

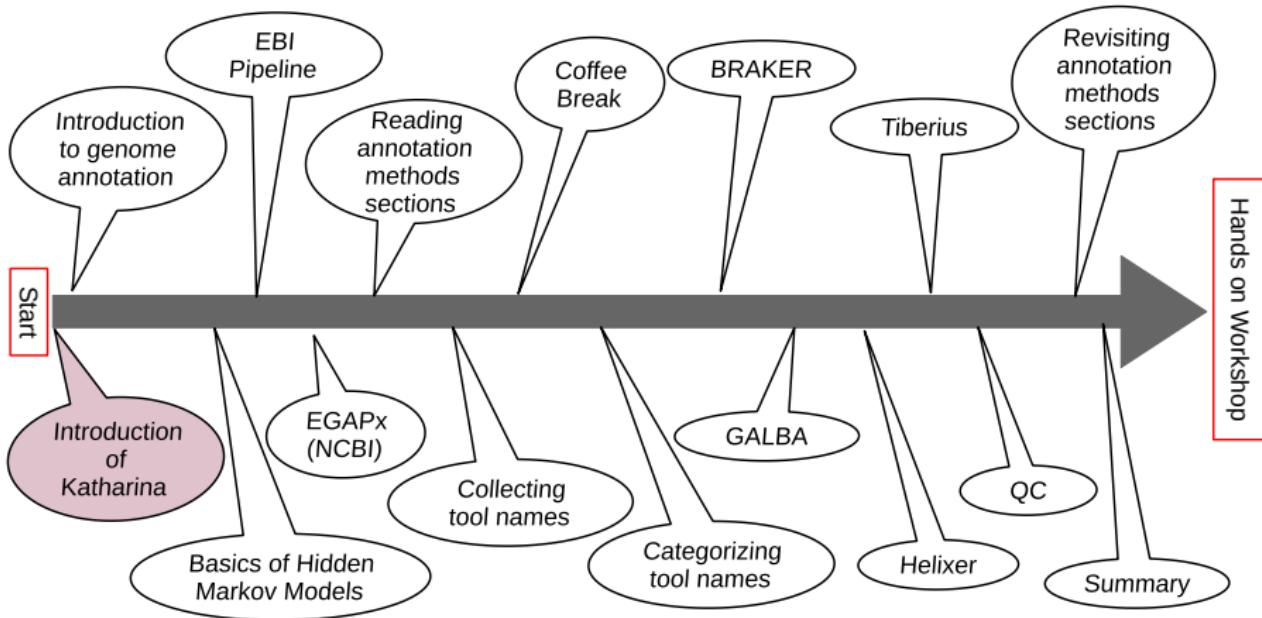
Annotation of Protein Coding Genes

May 6th 2025

Katharina J. Hoff

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Mastodon: @KatharinaHoff@fosstodon.org

E-Mail: katharina.hoff@uni-greifswald.de



Katharina J. Hoff

Group Leader in Applied Bioinformatics at University of Greifswald

Short CV

- 2005 B.Sc. Plant Biotechnology (Hanover, stays abroad: Budapest & Alnarp)
- 2009 Ph.D. Molecular Biology (Göttingen)
- 2022 Habilitation (Greifswald)

Research

- eukaryotic genome annotation, metagenomics
- best known for: **BRAKER** & other **Gaius-Augustus** software
- 38 peer-reviewed research articles with currently 7,902 citations

Teaching

- currently 1 postdoc, 4 (+4) PhD students, 1 MSc student, 3 BSc students
- applied bioinformatics, programming, statistics, & data science

... I love to sail, have a dog, a cat, and an 8-years old daughter...

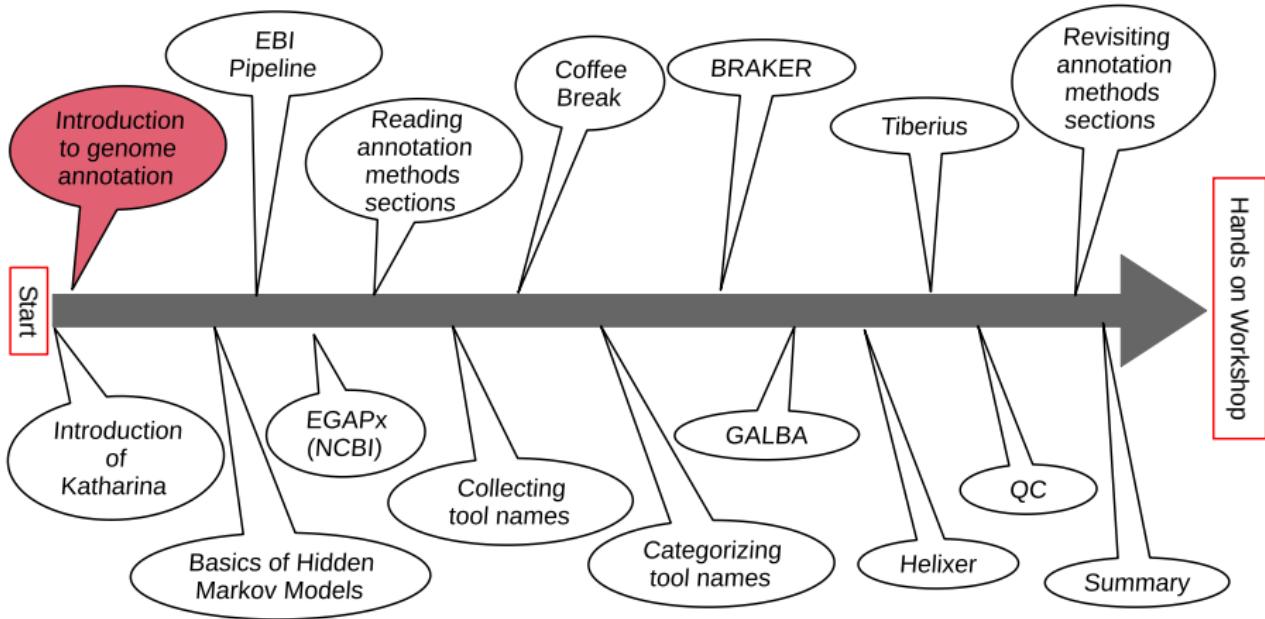
After this lecture, you will...

- understand what genome annotation in eukaryotes is
- know the basics of a Hidden Markov Model
- have a vague idea of INSDC annotation pipelines
- roughly understand methods sections on genome annotation
- know what's happening in BRAKER & GALBA
- be aware of the rapid advances with Deep Learning
- have an idea of quality control methods

Materials at

https://github.com/KatharinaHoff/GenomeAnnotation_Workshop_Barcelona

(Some images have been removed on Github because I do not have permission to share them.)



Where are the protein coding genes?

Genomic sequence: chicken

cctcacctctgagaaaacctcttgcaccaataccatgaagctctgcgtgactgtcctgtctctcc
gtgcttagtagtcgcctctgctcttagcacttcagcaccaagtaagtctactttgcagctgctatt
tcgagtcaagggttaggcagagtcctttctagtcggctggcaaacagtggatctgggatgg
acaaggcagcttaggaagattgccatgttagtctgtctaaatgttagagtctagatagatattcagtaa
cattcaagttcctatcccataagaatttagcaaccaggcagaggaaaacgatggctggaagtcagactg
ttgaattggcttcgccttaattatttgtcaagcaagccccgtccctctgtgccttggttcccc
atctgtcatatgaagggagtgcgtgttctgagactgaatccagttcaatcttctagatttcttc
tcgttcttctctgaagatccactattcagaataagactcctgtctatgttaggtggaaatggatacaag
ggaccatattgggttctggtagctccacaggatgctcaatgaagatgcaaattagaagtcaaaat
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gcctgctgtttcttacaccgcgaggaagcttcctcgcaacttgcgttagattactatgagaccagc
agcctctgtcccaagccagctgtgggtgagtatcaaccctggctccctggaggcaagggtgg
ctggattttaaggggcctgtttggggaggggtgatgagcgtggggaggcagctctcaggctg
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ggcagccgagacagaagggggttcctggggaggaatttgcgtggggaggcagcaggaaaggcag
acaggtccatgagatggaccatttcattaaaccatgctagaaaaacatgtggaaaagtcaactacca
ggctggcagggaatgggcaatttgcgtggggaggcagcttcattcatactgattgcattgc
cctggggccacagctaatttcattcattcatactgattgcattgcattgcggggaggcag
ggatccatccaccagagctccccacatggaccatggcaggcagaggaaatgcctaccacaggca
gggataaaggccagatgacctaagggtccatgggattctaatttcattgcgtggggaggcag
caaaccaaaaggcagcaagtcgtgcgtgacccaggatgcgtggggaggcagtcgtatgac
ctggaaactgaactgagctgcctcagagacaggaaatgttc

Examples for the importance of genome annotation

Silencing polygalacturonase activity in tomato



Sheeny et al. (1988) Proc. Natl. Acad. Sci. USA 85:8805-8809; Image: adapted from

<http://luisbarbosa2.blogspot.com/2013/06/flavr-savr-tomato.html>, Original: Asia Datta, Subhra Chakraborty, National Institute of Plant

Genome Research, New Delhi

Examples for the importance of genome annotation

Bacillus thuringiensis toxin against European corn borer

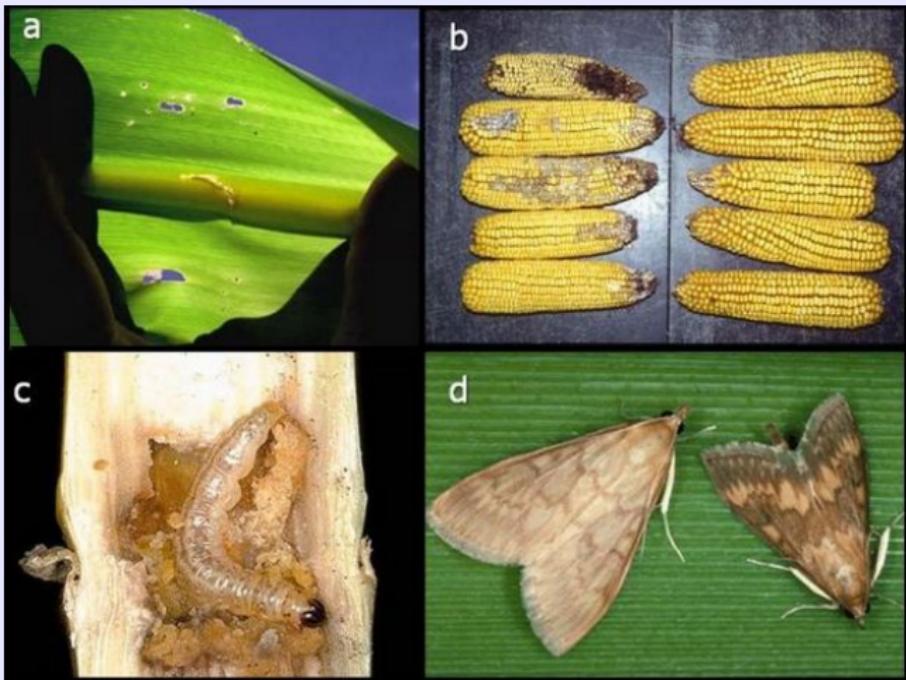


Image: Hellmich & Hellmich (2012) Nature Education Knowledge 3(10):4

http://www.nature.com/scitable/content/ne0000/ne0000/ne0000/ne0000/46977030/l_2.jpg

It does not take a village to publish a genome!

- In the past:

- ▶ Human: International Human Genome Sequencing Consortium (2001),
Nature 409(6822), 860 **248 authors**
- ▶ Mosquito: Nene et. al (2007) **95 authors**

It does not take a village to publish a genome!

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 - ▶ Human: International Human Genome Sequencing Consortium (2001), Nature 409(6822), **860 248 authors**
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- More recently:
 - ▶ 4 *Botrytis cinerea*: Adhikari et al. (2025), **5 authors**
 - ▶ European harvest mouse: O'Brien & Colom (2024), **2 authors**
 - ▶ Great wood-rush: Goodwin et al. (2024), **4 authors**

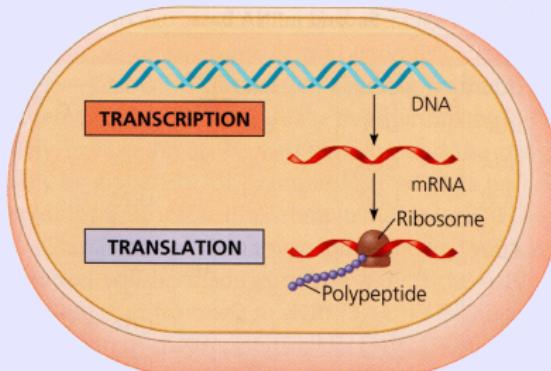
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 - ▶ Great wood-rush: Goodwin et al. (2024), **4 authors**
- **You can do it!**

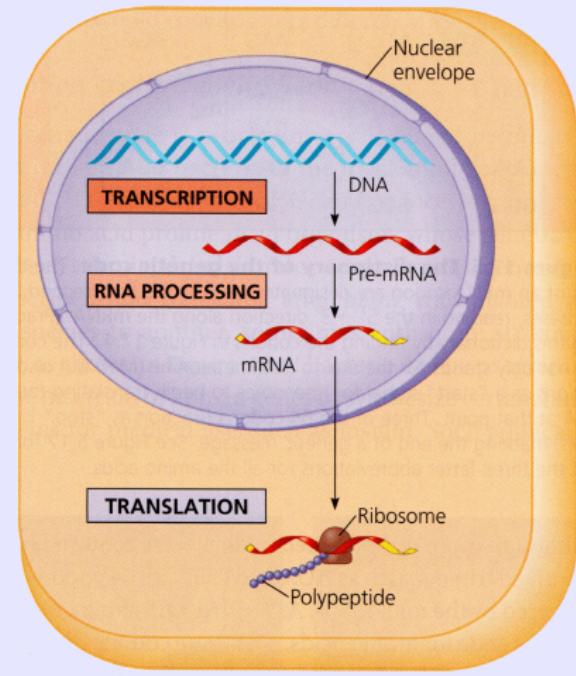
How does a cell recognize protein-coding genes?

Transcription & Translation

Prokaryotes



Eukaryotes



Images: Campbell et al., Biology, San Francisco, 2008, p. 329, Fig. 17.3

How does a cell recognize protein-coding genes?

Prokaryotes & Eukaryotes*

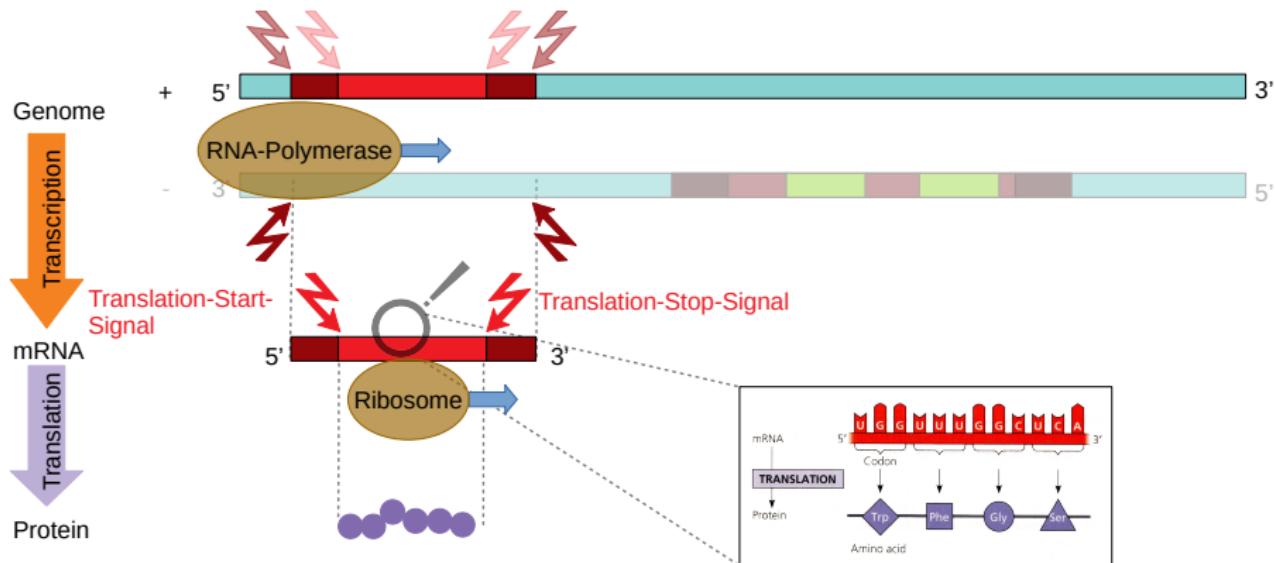
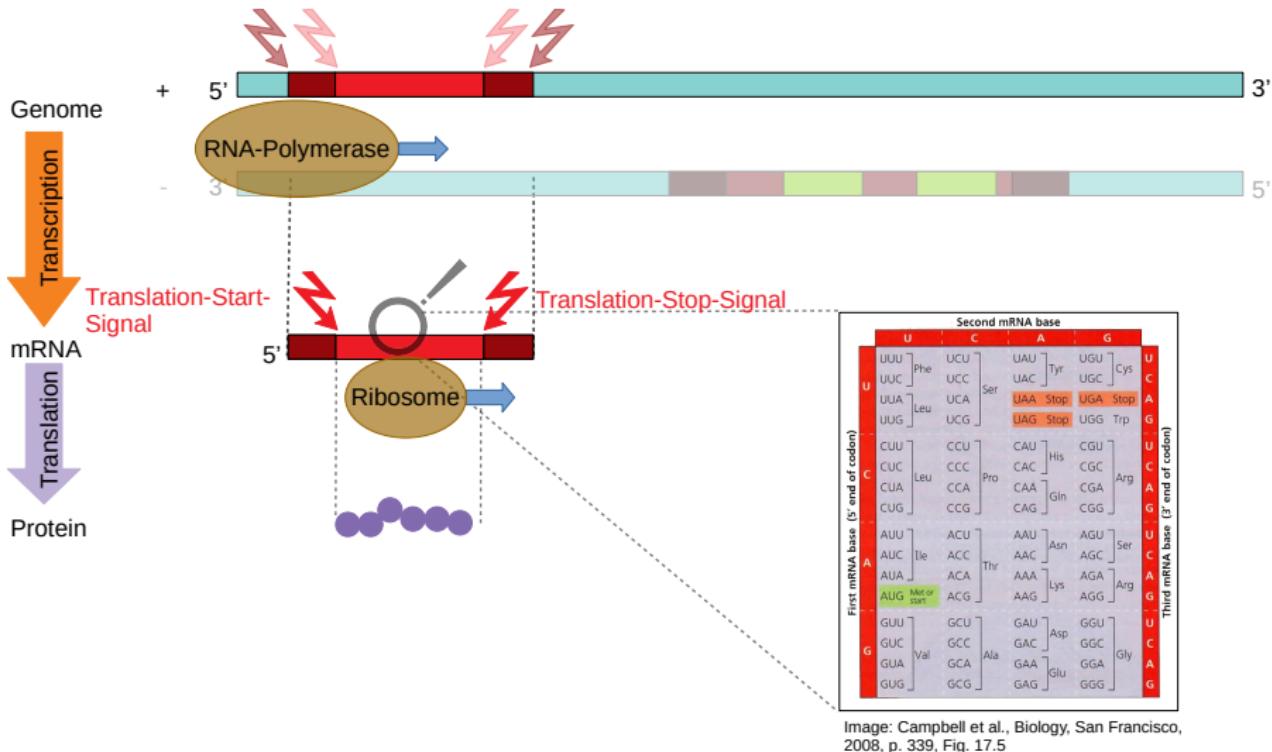


Image: Campbell et al., Biology, San Francisco, 2008, p. 329, Fig. 17.4

*) only some of the genes in eukaryotes

How does a cell recognize protein-coding genes?

