* **9:** e94554 PubMed: 24728327	Additional literature report	✗	found in healthy ancestrally diverse cohort. Table S1.
4. Feliubadaló (2013) *Eur J Hum Genet* **21:** 864 PubMed: 23249957	Additional literature report	✗	Descr. as polymorphism in Suppl. Table 1 (online).
5. Guidugli (2014) *Hum Mutat* **35:** 151 PubMed: 24323938	Additional literature report	✗	IARC Class 1 - not pathogenic
6. Hondow (2011) *BMC Cancer* **11:** 265 PubMed: 21702907	Additional literature report	✗	Descr. as polymorphism (in Table S3, online).
7. Hu (2008) *Sichuan Da Xue Xue Bao Yi Xue Ban* **39:** 973 PubMed: 19253839	Additional phenotype	✓	Breast cancer, association with
8. Johnston (2012) *Am J Hum Genet* **91:** 97 PubMed: 22703879	Additional literature report	–	found in 298/572 individuals
9. Kote-Jarai (2011) *Br J Cancer* **105:** 1230 PubMed: 21952622	Additional phenotype	–	Prostate cancer ?; descr as unclassified variant
10. Maxwell (2016) *Am J Hum Genet* **98:** 801 PubMed: 27153395	Additional literature report	✗	Table S5. Final call Benign.
11. Minucci (2015) *Expert Rev Mol Diagn* **15:** 1383 PubMed: 26306726	Additional literature report	✗	no clinical significance. Table 8.
12. Palli (2007) *BMC Cancer* **7:** 170 PubMed: 17767707	Additional phenotype	✓	Male BC risk
13. Pilato (2011) *Breast Cancer Res Treat* **125:** 651 PubMed: 20352487	Additional literature report		?
14. Qiu (2010) *Breast Cancer Res Treat* **123:** 487 PubMed: 20135345	Additional phenotype	✓	Breast cancer, susceptibility to, association with; low penetrance allele.
15. Seymour (2008) *Oncol Rep* **19:** 783 PubMed: 18288416	Additional literature report		None
16. Wenham (2003) *Clin Cancer Res* **9:** 4396 PubMed: 14555511	Additional literature report		no association with ovarian cancer
17. Wu (2005) *Cancer Res* **65:** 417 PubMed: 15695382	Functional characterisation		None

DIAGNOSIS

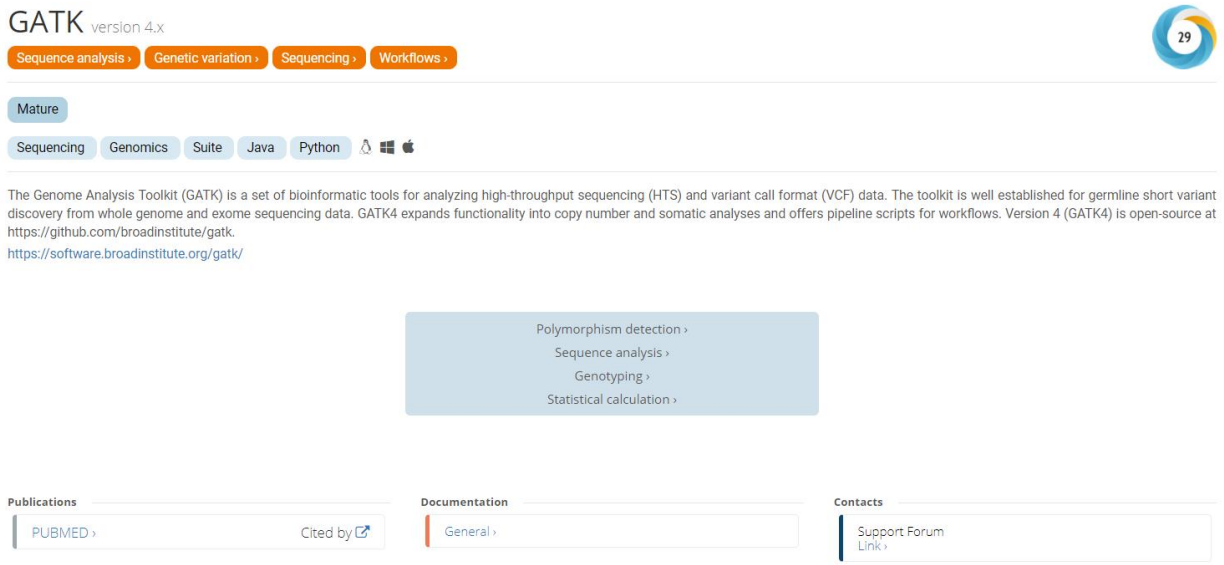
UCSC genome browser

- Nueikite į UCSC genome browser‘į (https://genome.ucsc.edu/) ir pasirinkite *Genomes,* Human hg19
- Nueikite į chr17:41,155,717-41,318,094
- Žemiau galima pasirinkti skirtingus track‘us priklausomai nuo to, ko ieškote
- Spustelėjus ant track‘o pateikiama informacija apie jį
- Galimybė kurti custom track‘us