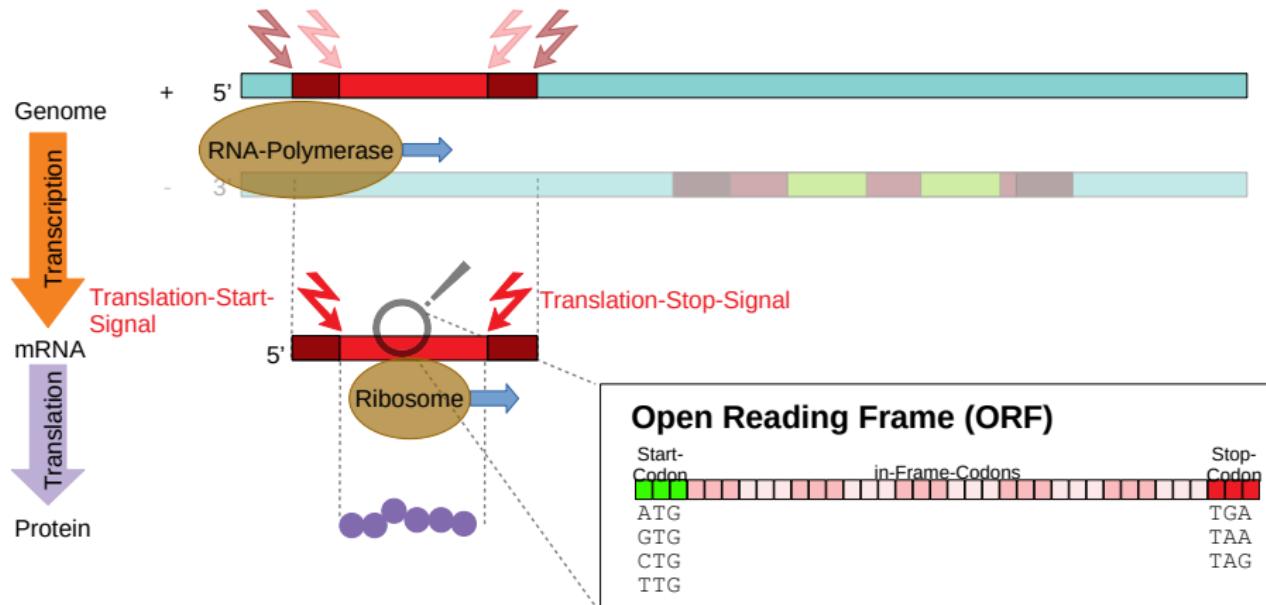
Prokaryotes & Eukaryotes*



*) only some of the genes in eukaryotes

How does a cell recognize protein-coding genes?

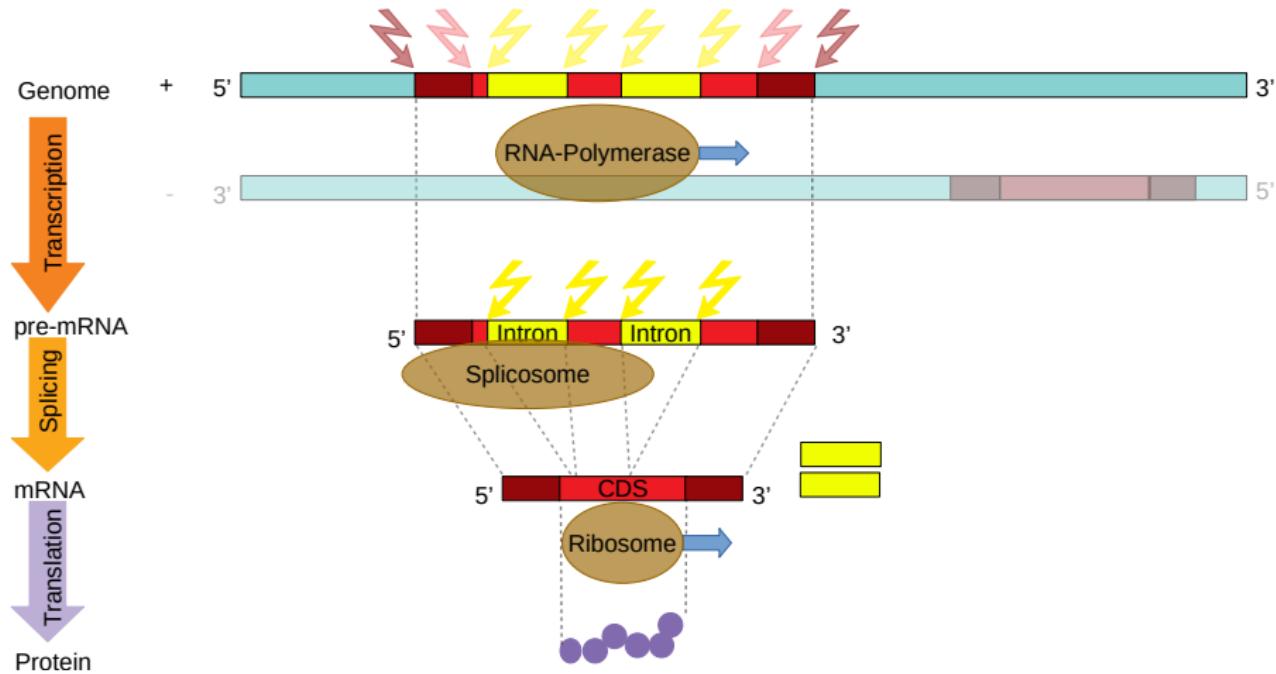
Prokaryotes & Eukaryotes*



- every protein coding gene has an ORF
- not every ORF is a protein coding gene

How does a cell recognize protein-coding genes?

Eukaryotes: Splicing of introns



The Genome Annotation Problem

Genomic Sequence: chicken

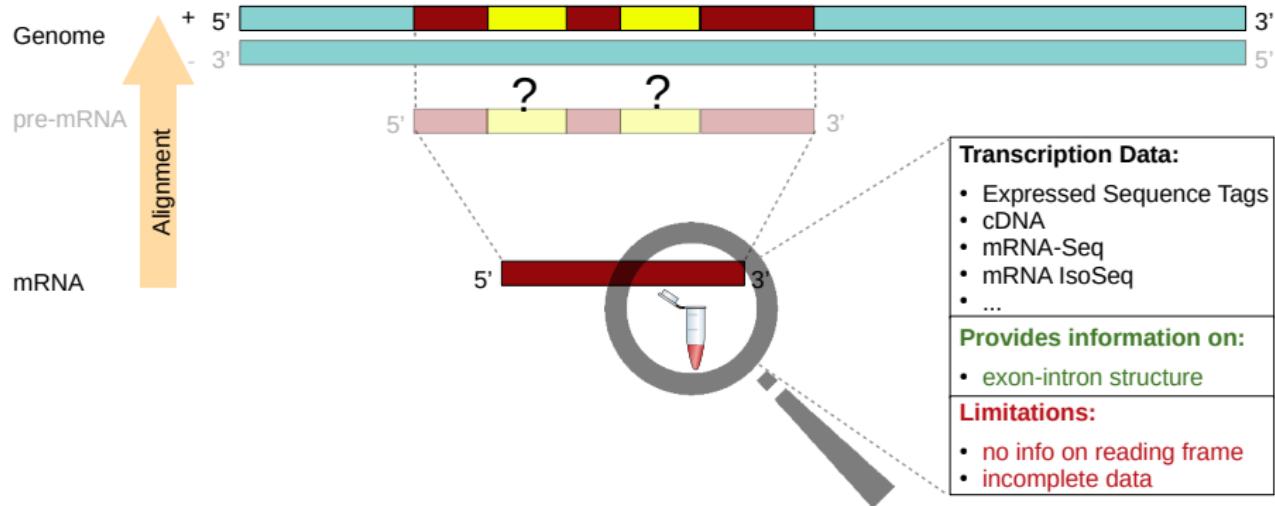
The Genome Annotation Problem

Genomic sequence: chicken (1 gene: macrophage inflammatory protein-1 b)

cctcacctctgagaaaacctcttgccaccaataccatgaagctctgcgtgactgtcctgtctctcc
gtgcttagtgcctctgctcttagcacttcagcaccaagtaagtctactttgcagctgctatt
tcgagtcaagggttaggcagagtcctttctagtcggctggcaaacacgtggatctgggatgg
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cattcaagttcctatttcttaagaatttagcaaccaggagaaaacgatggctggaagtcagact
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ggaccatattgggttctggtagctccacaggatgctcaatgaagatgcaaaattagaagtcaaaat
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ggctggcagggaatgggcaatcttactgattgcacccactggctccatctggcaacc
cctggggccacagctaaatccatgtggtagttacaggagtcgtccatgtgcgtgg
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gggataaaggccagatgacctaaggcccattggattctatctgtctgccttgcgt
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tc

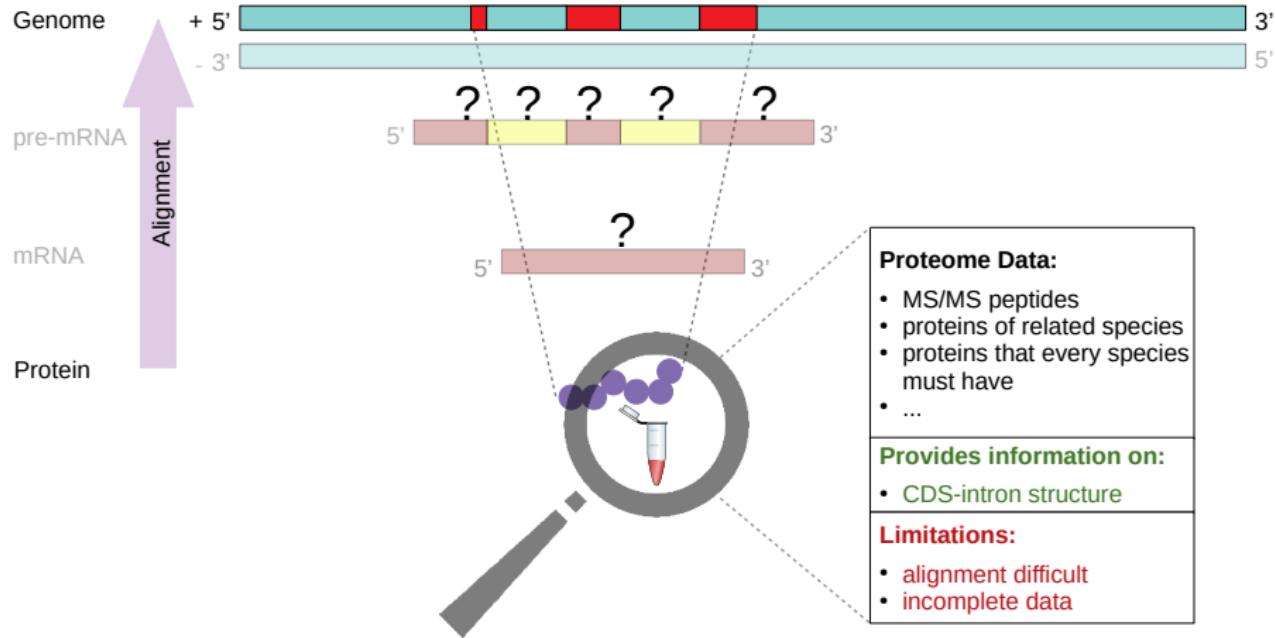
What aids in the identification of genes in genomes?

Evidence data from transcription



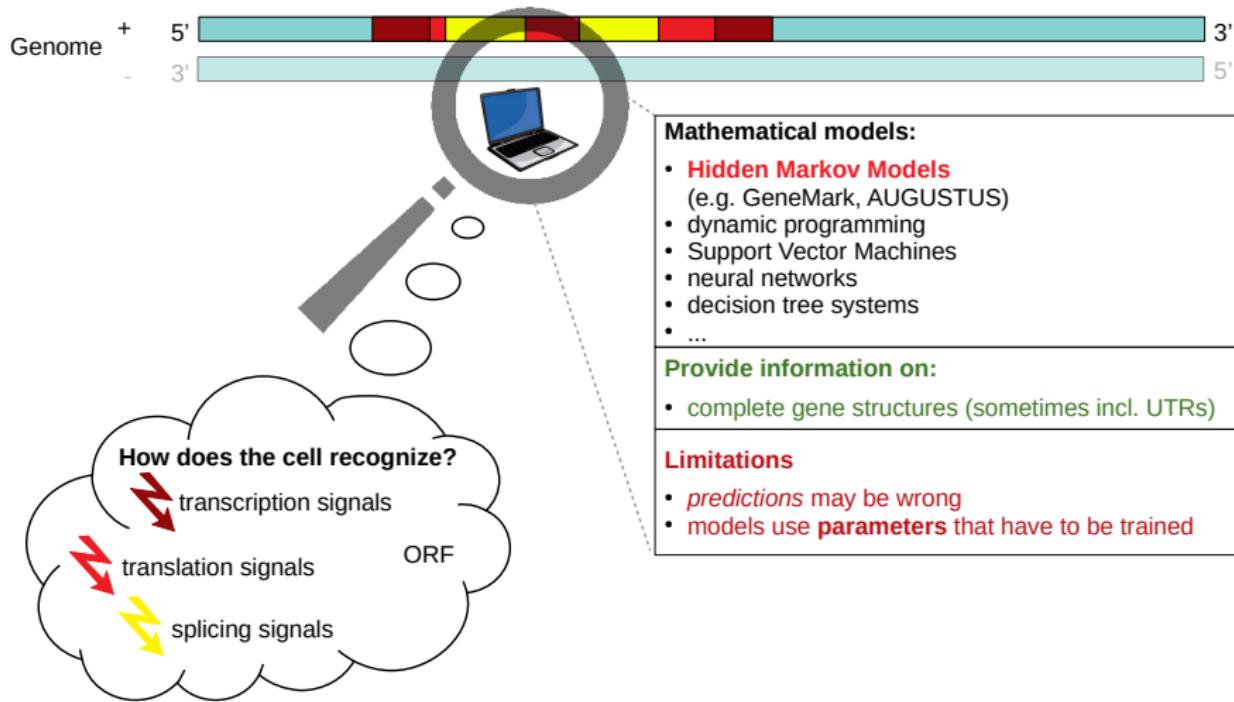
What aids in the identification of genes in genomes?

Evidence data from translation



What aids in the identification of genes in genomes?

Mathematical models



What aids in the identification of genes in genomes?

Mathematical models



A Hidden Markov Model

can read the genome sequence from left to right and, through knowledge of signals for transcription and translation, assign a probable state to each nucleotide (e.g., intergenic region or CDS).



Mathematical models:

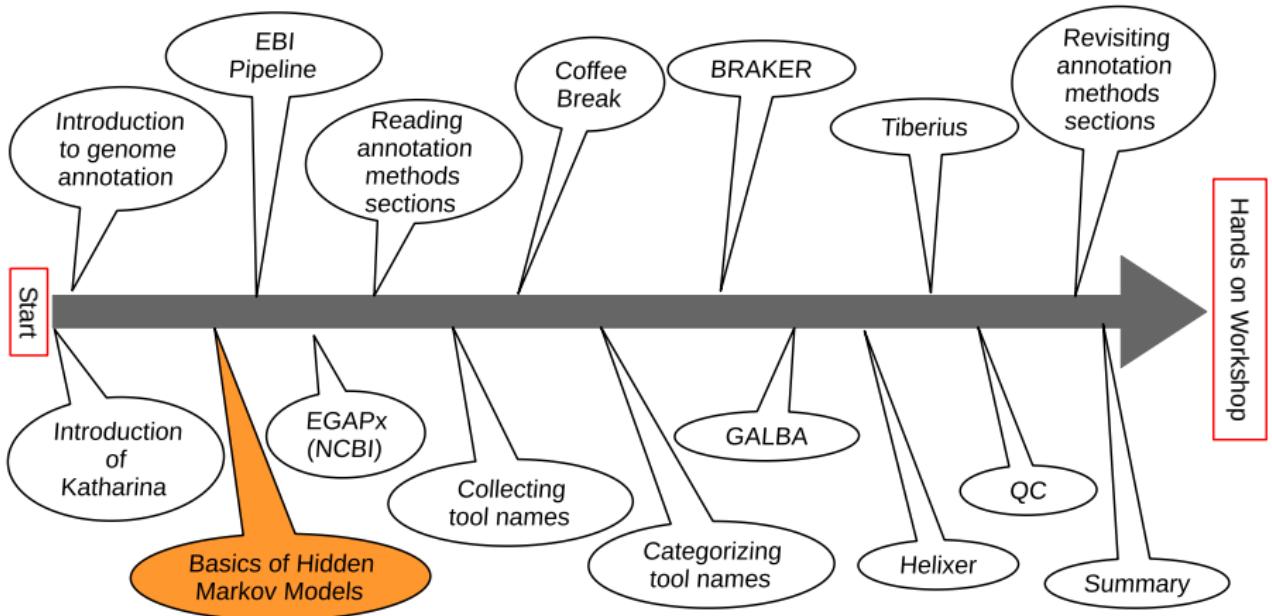
- **Hidden Markov Models**
(e.g. GeneMark, AUGUSTUS)
- dynamic programming
- Support Vector Machines
- neural networks
- decision tree systems
- ...

Provide information on:

- complete gene structures (sometimes incl. UTRs)

Limitations

- *predictions may be wrong*
- models use **parameters** that have to be trained



Basis of highly accurate gene prediction tools

Hidden Markov Model

Simplifications

- There are only 2 nucleotides: A, B
- There are only 2 sequence states: intergenic (I), coding sequence (K)

Input: “Genome sequence”

e.g. AABBBAB

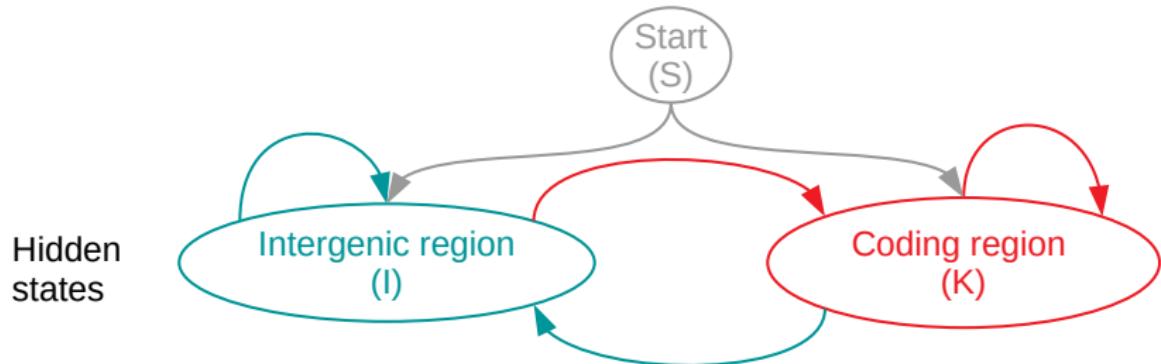
Goal: “Most likely path through hidden states”

e.g. **AABBBAA**

or **IIKKKIKI** $P(\text{path}) = 0.3\%$

Basis of highly accurate gene prediction tools

Hidden Markov Model

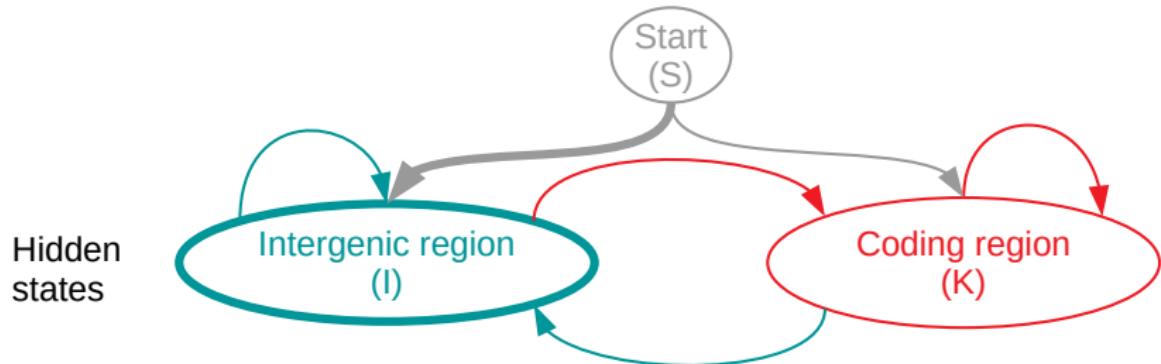


A possible 'state path' for the genome sequence:

AABBBA

Basis of highly accurate gene prediction tools

Hidden Markov Model

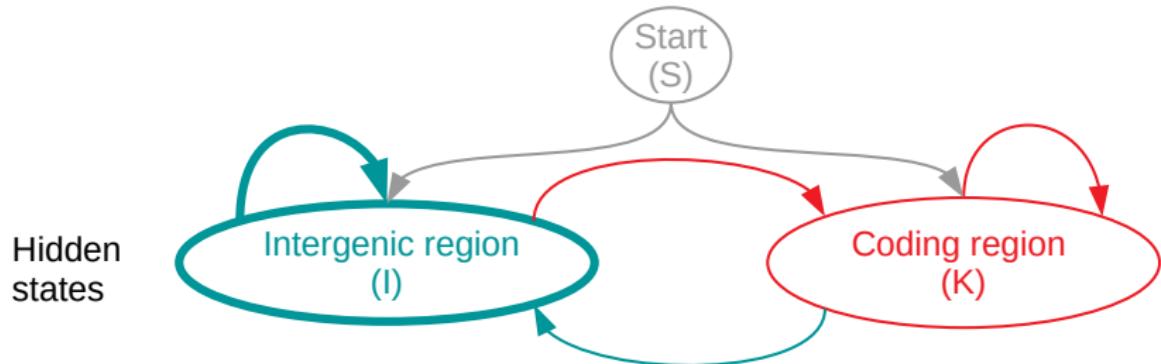


A possible 'state path' for the genome sequence:

AABBBA
I

Basis of highly accurate gene prediction tools

Hidden Markov Model

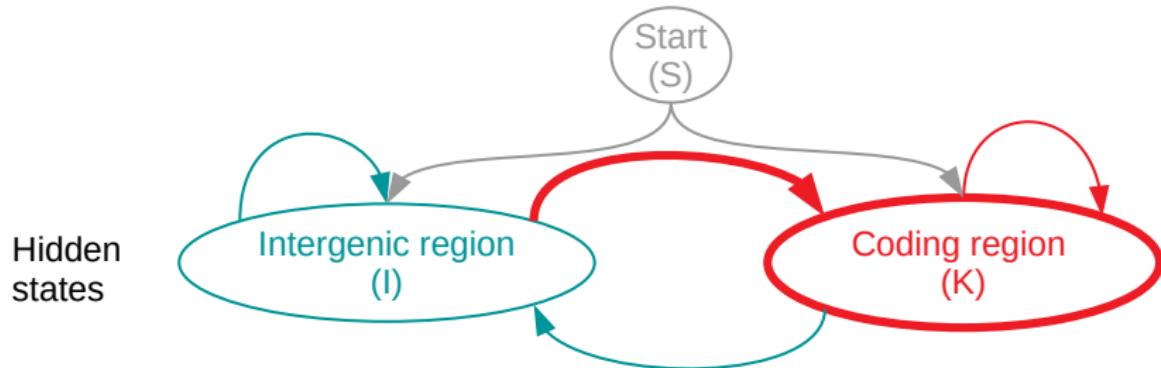


A possible 'state path' for the genome sequence:

AABBBA
II

Basis of highly accurate gene prediction tools

Hidden Markov Model



A possible 'state path' for the genome sequence:

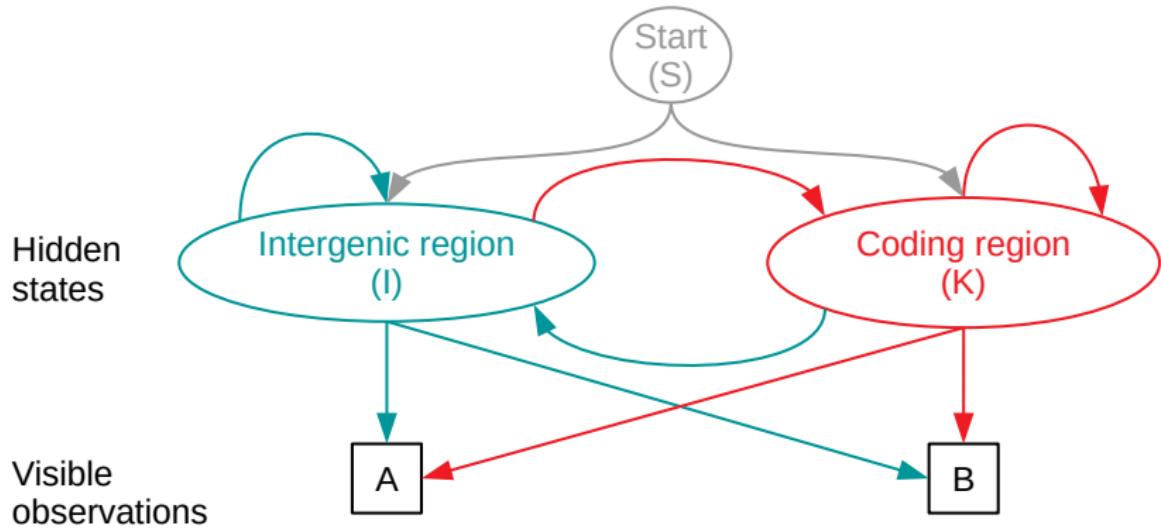
AABBBAA
IIK...

Model properties

- 1 The current value of the hidden state depends exclusively on the state of its predecessor.

Basis of highly accurate gene prediction tools

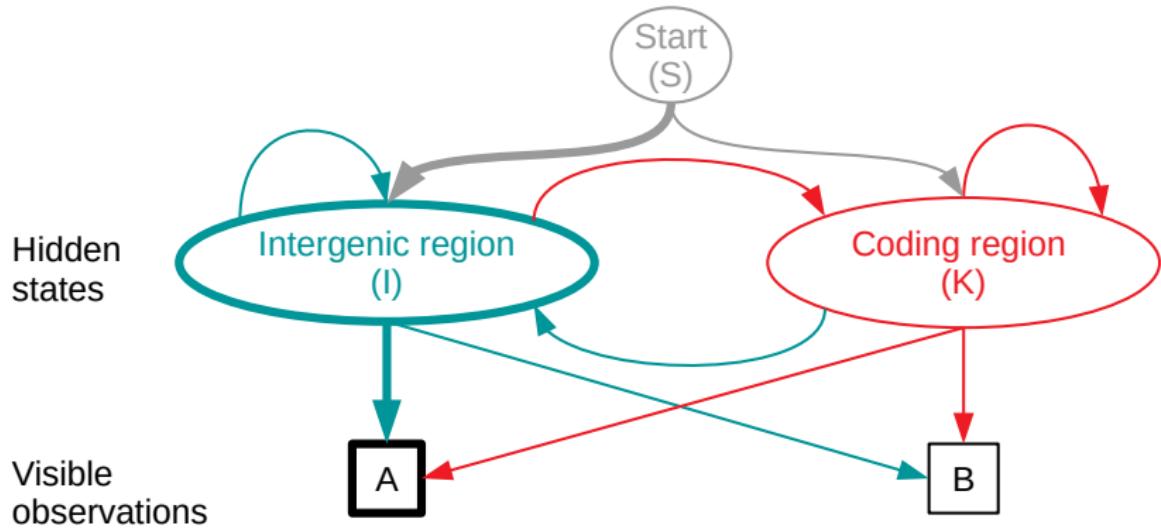
Hidden Markov Model



A possible 'state path' for the genome sequence:

Basis of highly accurate gene prediction tools

Hidden Markov Model

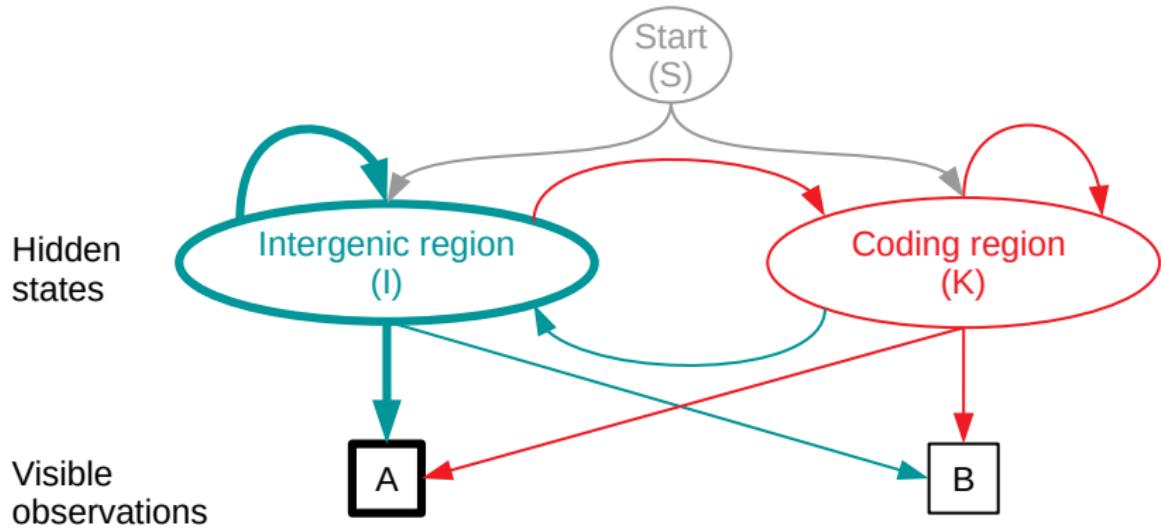


A possible 'state path' for the genome sequence:

A
I

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Hidden Markov Model

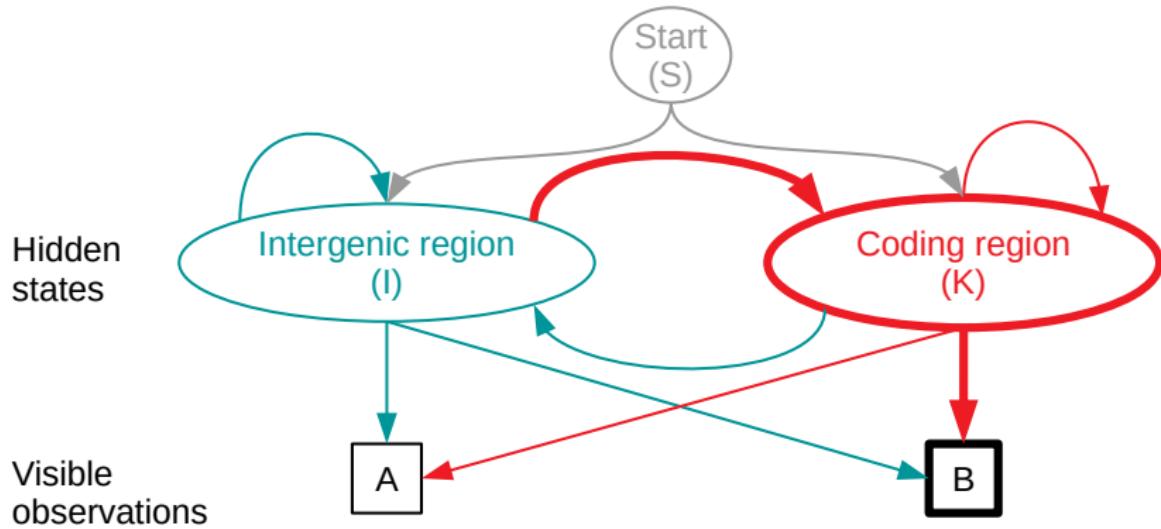


A possible 'state path' for the genome sequence:

AA
II

Basis of highly accurate gene prediction tools

Hidden Markov Model

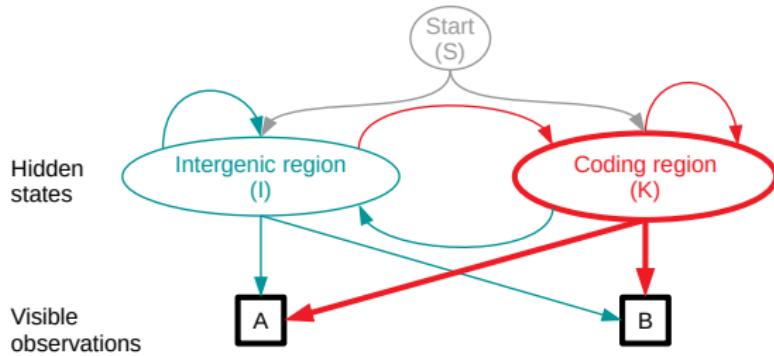


A possible 'state path' for the genome sequence:

AAB...
IIK...

Basis of highly accurate gene prediction tools

Hidden Markov Model

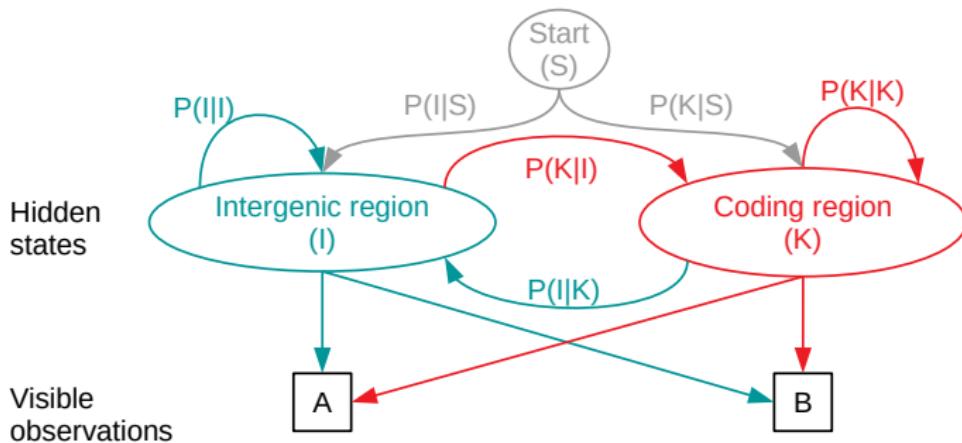


Model properties

- ① The current value of the hidden state depends exclusively on the state of its predecessor.
- ② The current value of the visible observation depends exclusively on the value of the current, hidden state.

Basis of highly accurate gene prediction tools

Hidden Markov Model



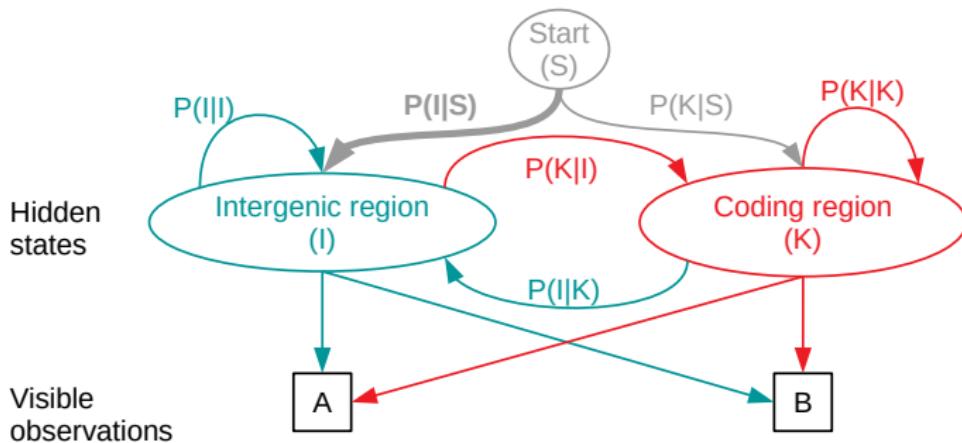
How likely are the state transitions?

Use data with known state transitions for learning!



Basis of highly accurate gene prediction tools

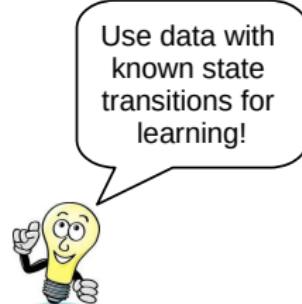
Hidden Markov Model



Training data:

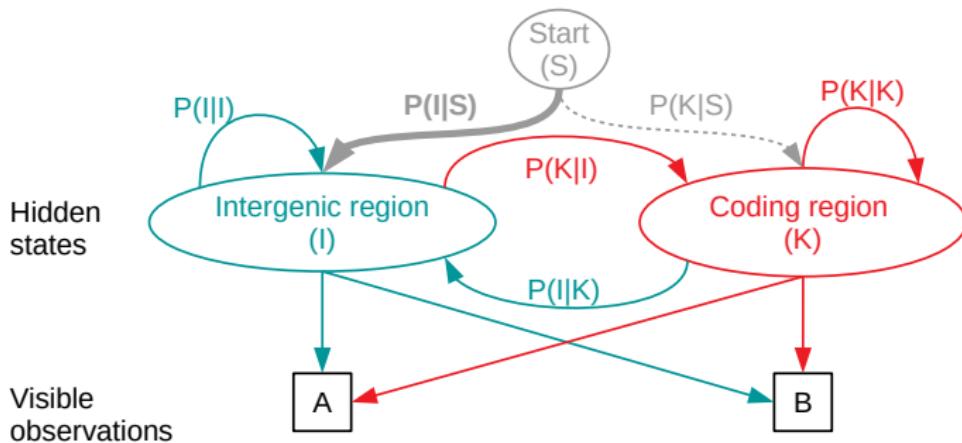
AABABA
IKKIII

Start probability
 $P(I|S) = ?$



Basis of highly accurate gene prediction tools

Hidden Markov Model



Training data:

AABABA

IKKIII

+

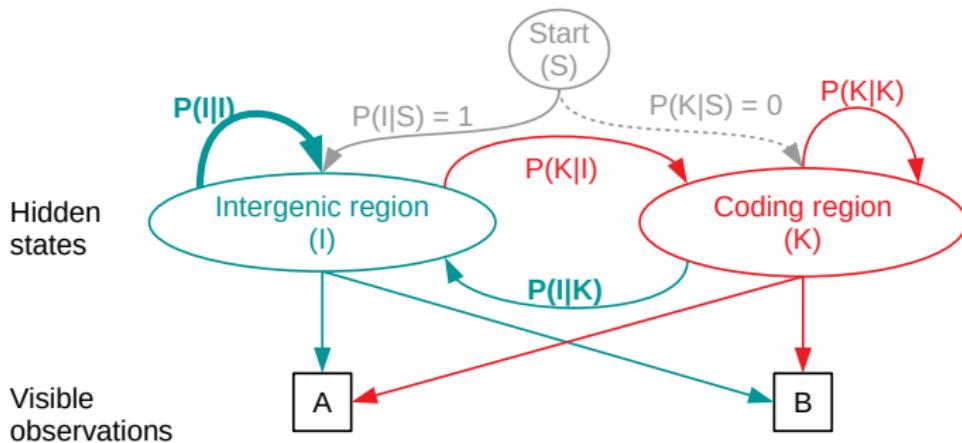
Start probability
 $P(I|S) = 1$

Use data with known state transitions for learning!



Basis of highly accurate gene prediction tools

Hidden Markov Model



Training data:

AABABA
IKKIII

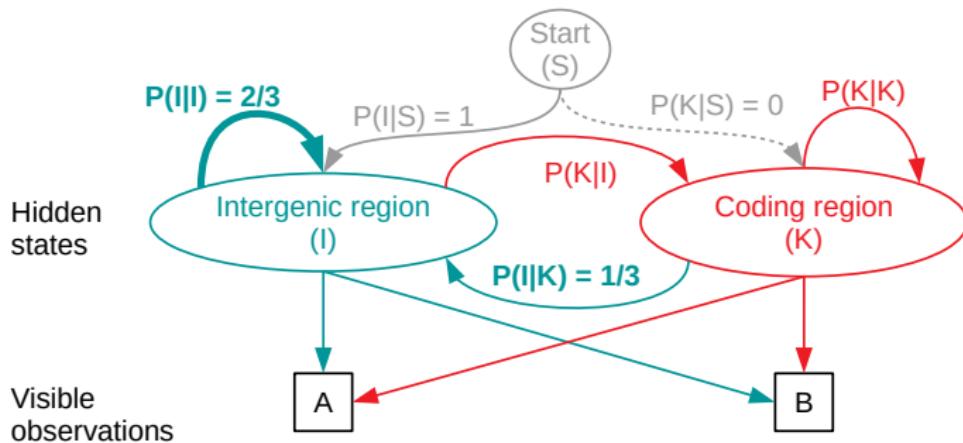
$P(I|I) = ?$

Use data with known state transitions for learning!