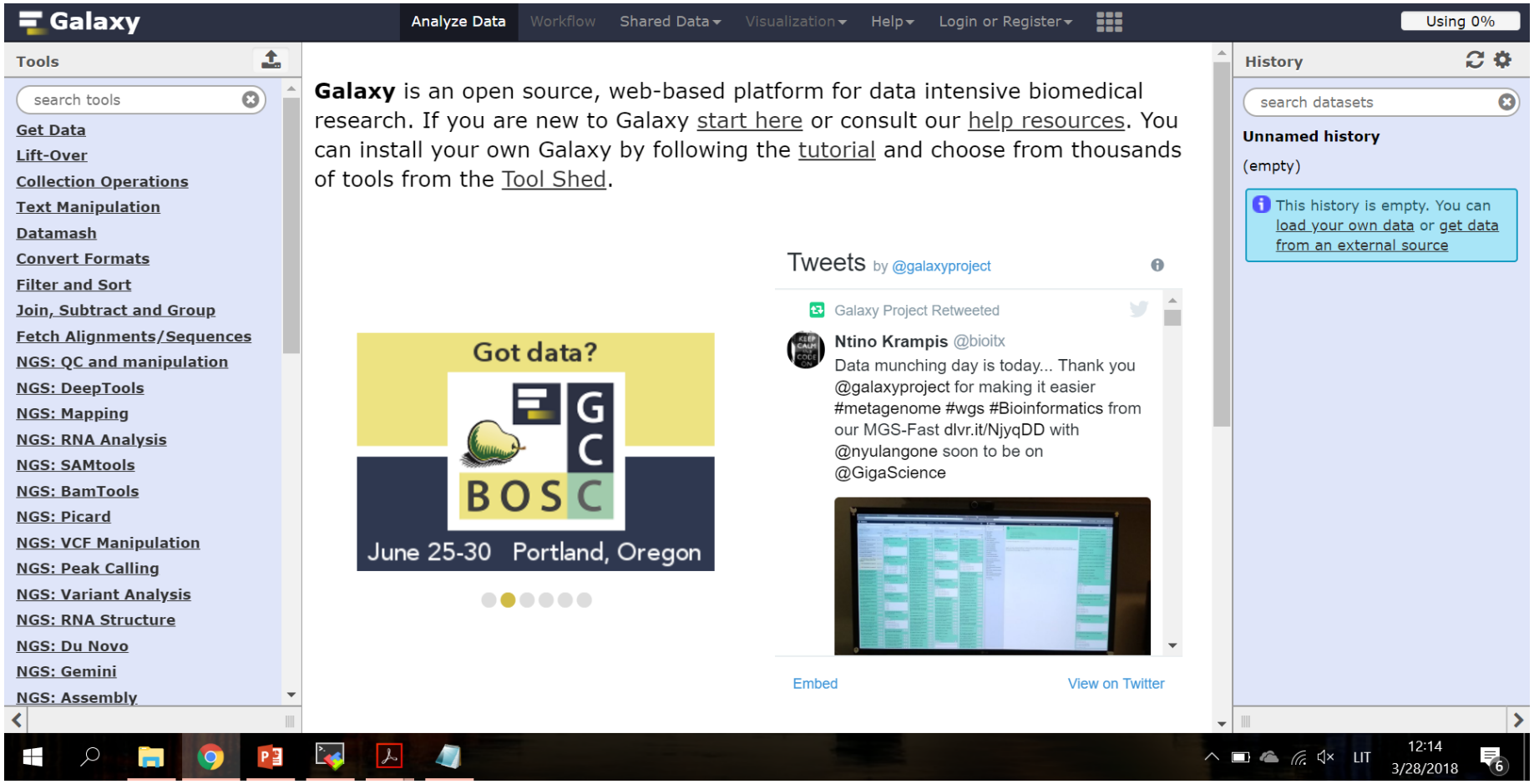

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x
chr17:41,155,717-41,318,094 162,378 bp.
enter position, gene symbol, HGVS or search terms
go
chr17 (q21.31)
Scale
chr17:
50 kb
hg19
41,200,000
41,250,000
41,300,000
UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)
IFI35
RND2
VAT1
BRCA1
NBR2
AK093551
AK311131
RefSeq Genes
Publications: Sequences in Scientific Articles
Sequences
SNPs
ClinVar Variants
ar Short Variants
Var Long Variants
4.88
100 vertebrates Basewise Conservation by PhyloP
100 Vert. Cons
0
-4.5
Multiz Alignments of 100 Vertebrates
Rhesus
Mouse
Dog
Elephant
Chicken
X_tropicalis
Zebrafish
Lamprey
Simple Nucleotide Polymorphisms (dbSNP 150) Found in >= 1% of Samples
Common SNPs(150)
Repeating Elements by RepeatMasker
RepeatMasker

Kur rasti specifinių bioinformatinių tools‘ų?

- Google
- bio.tools
- omictools.com
- mybiosoftware.com
- Kolegos, draugai, forumai



Galaxy - usegalaxy.org/ arba galaxy.pasteur.fr/



Išvados