Basis of highly accurate gene prediction tools

Hidden Markov Model



Training data:

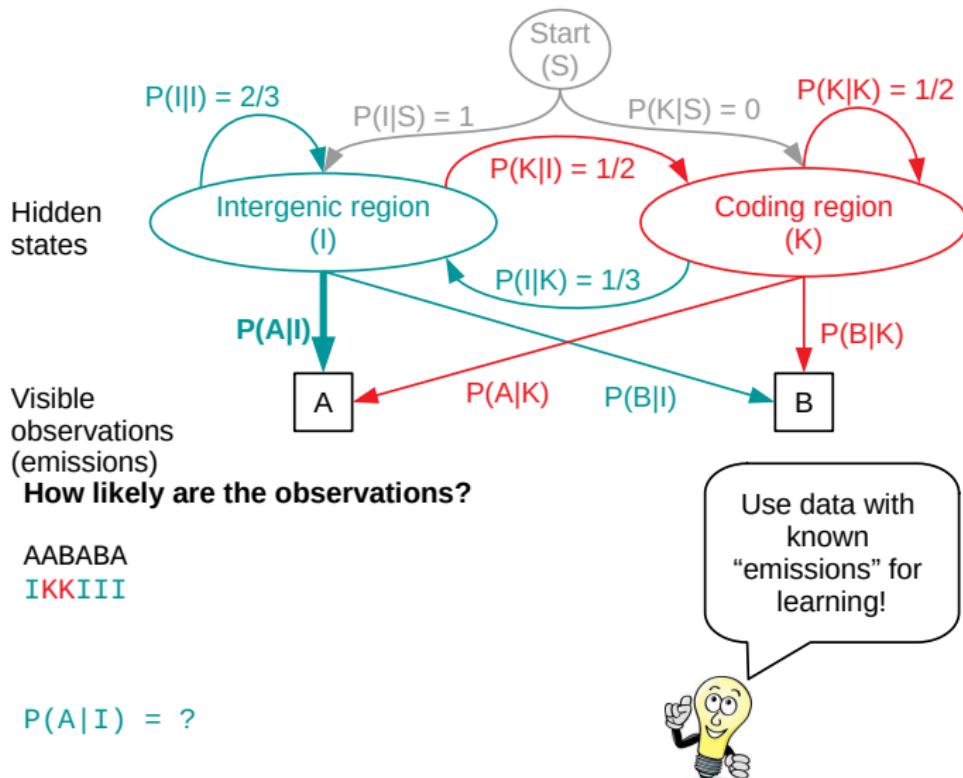
AABABA
IKKIII
-++

$$P(I|I) = 2/3$$

$$P(I|K) = 1 - P(I|I) = 1/3$$

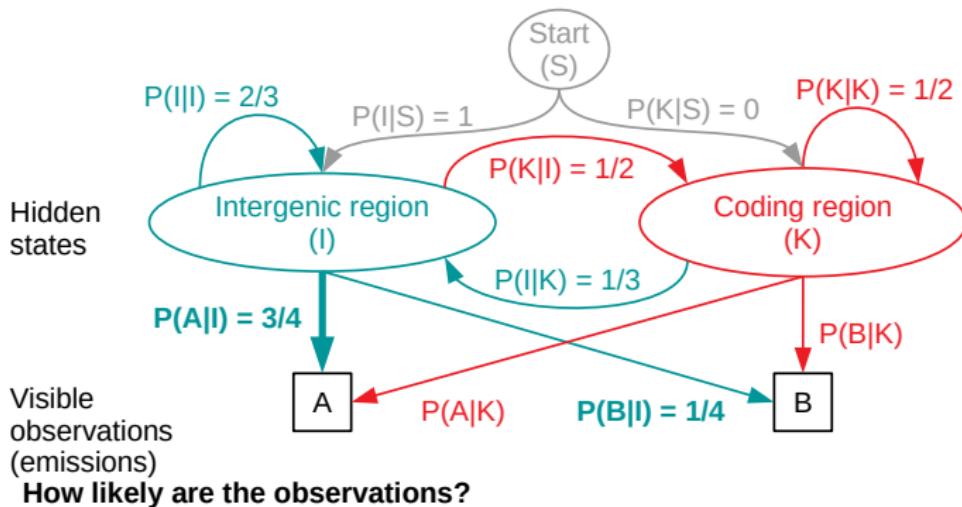
Basis of highly accurate gene prediction tools

Hidden Markov Model



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AABABA

IKKIII

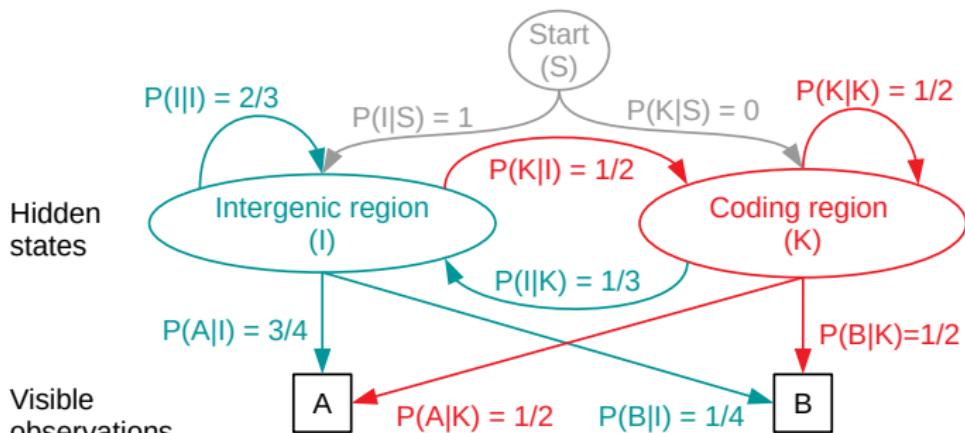
+ + - +

$$P(A|I) = \frac{3}{4}$$

$$P(B|I) = 1 - P(A|I) = 1 - \frac{3}{4} = \frac{1}{4}$$

Basis of highly accurate gene prediction tools

Hidden Markov Model



Training data:

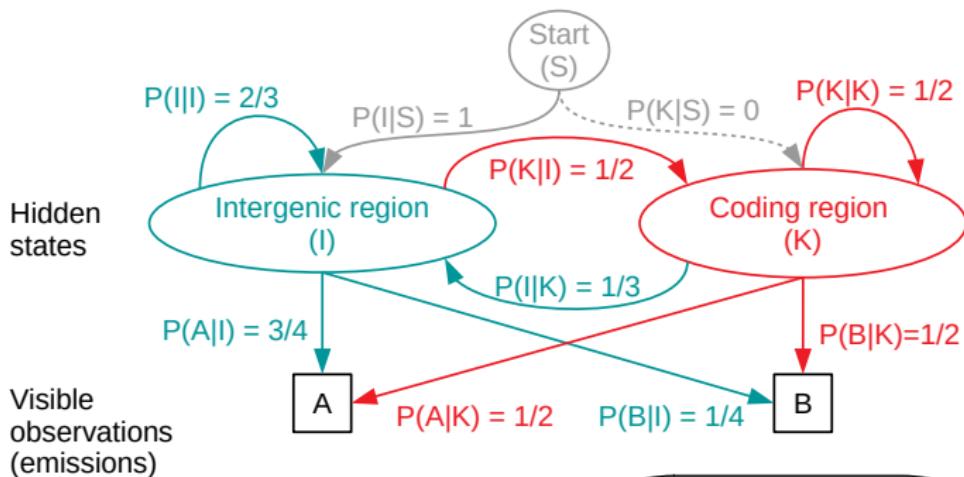
AABABA
IKKIII

In practice, more training data and training algorithm!



Basis of highly accurate gene prediction tools

Hidden Markov Model



How likely is a given state-emission path?

Path = AAB
IKK

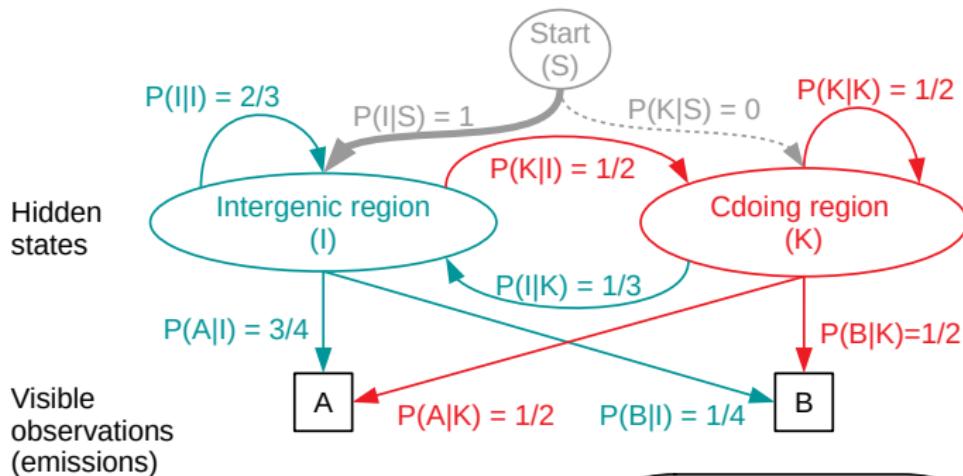
$P(\text{Path}) = ?$

Multiply the probabilities along the state-emission path!



Basis of highly accurate gene prediction tools

Hidden Markov Model



How likely is a given state-emission path?

Path = AAB
IKK

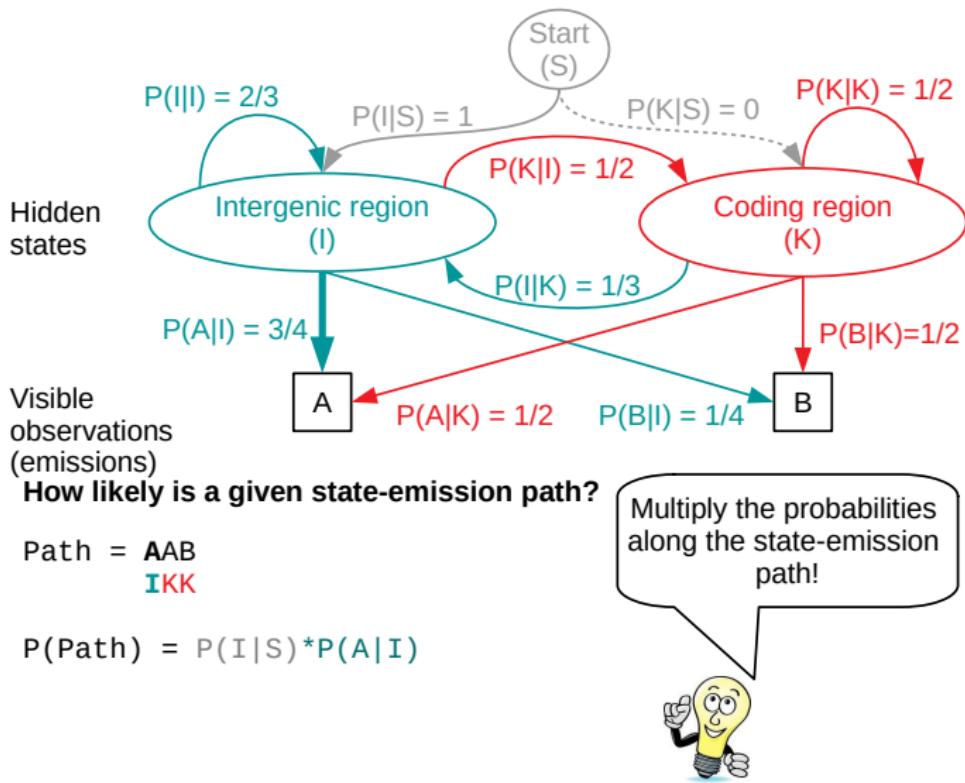
$P(\text{Path}) = P(I|S)$

Multiply the probabilities along the state-emission path!



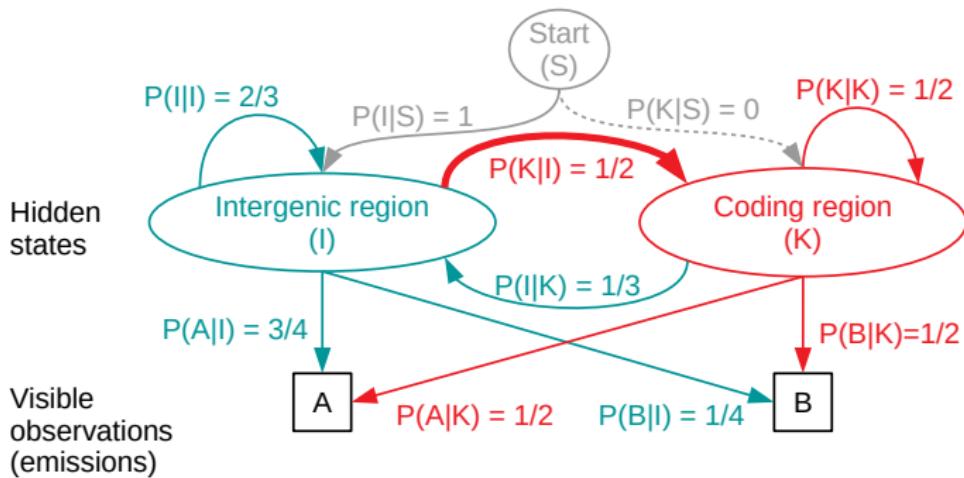
Basis of highly accurate gene prediction tools

Hidden Markov Model



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Hidden Markov Model



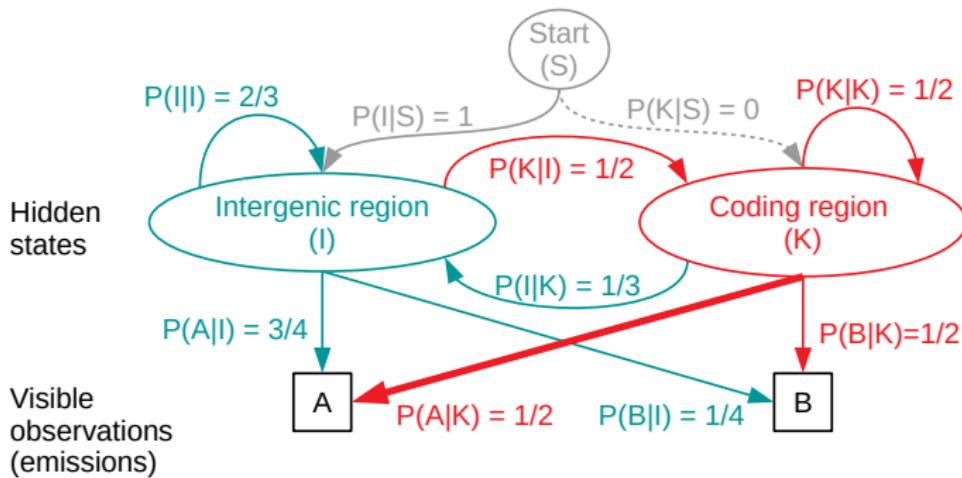
How likely is a given state-emission path?

Path = AAB
IKK

$$P(\text{Path}) = P(I|S) * P(A|I) * P(K|I)$$

Basis of highly accurate gene prediction tools

Hidden Markov Model



How likely is a given state-emission path?

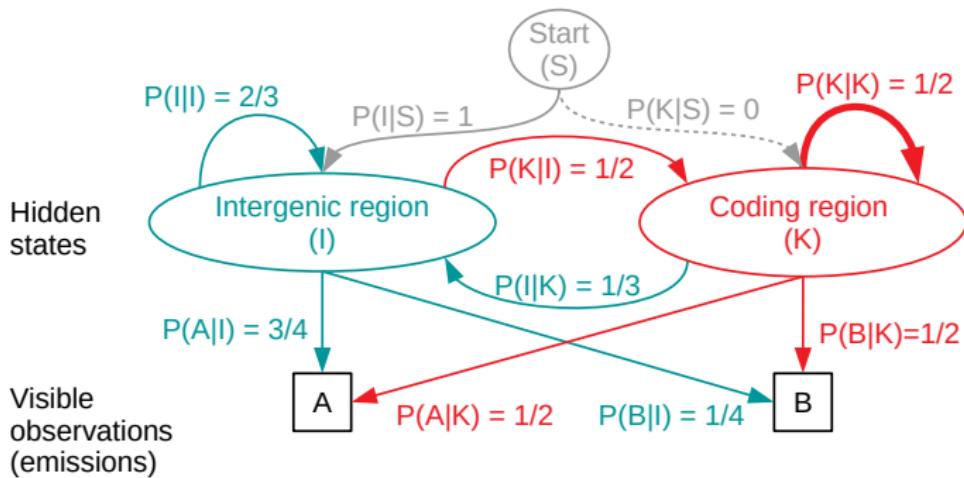
Path = AAB

IKK

$$P(\text{Path}) = P(I|S) * P(A|I) * P(K|I) * P(A|K)$$

Basis of highly accurate gene prediction tools

Hidden Markov Model



How likely is a given state-emission path?

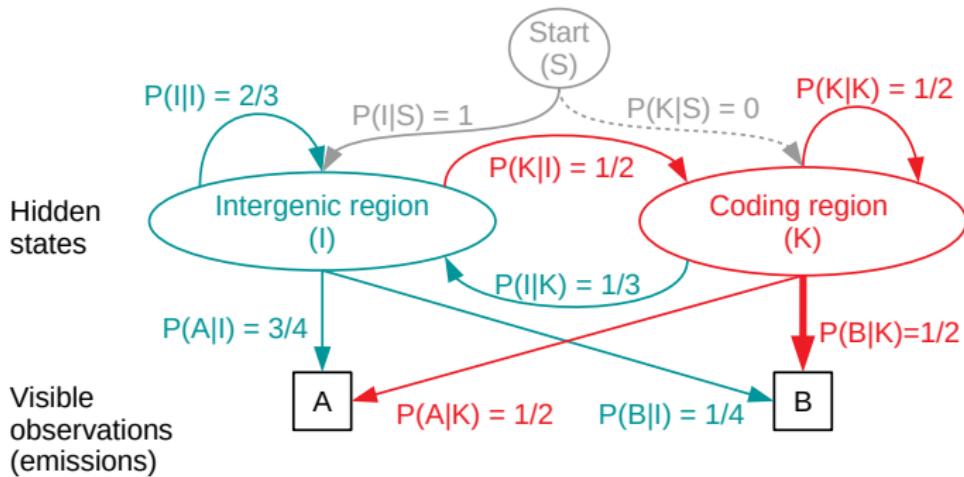
Path = AAB

IKK

$$P(\text{Path}) = P(I|S) * P(A|I) * P(K|I) * P(A|K) * P(K|K)$$

Basis of highly accurate gene prediction tools

Hidden Markov Model



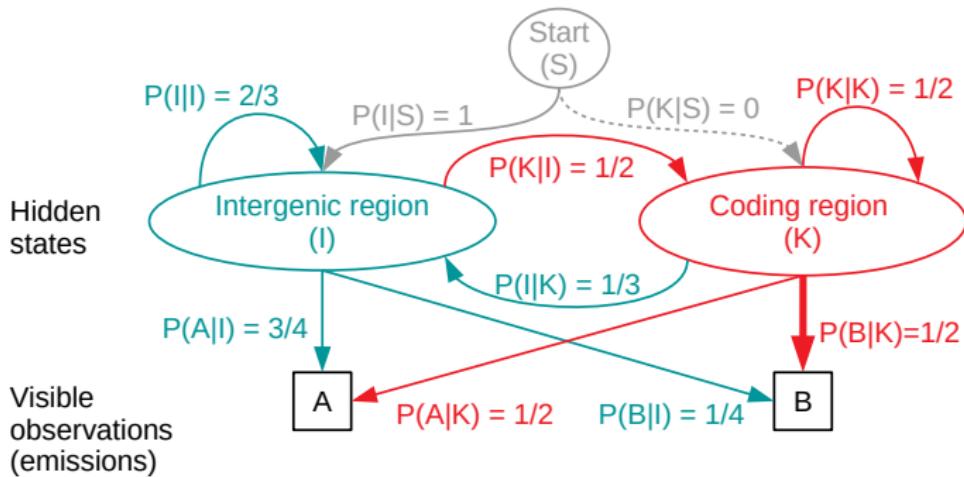
How likely is a given state-emission path?

Path = AAB
IKK

$$P(\text{Path}) = P(I|S) * P(A|I) * P(K|I) * P(A|K) * P(K|K) * P(B|K)$$

Basis of highly accurate gene prediction tools

Hidden Markov Model



How likely is a given state-emission path?

Path = AAB

I**KK**

$$\begin{aligned}P(\text{Path}) &= P(I|S) * P(A|I) * P(K|I) * P(A|K) * P(K|K) * P(B|K) \\&= 1 * \frac{3}{4} * \frac{1}{2} * \frac{1}{2} * \frac{1}{2} * \frac{1}{2} \\&= 3/64\end{aligned}$$

Basis of highly accurate gene prediction tools

Hidden Markov Model

Find the most probable state sequence for a given sequence

Input: "genome sequence"

AABBBA

Problem: "too many possible state sequences"

IIIKKKKK

KKIKKIIIK

IIKIIIIKIK

IKKIKIIIK

KIKIKKKIK

KKKIKIKKK

...

Idea:

- ➊ Generate all possible state sequences
- ➋ Calculate the probability for each state sequence
- ➌ Choose the state sequence with the highest probability

⇒ too expensive!

Basis of highly accurate gene prediction tools

Hidden Markov Model

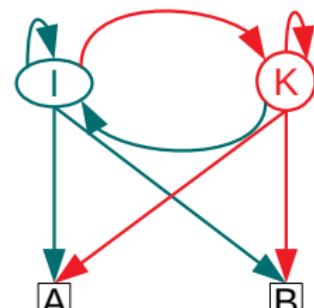
Find the most probable state sequence for a sequence: Viterbi Algorithm.

Transition probabilities
Emission probabilities

AABBBA



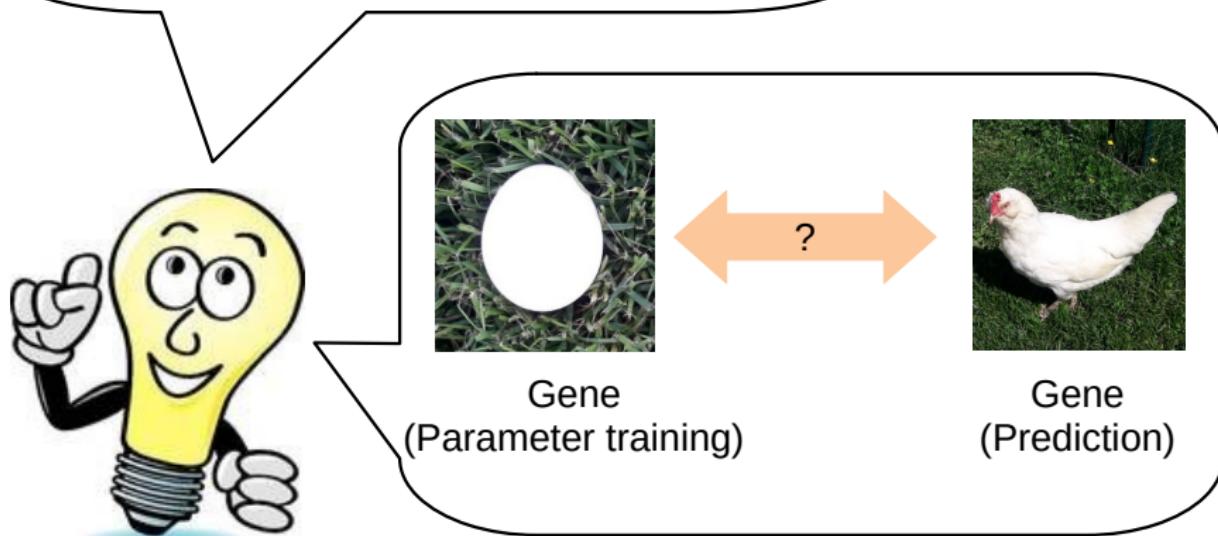
Viterbi



Most probable state sequence:
IIKKKIII

Hidden Markov Model for gene identification in practice

- 4096 observed nucleotide hexamers
- Many more hidden states
(e.g. 3'-UTR, 5'-UTR, Intron, ...)





Transcription data:

- Expressed Sequence Tags
- cDNA
- mRNA-Seq
- mRNA IsoSeq
- ...

Proteome data:

- MS/MS peptides
- proteins of related species
- proteins that every species must have
- ...

Mathematical models:

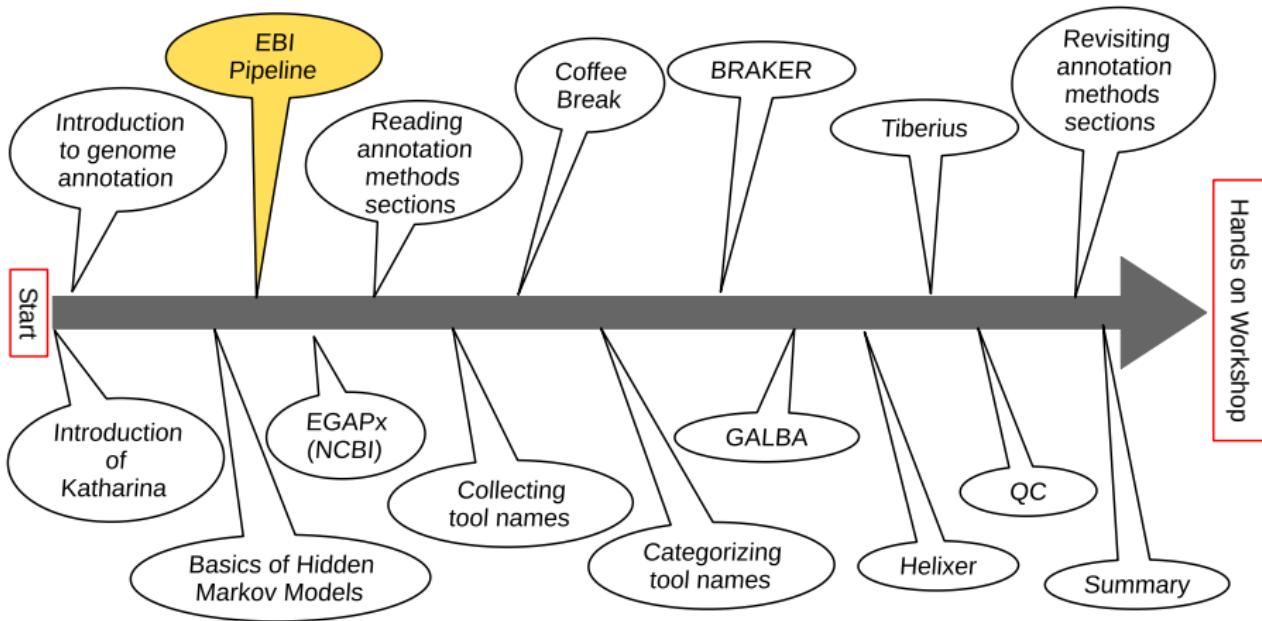
- **Hidden Markov Models**
(e.g. GeneMark, AUGUSTUS)
- dynamic programming
- Support Vector Machines
- neural networks
- decision tree systems
- ...

Provide information on:

- complete gene structures (sometimes incl. UTRs)

Limitations

- *predictions* may be wrong
- models use **parameters** that have to be trained



EBI: Ensembl annotation system

Ensembl annotation pipelines

Ensembl annotation pipeline for non-vertebrates

Documentation

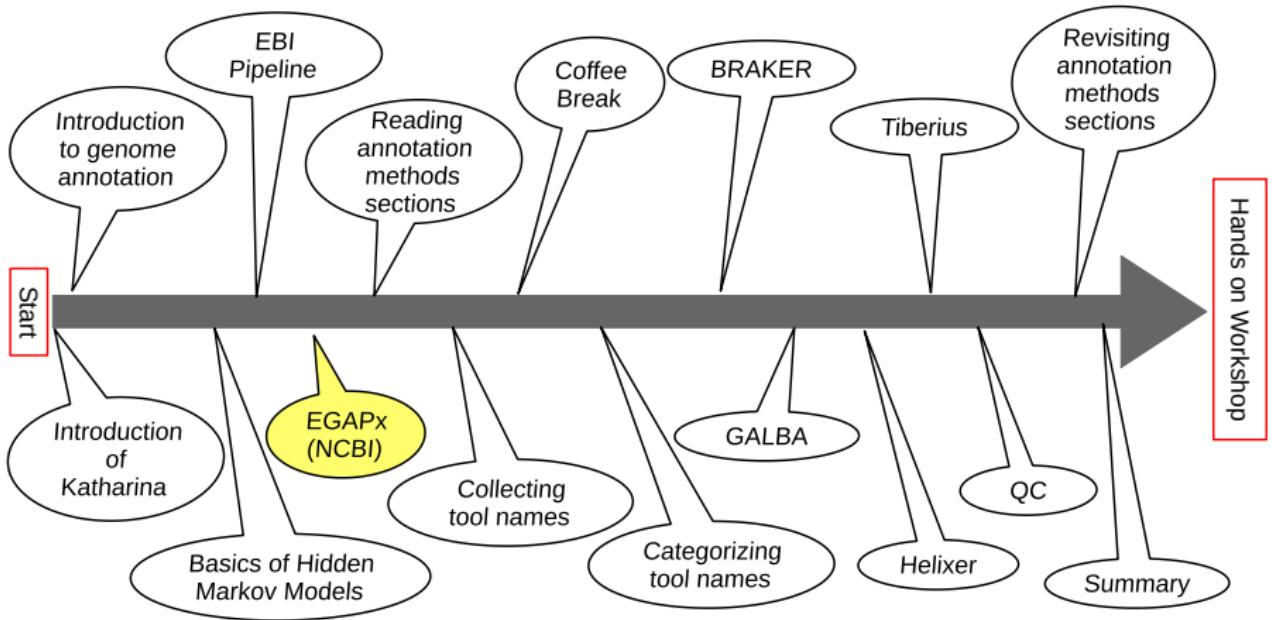
- Ensembl vertebrate pipeline: https://rapid.ensembl.org/info/genome/genebuild/full_genebuild.html
- Ensembl non-vertebrate pipeline: <https://rapid.ensembl.org/info/genome/genebuild/anno.html>
- BRAKER2 in Ensembl: <https://rapid.ensembl.org/info/genome/genebuild/braker.html>

Where to find annotations

- ENSEMBL: <https://beta.ensembl.org/>

Notes by Katharina

- Can (probably) only be installed and executed by EBI
- Not publicly benchmarked against other pipelines



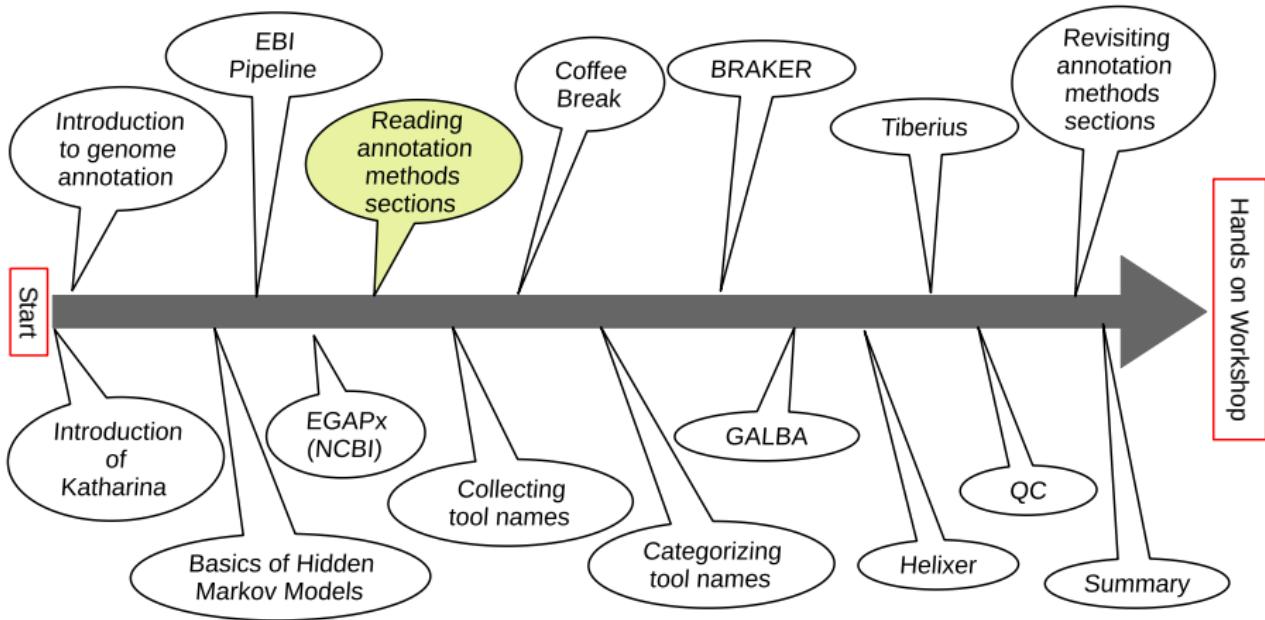
Different Annotation Scenarios

- Internal: The NCBI Eukaryotic Genome Annotation Pipeline (EGAP)
- (Internal: RefSeq curation)
- You can run it: **EGAPx**

Annotation with EGAPx (NCBI)

Annotation with EGAPx (NCBI)

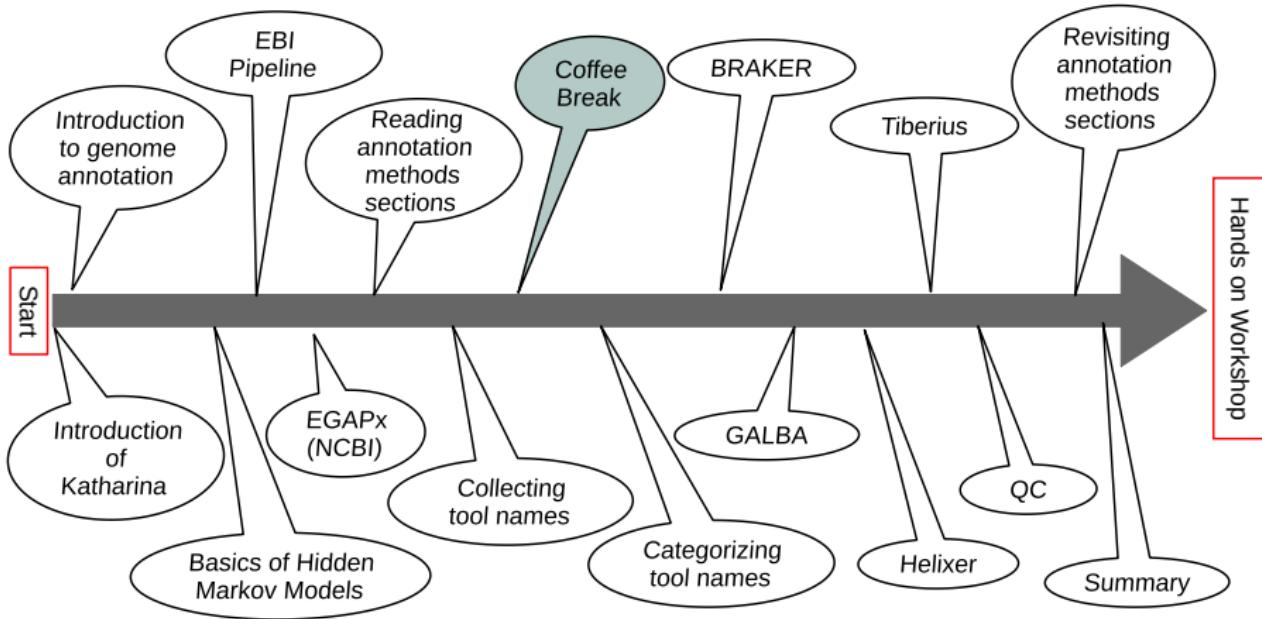
- Containerized with Docker/Singularity
- Documentation: <https://github.com/ncbi/egapx>
- Currently supported clades (protein sets):
 - ▶ Chordata
 - ▶ Insecta
 - ▶ Arthropoda
 - ▶ Monocots
 - ▶ Eudicots
- Easy to use
- Benchmarking possible: good accuracy!

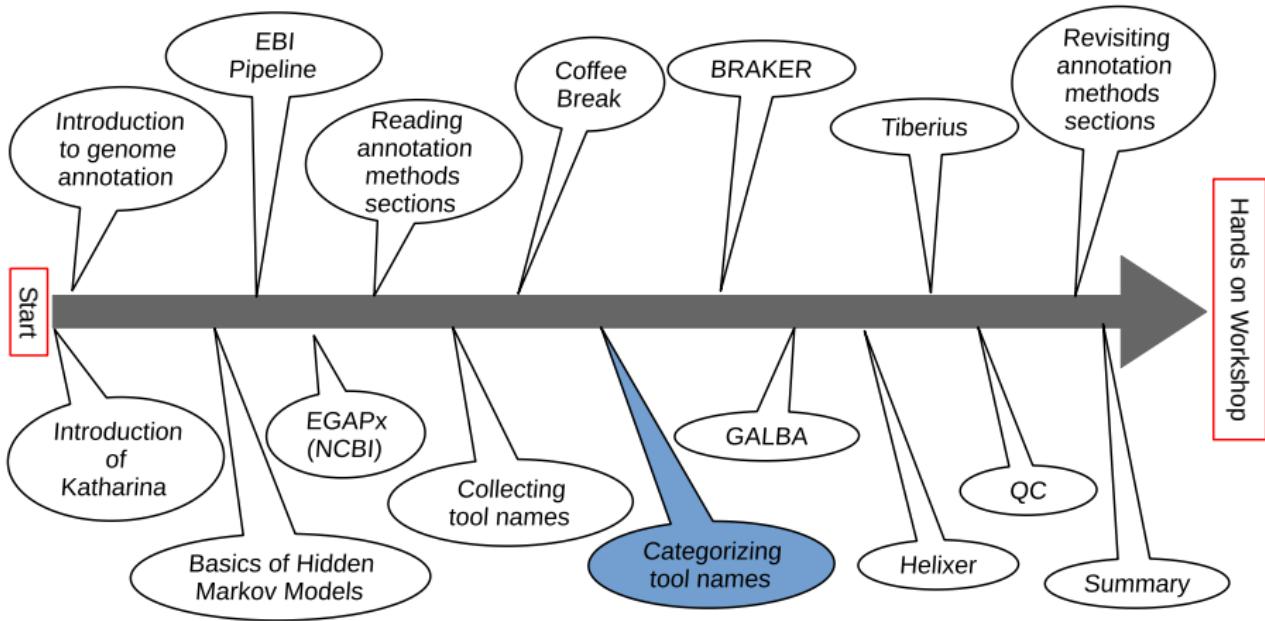


Read your methods snippet

Focus on structural annotation of protein coding genes only!

- ➊ We move to Wooclap
- ➋ Enter the names of tools involved in structural annotation of protein coding genes





Categorize tool names

Go to

<https://shorturl.at/uA0Tg>

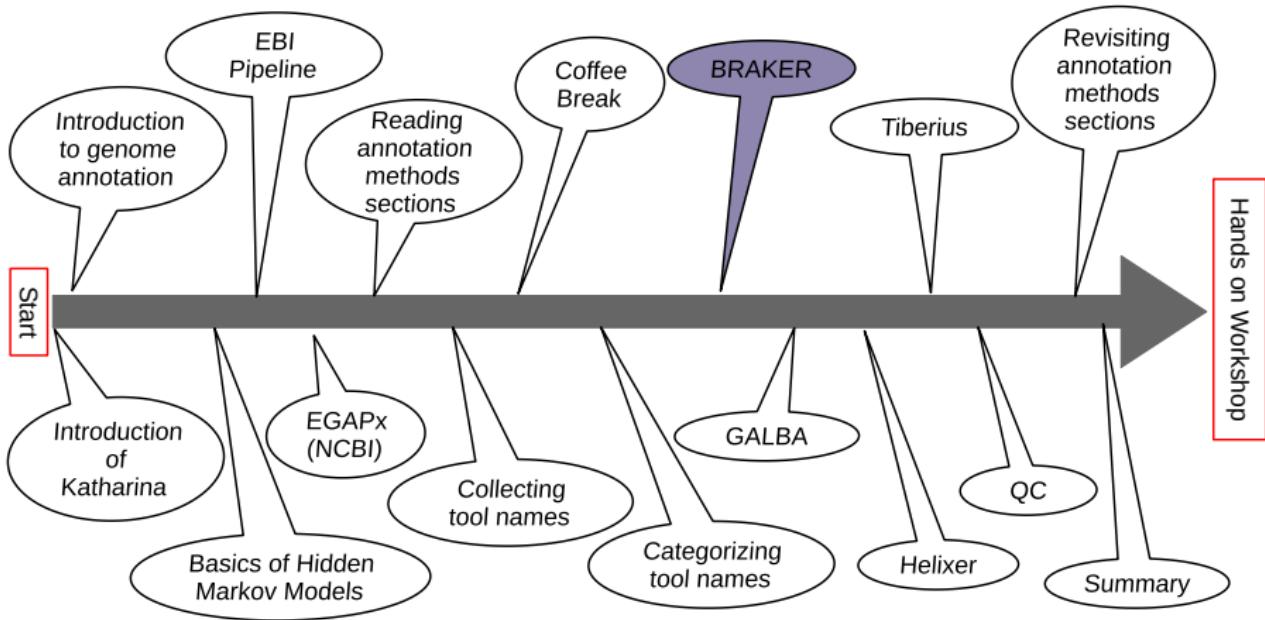
and sort the tools names from your methods snippet into categories



The aera of genome annotation super heroes



Image: credits to DALL-E2, modified by human



The BRAKER Team

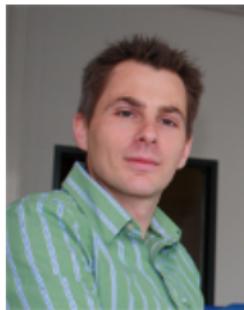
University of Greifswald & Georgia Tech University



Lars Gabriel



Alexandre Lomsadze, Katharina Hoff, Tomáš Brůna



Mario Stanke



Mark Borodovsky

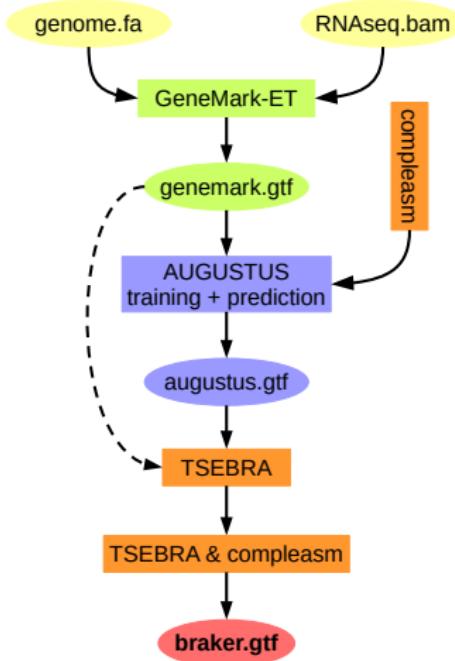
Also: Simone Lange, Matthias Ebel, Hannah Thierfeldt, Anica Hoppe, Neng Huang

BRAKER1: Unsupervised RNA-Seq-Based Genome Annotation with GeneMark-ET and AUGUSTUS FREE

Katharina J. Hoff ✉, Simone Lange, Alexandre Lomsadze, Mark Borodovsky ✉, Mario Stanke

Bioinformatics, Volume 32, Issue 5, 1 March 2016, Pages 767–769,

<https://doi.org/10.1093/bioinformatics/btv661>



- spliced alignments of RNA-Seq are used by GeneMark-ET and AUGUSTUS
- 2,174 citations (Google Scholar)

Whole-Genome Annotation with BRAKER

Katharina J. Hoff, Alexandre Lomsadze, Mark Borodovsky, and Mario Stanke

in Kolmar M. (eds) Gene Prediction. Methods in Molecular Biology, vol 1962. Humana, New York, NY, 2019

GeneMark-ET uses RNA-Seq for Training

Anchors from RNA-Seq for training

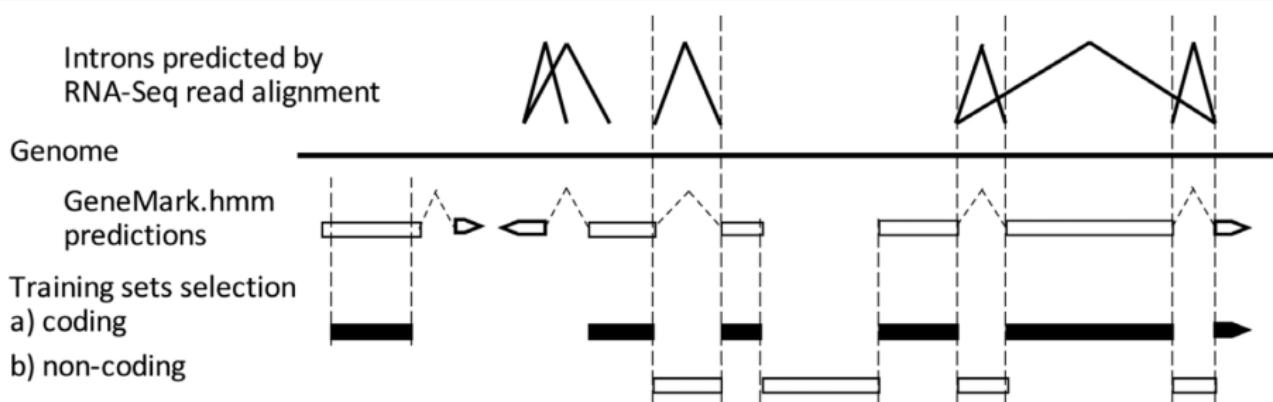


Figure 3. Selection of elements of training set in GeneMark-ET for the next iteration. The new training set of protein-coding regions is comprised from exons with at least one 'anchored splice site' as well as long exons predicted *ab initio* (>800 nt).

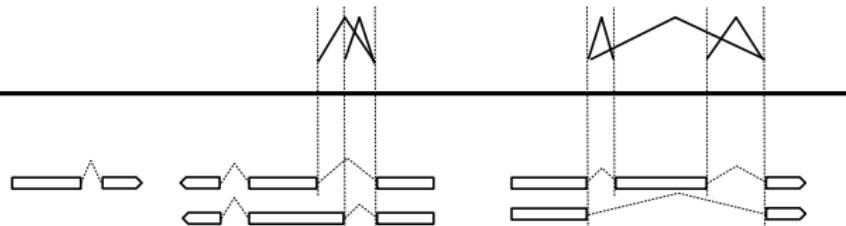
- employs unsupervised training
- training includes introns and exons anchored by mapped RNA-Seq reads
- does not require RNA-Seq reads assembly
- does not use RNA-Seq information in the *prediction* step

AUGUSTUS uses RNA-Seq for **Prediction**

Introns predicted by RNA-Seq read alignment

Genome

AUGUSTUS gene predictions with “hints” from RNA-Seq



- requires “prior data” for training
- uses intron information from RNA-seq for *prediction*
- no RNA-Seq assembly required
- optional input: BUSCO lineage (compleasm)

Measuring accuracy of genome annotation

Experiments

Accuracy assessment after applying tool to genome with reference annotation:

Species	Genome Size (Mb)	# Genes in Annotation
<i>Arabidopsis thaliana</i> (thale cress)	119	27,444
<i>Bombus terrestris</i> (bumble bee)	249	10,581
<i>Caenorhabditis elegans</i> (nematode)	100	20,172
<i>Danio rerio</i> (zebrafish)	1,345	25,611
<i>Drosophila melanogaster</i> (fruit fly)	137	13,928
<i>Gallus gallus</i> (chicken)	1,040	17,279
<i>Medicago truncatula</i> (barrelclover)	420	44,464
<i>Mus musculus</i> (mouse)	2,650	22,378
<i>Parasteatoda tepidariorium</i> (house spider)	1,445	18,602
<i>Populus trichocarpa</i> (poppy)	389	34,488
<i>Solanum lycopersicum</i> (tomato)	772	33,562

Accuracy metrics

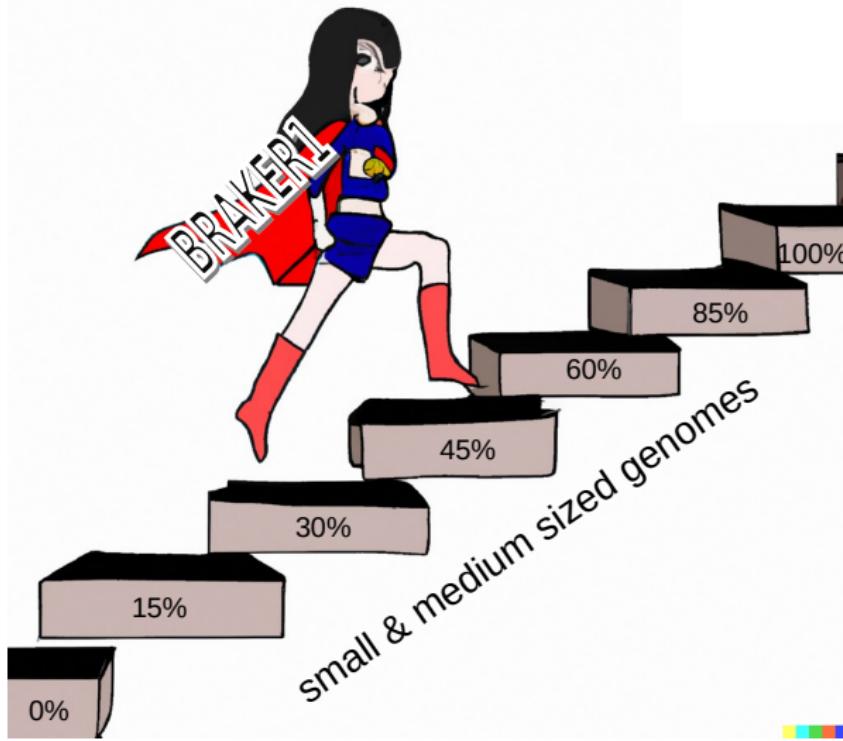
Precision = Specificity: Percentage of correctly found genes/transcripts/exons in the **predicted gene set**.

Recall = Sensitivity: Percentage of correctly found genes/transcripts/exons in the **reference annotation**.

$$\text{F1-Score: } \frac{2 \cdot \text{Recall} \cdot \text{Precision}}{\text{Recall} + \text{Precision}}$$

BRAKER1 gene F1 accuracy

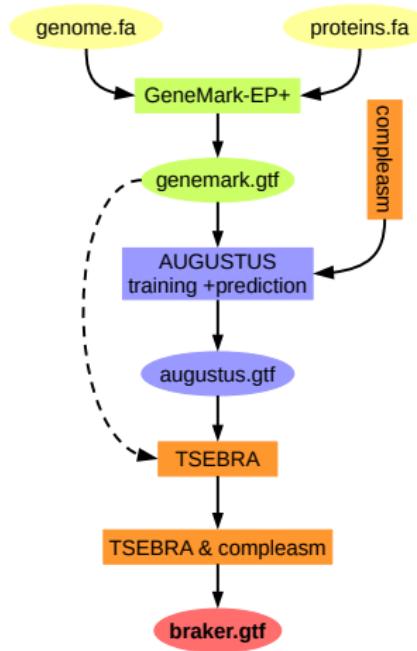
Image: credits to DALL-E2, human modification



Use only if not enough RNA-Seq for BRAKER3!

BRAKER2: automatic eukaryotic genome annotation with GeneMark-EP+ and AUGUSTUS supported by a protein database

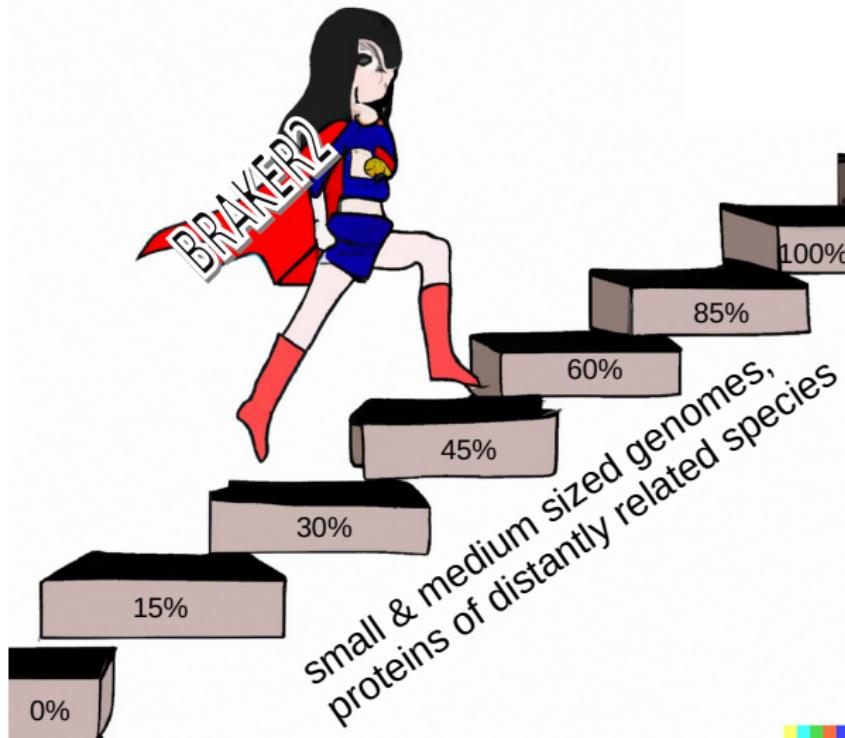
Tomáš Brúna^{1,†}, Katharina J. Hoff^{2,3,†}, Alexandre Lomsadze⁴, Mario Stanke^{2,3,‡} and Mark Borodovsky^{④,5,*‡}



- spliced alignments of a large number of proteins (e.g. OrthoDB partition)
- optional input: BUSCO lineage (compleasm)
- 1,480 citations (Google Scholar)

BRAKER2 gene F1 accuracy

Image: credits to DALL-E2, human modification



Use only if you have no RNA-Seq data on genomes <1 Gbp

BRAKER3 gene F1 accuracy - climbing the top

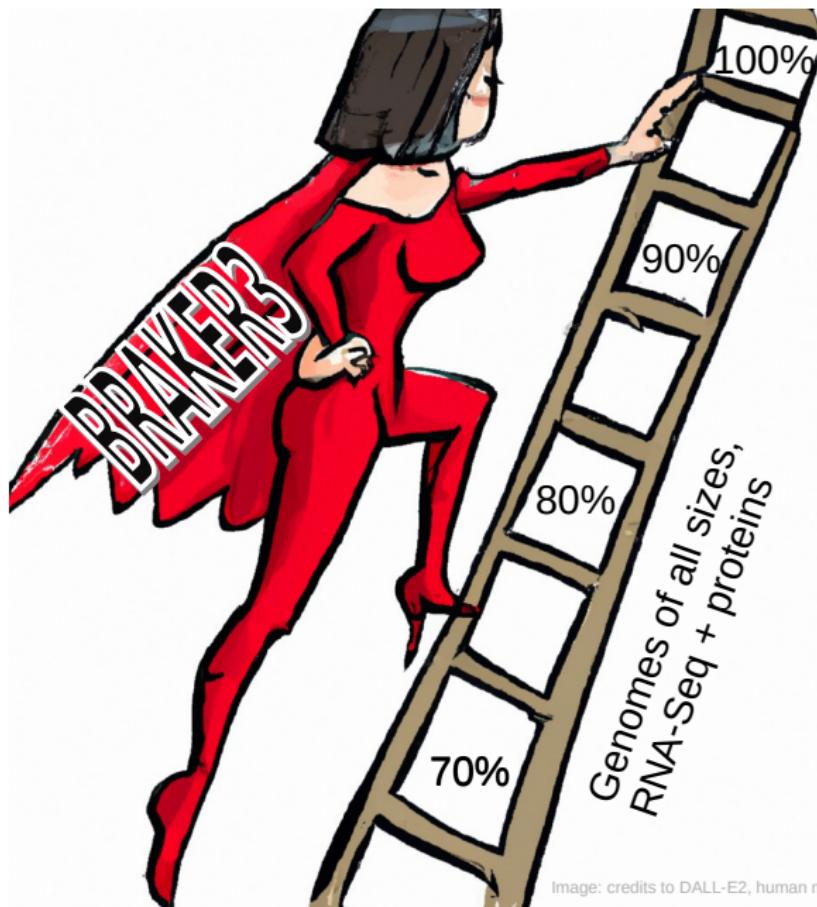
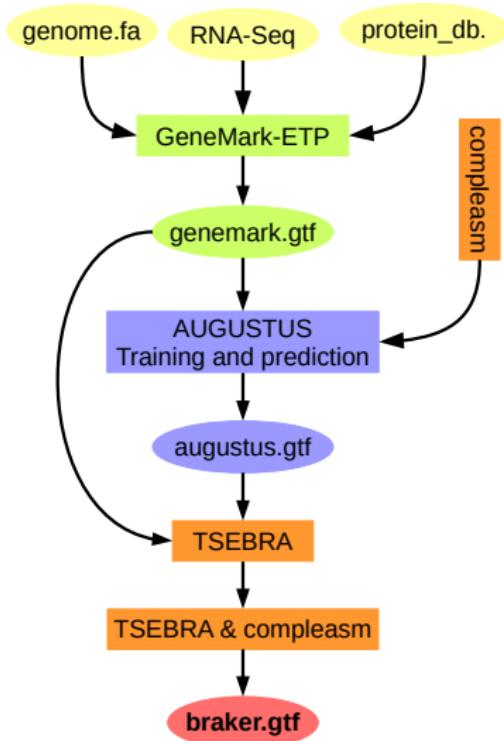


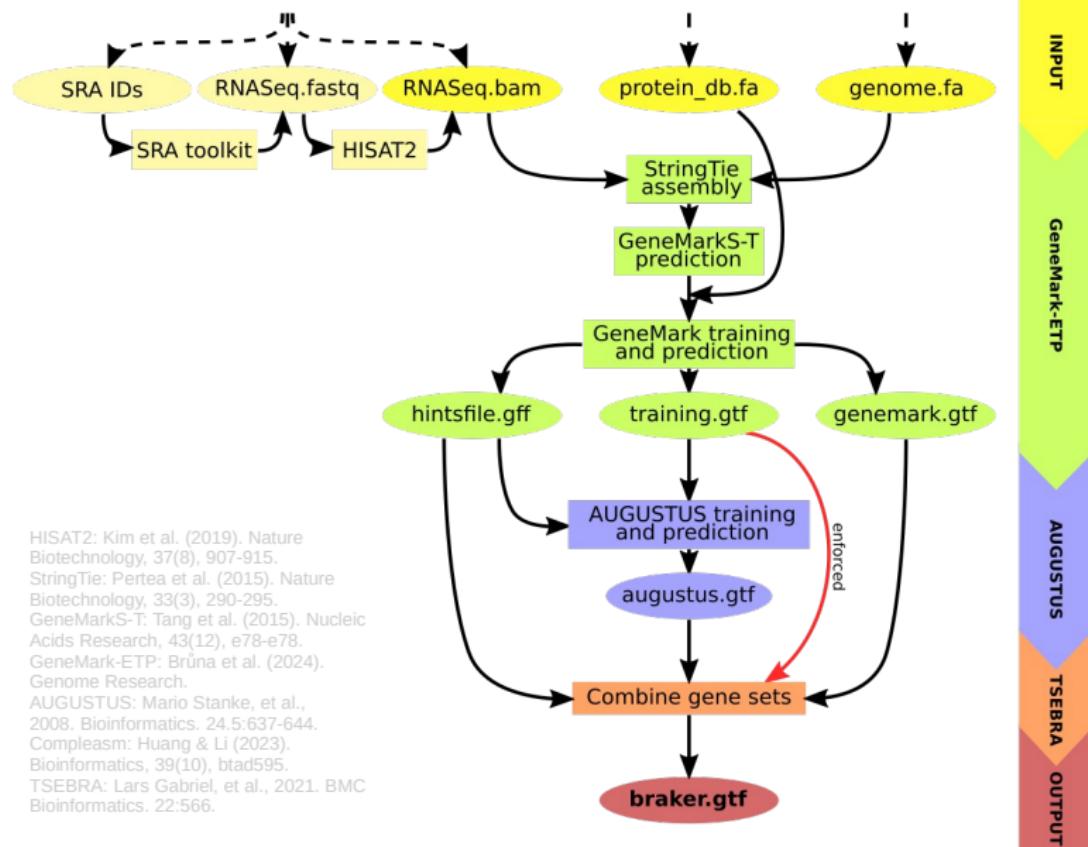
Image: credits to DALL-E2, human modification

BRAKER3: using RNA-Seq and protein evidence with GeneMark-ETP, AUGUSTUS and TSEBRA



- Gabriel *et al.* (2024)
- 249 citations (Google Scholar)
- spliced aligned and **assembled** RNA-Seq
- large protein database
- optional input: BUSCO lineage (compleasm)
- combines GeneMark-ETP and AUGUSTUS gene sets with TSEBRA

BRAKER3: using RNA-Seq and protein evidence with GeneMark-ETP, AUGUSTUS and TSEBRA



HISAT2: Kim et al. (2019). Nature Biotechnology, 37(8), 907-915.

StringTie: Pertea et al. (2015). Nature Biotechnology, 33(3), 290-295.

GeneMarkS-T: Tang et al. (2015). Nucleic Acids Research, 43(12), e78-e78.

GeneMark-ETP: Brúna et al. (2024). Genome Research.

AUGUSTUS: Mario Stanke, et al., 2008. Bioinformatics. 24:5:637-644.

Compleasim: Huang & Li (2023). Bioinformatics, 39(10), btad595.

TSEBRA: Lars Gábel, et al., 2021. BMC Bioinformatics. 22:566.

SOFTWARE

Open Access

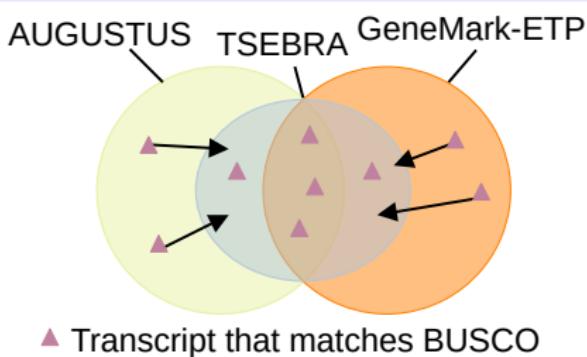


TSEBRA: transcript selector for BRAKER

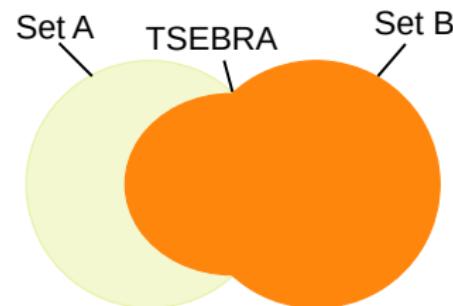
Lars Gabriel^{1,2}, Katharina J. Hoff^{1,2}, Tomáš Brůna³, Mark Borodovsky^{4,5} and Mario Stanke^{1,2*}

- **combines** several gene sets according to evidence
- 224 citations (Google Scholar)

TSEBRA in BRAKER



Manually enforcing a gene set



enforce Set B with -k setb.gtf

Can be used to combine BRAKER1 and BRAKER2 output if BRAKER3 fails.

Accuracy of genome annotation approaches by BRAKER team

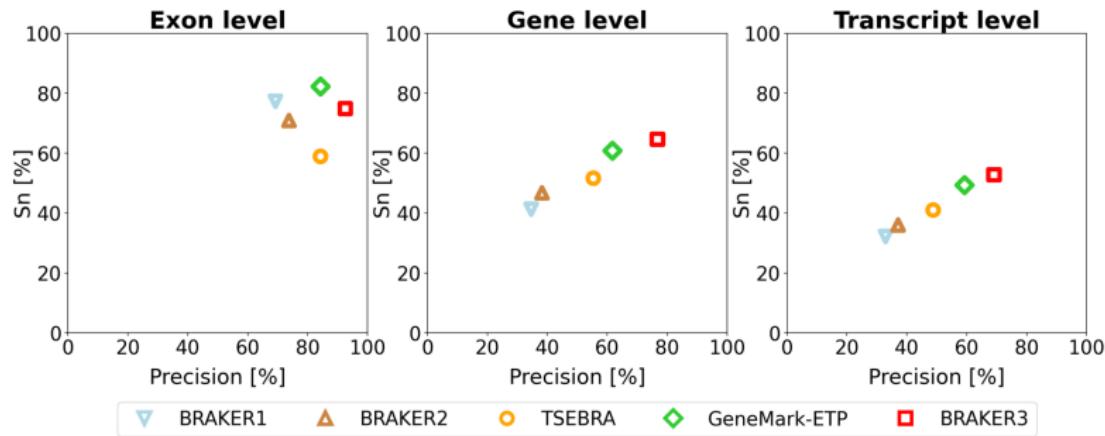


Figure 2. Average precision and sensitivity of gene predictions made by BRAKER1, BRAKER2, TSEBRA, GeneMark-ETP, and BRAKER3 for the genomes of 11 different species (listed in [Supplemental Table S1](#)). Inputs were the genomic sequences, short-read RNA-seq libraries, and protein databases (*order excluded*).

Image: Gabriel *et al.* (2024), Genome Research

Availability

GitHub

<https://github.com/Gaius-Augustus/BRAKER>

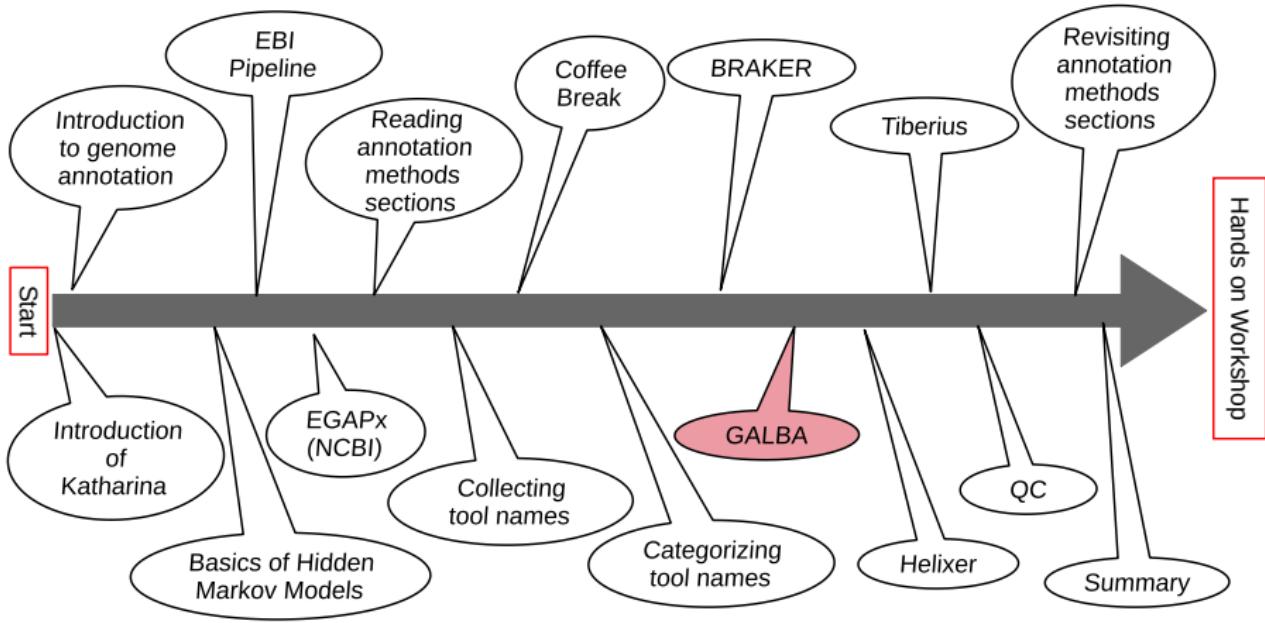
Docker/Singularity

```
singularity build braker.sif \
    docker://teambraker/braker:latest
```

```
singularity exec braker.sif braker.pl [OPTIONS]
```

Licenses

- BRAKER: Artistic License
- most components under open source software licenses
- GeneMark-ETP: CC BY-NC



GALBA Contributors



Tomáš Brůna



Heng Li



Joseph Guhlin



Lars Gabriel



Natalia Nenasheva



Ethan Tolman



Paul Frandsen



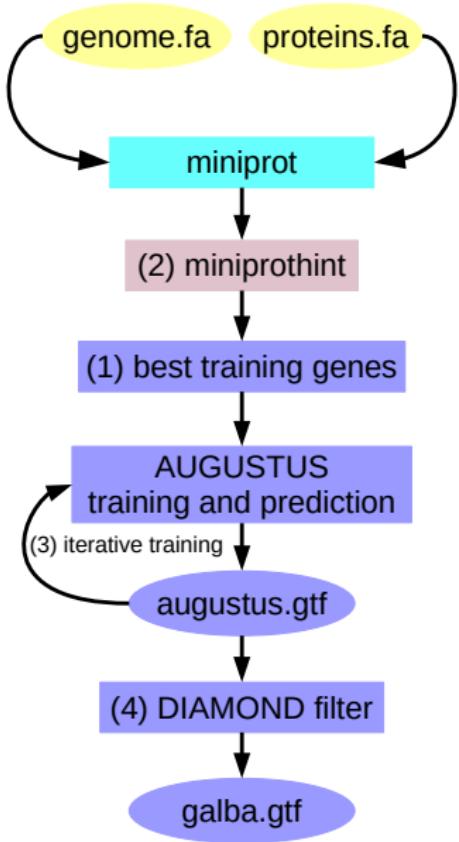
Matthias Ebel



Mario Stanke



Katharina Hoff



RESEARCH

Open Access

Galba: genome annotation with miniprot and AUGUSTUS

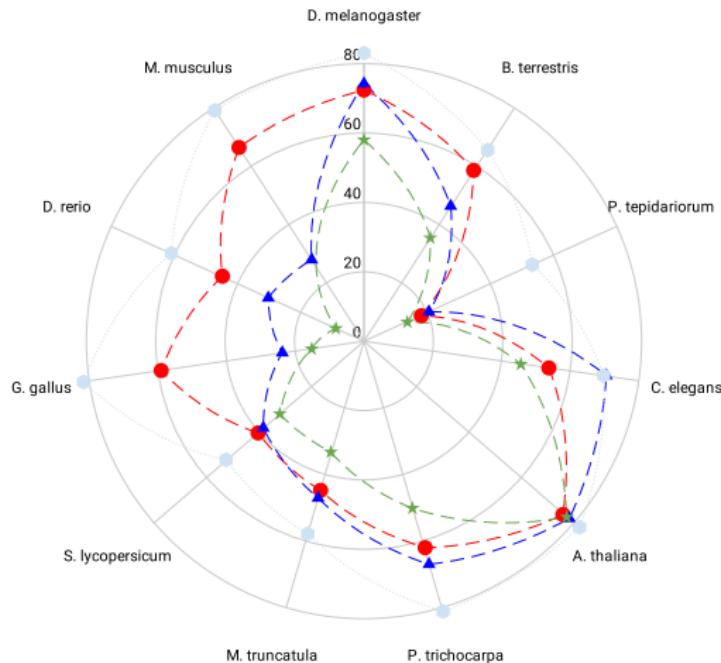


- 42 citations (Google Scholar)
- for genomes >1Gbp
- proteins of close relatives

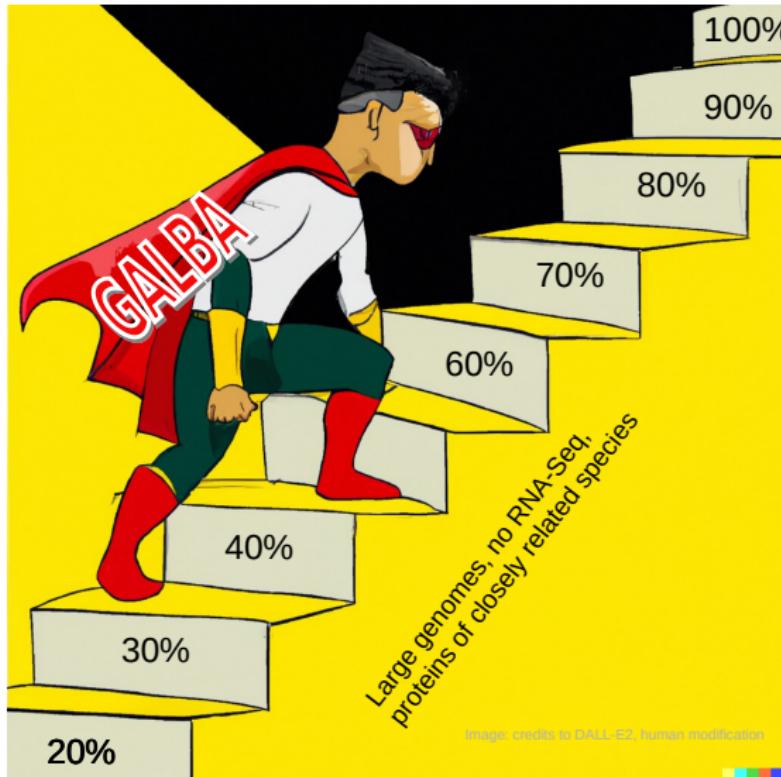
Proteins Only (GALBA, BRAKER2, FunAnnotate) vs. BRAKER3 with RNA-Seq & Proteins

Gene F1 (%)

● GALBA v1.0.10 ▲ BRAKER2 ★ FunAnnotate ● BRAKER3



GALBA: Gene F1 Accuracy



If you have RNA-Seq, use BRAKER3!

Availability

GitHub

<https://github.com/Gaius-Augustus/GALBA>

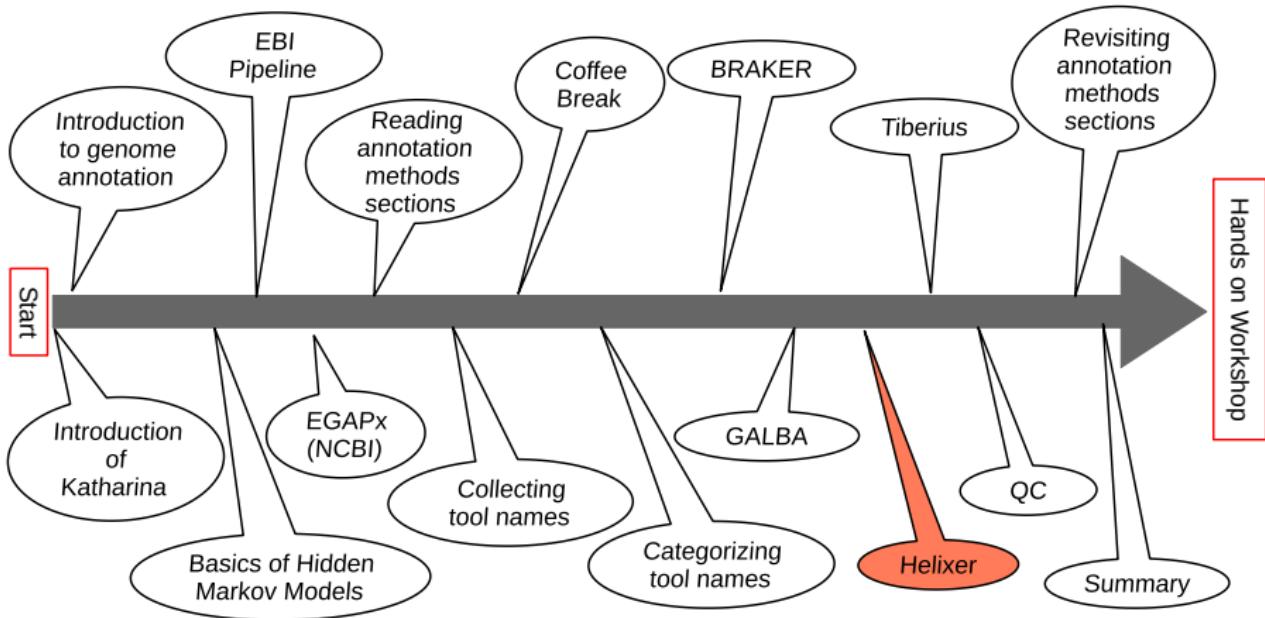
Docker/Singularity

```
singularity build galba.sif \
    docker://katharinahoff/galba:latest
```

```
singularity exec galba.sif galba.pl [OPTIONS]
```

Licenses

- GALBA: Artistic License
- all dependencies have Open Source Licenses



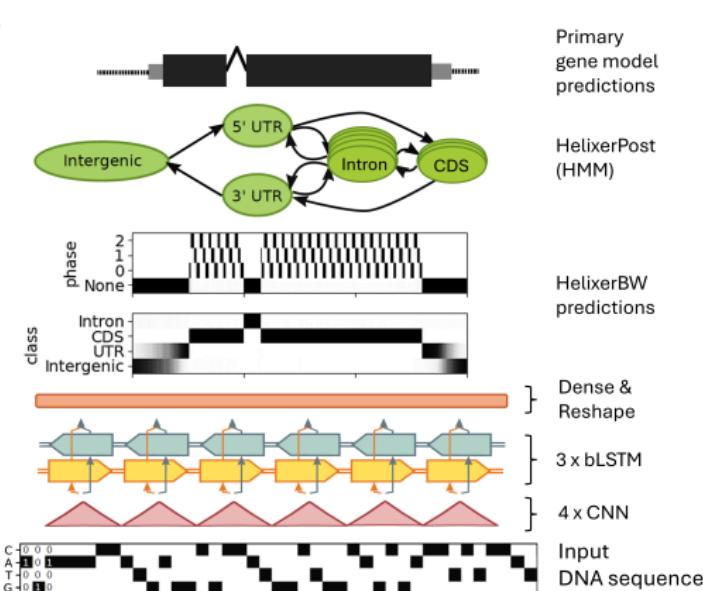
Helixer: bringing deep learning into genome annotation



Image: ChatGPT by OpenAI, manual editing

HELIXER—*de novo* PREDICTION OF PRIMARY EUKARYOTIC GENE MODELS COMBINING DEEP LEARNING AND A HIDDEN MARKOV MODEL

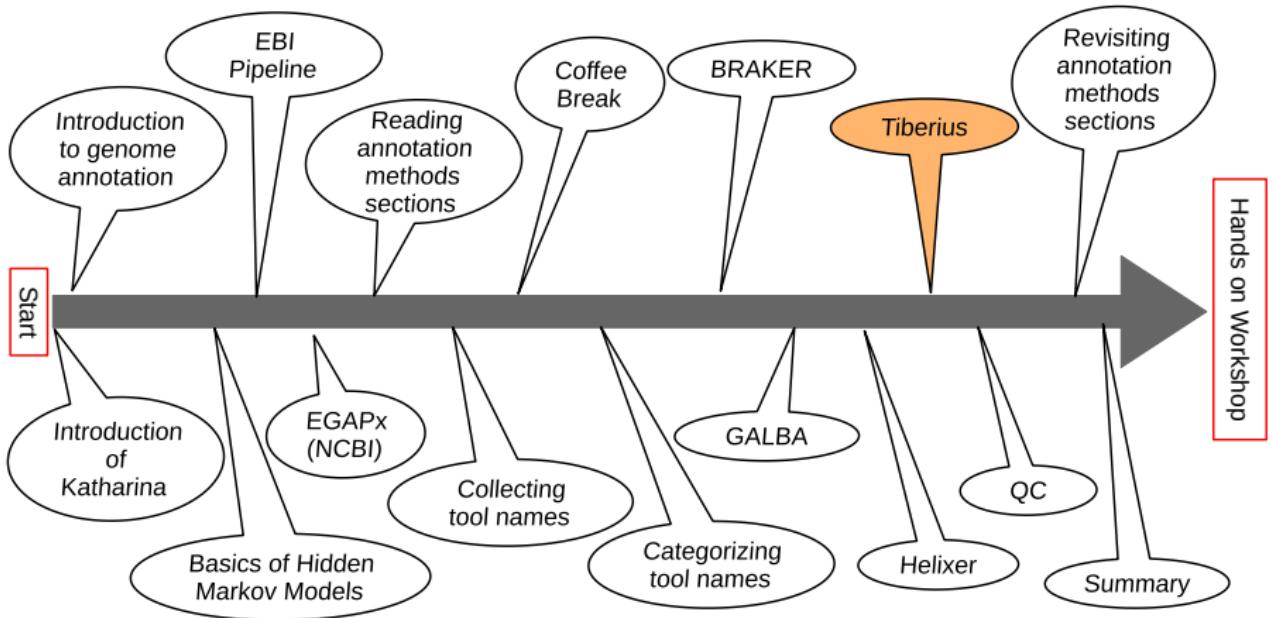
Felix Holst^{1†}, Anthony Bolger^{2†}, Christopher Günther¹, Janina Maß³,
Sebastian Triesch^{1,4}, Felicitas Kindel¹, Niklas Kiel^{1,4}, Nima Saadat^{3,4}, Oliver Ebenhöh^{3,4},
Björn Usadel^{2,4,5}, Rainer Schwacke², Marie Bolger², Andreas P.M. Weber^{1,4}, Alisandra K. Denton^{1,4}



- 27 citations (Google Scholar)
- cross-species gene finder
- *ab initio* prediction
- Pre-trained models for:
 - ▶ fungi
 - ▶ land plant
 - ▶ vertebrate
 - ▶ invertebrate
- accuracy (BUSCO): good
- web service

Availability: <https://github.com/weberlab-hhu/Helixer>

Image of Helixer: <https://github.com/weberlab-hhu/Helixer/blob/main/img/network.png>



Tiberius: improved genome annotation with deep learning

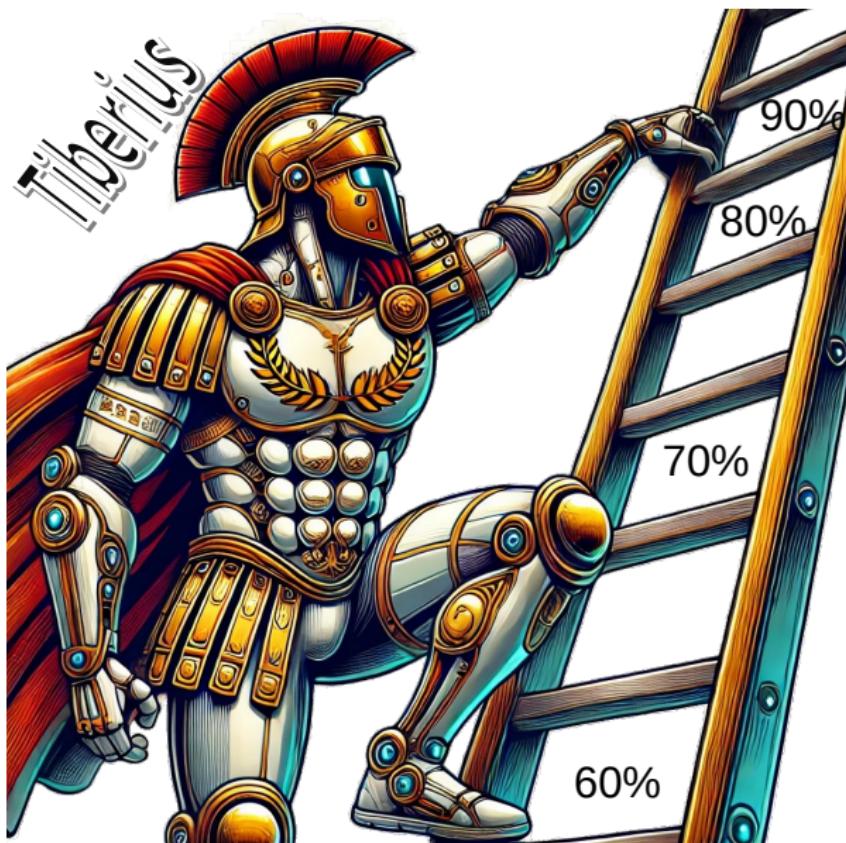


Image: ChatGPT by OpenAI, manual editing

The Tiberius Team

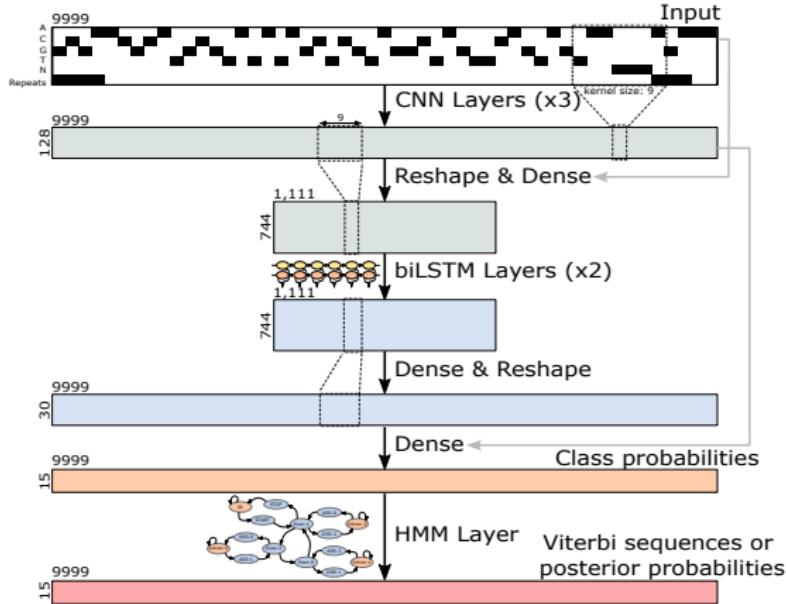
University of Greifswald



Lars Gabriel, Felix Becker, Katharina Hoff, Mario Stanke

Tiberius: end-to-end deep learning with an HMM for gene prediction

Lars Gabriel  ^{1,2,*}, Felix Becker  ^{1,2}, Katharina J. Hoff ^{1,2}, Mario Stanke  ^{1,2,*}



- builds on findings by Helixer team
- cross-species gene finder
- faster
- higher accuracy
- *ab initio* prediction
- Pre-trained model(s) for:
 - ▶ mammals
 - ▶ (diatoms)
- container for A100 GPU

Availability: <https://github.com/Gaius-Augustus/Tiberius>

Accuracy of state of the art gene finders

No alternative splicing isoforms

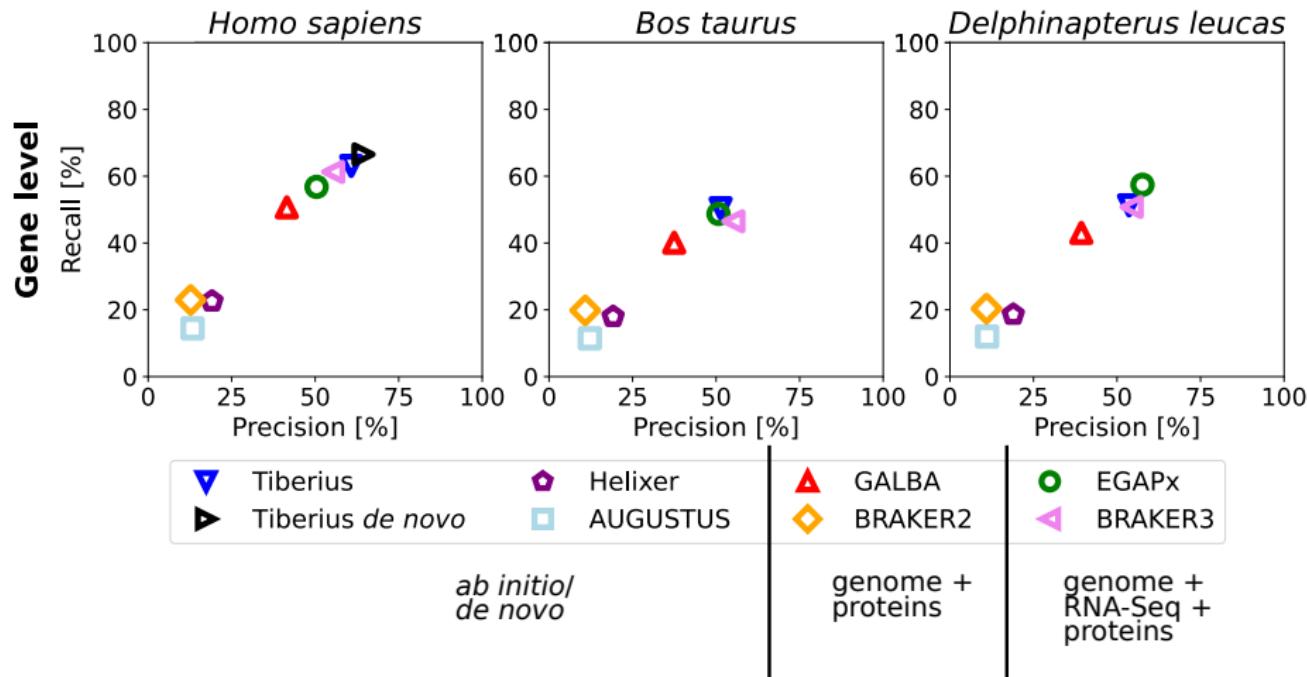
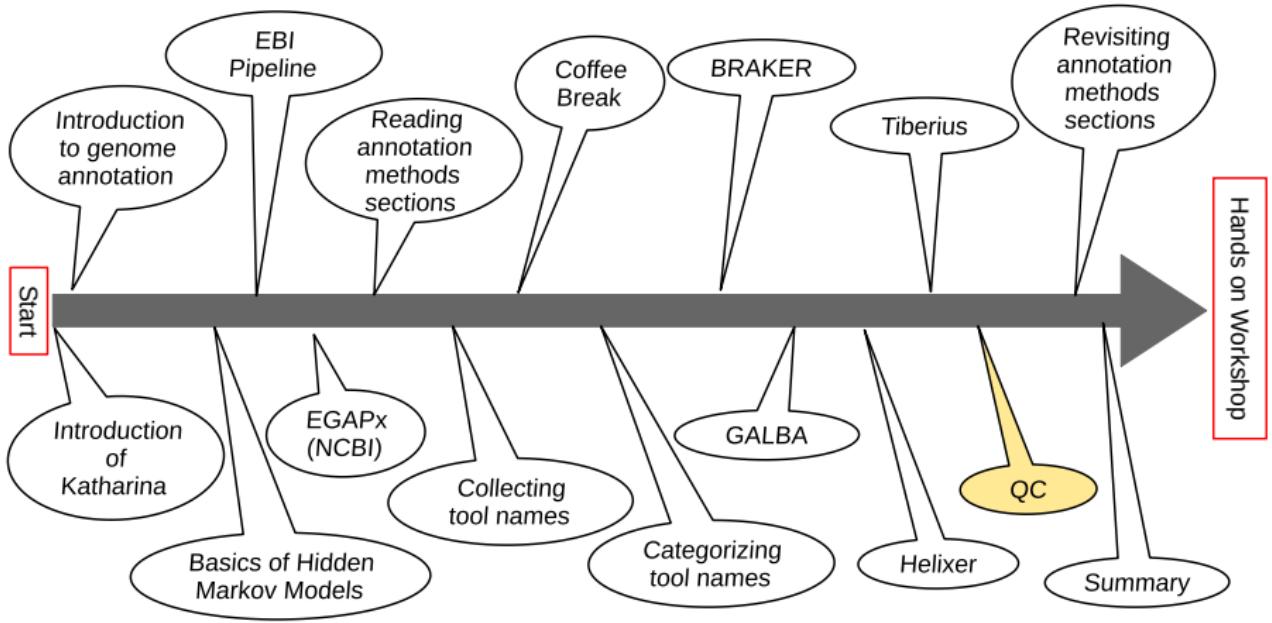


Image: Lars Gabriel, PAG presentation 2025

Current shortcomings of deep learning gene finders

- no evidence integration
- no alternative splicing isoform prediction
- require expensive GPU for feasible runtime
- limited to specific clades

→ BRAKER3, Galba & EGAPx currently remain important



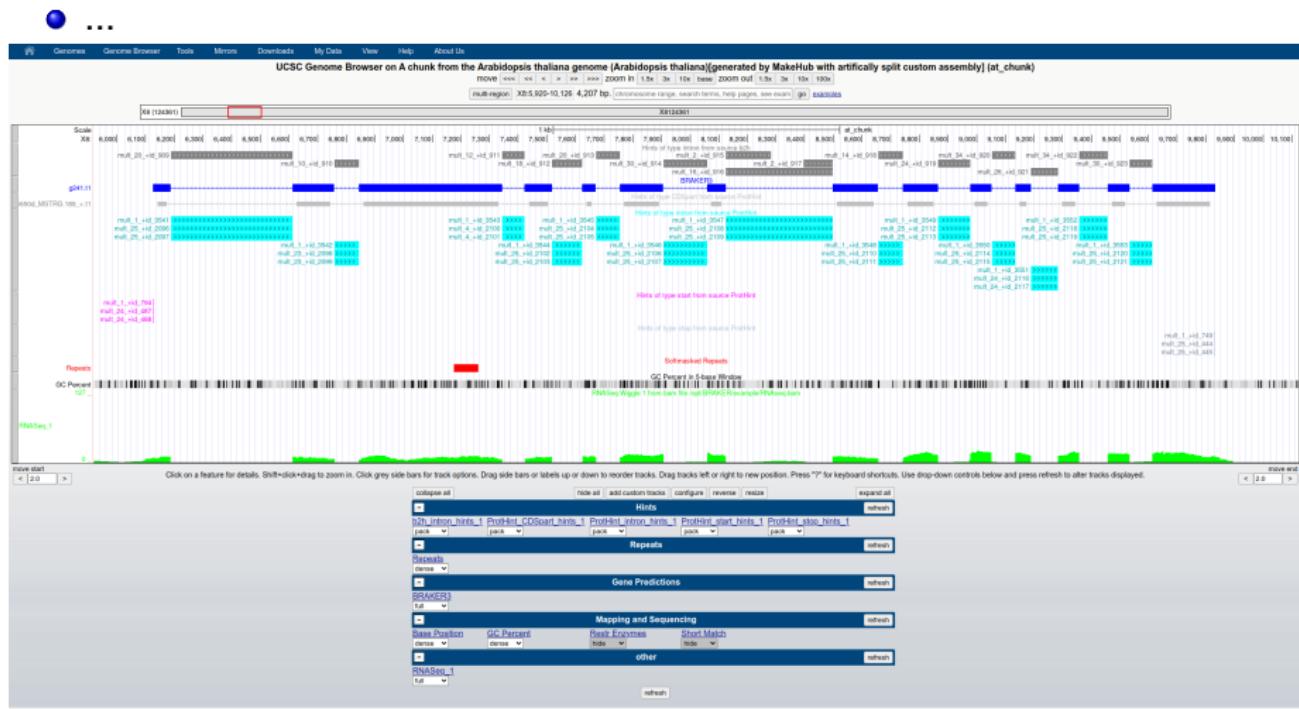
Did We Do a Good Job?



Genome Browsers

Visualize your Annotation in Context with Evidence

- UCSC Genome Browser, MakeHub
 - JBrowse



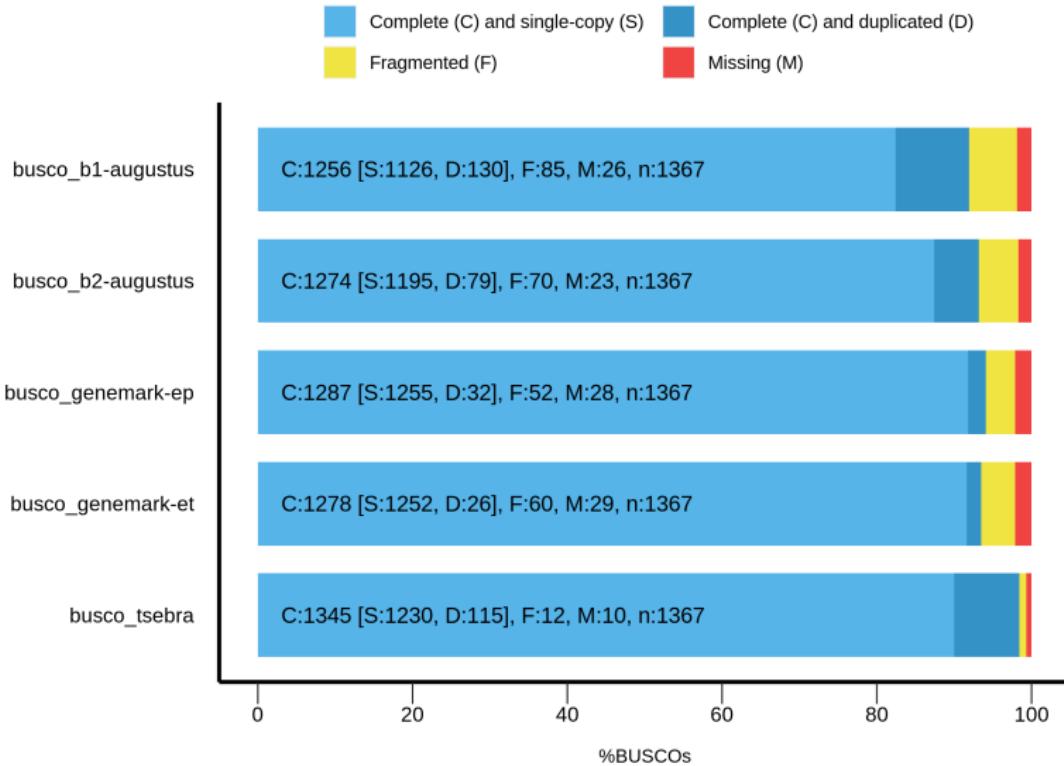
Describe Your Annotation

- number of genes
- number of transcripts
- ratio of mono-exonic to multi-exonic genes
- median number of exons per transcript
- maximal number of exons per transcript
- median transcript length
- ...

If possible, compare to annotated close relatives.
Consider effect of individual annotation pipelines.

BUSCO: Sensitivity in Clade-Specific Conserved Genes

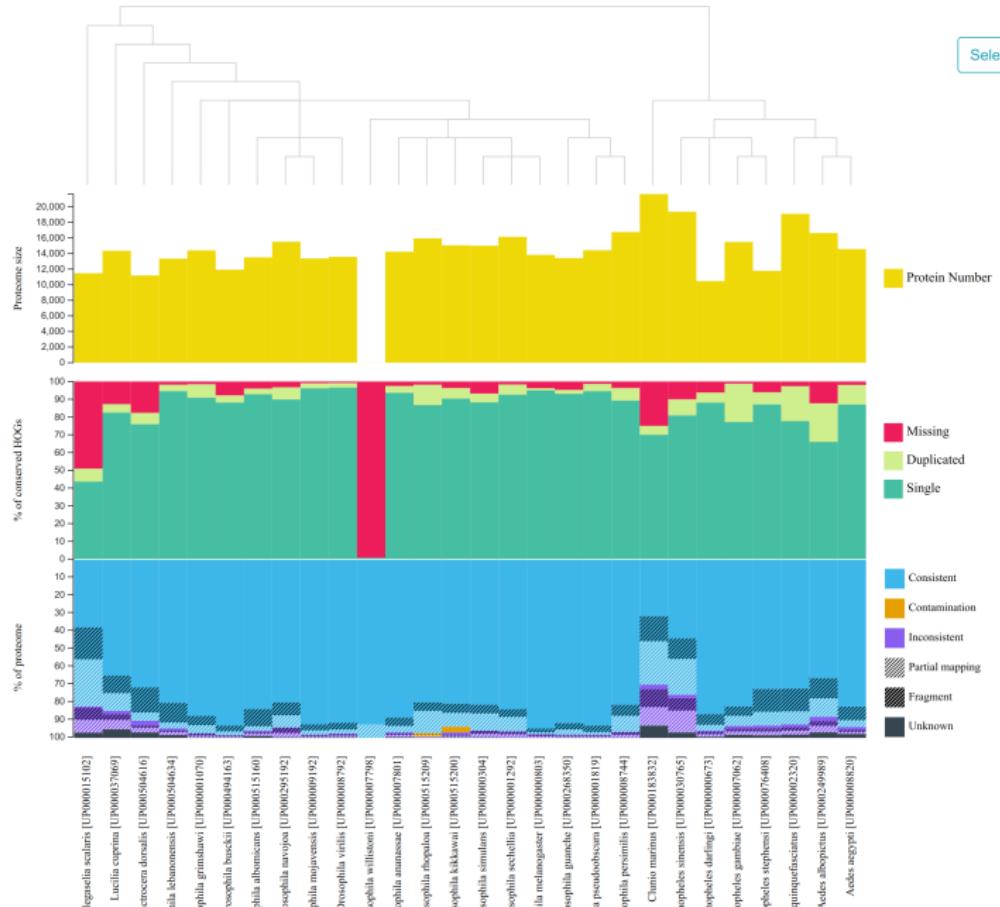
BUSCO Assessment Results



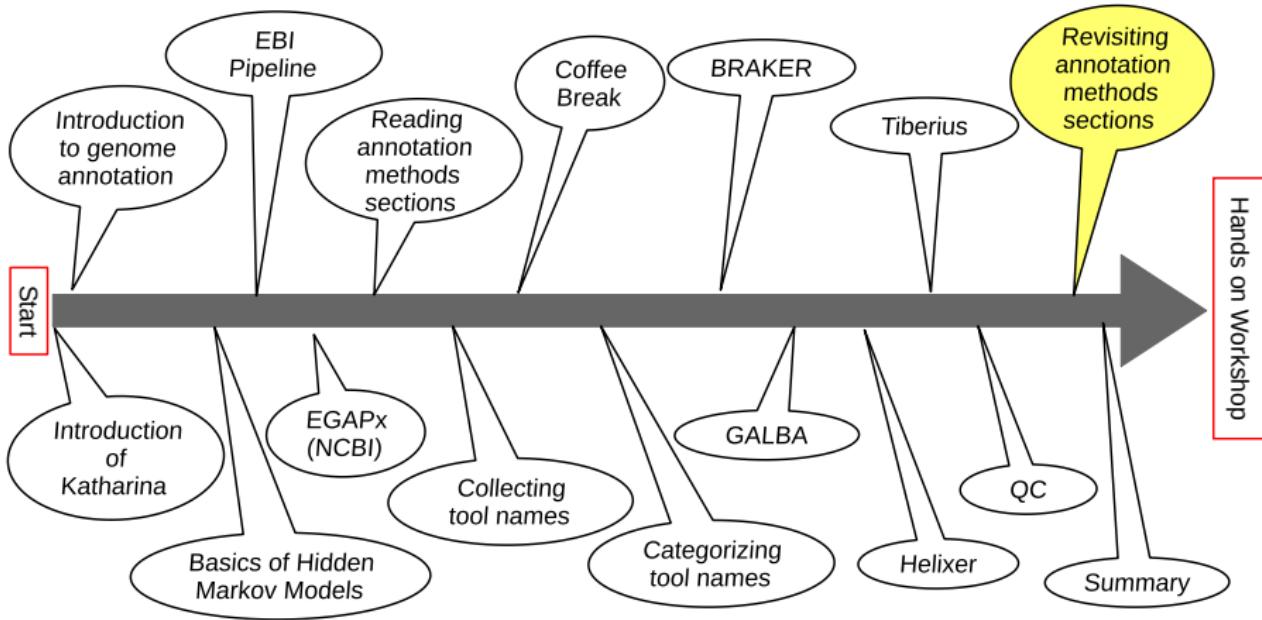
Beware! BUSCO completeness does not warrant correct gene structures!

OMArk: Sensitivity, Contaminations, & More

Select Taxon ▾



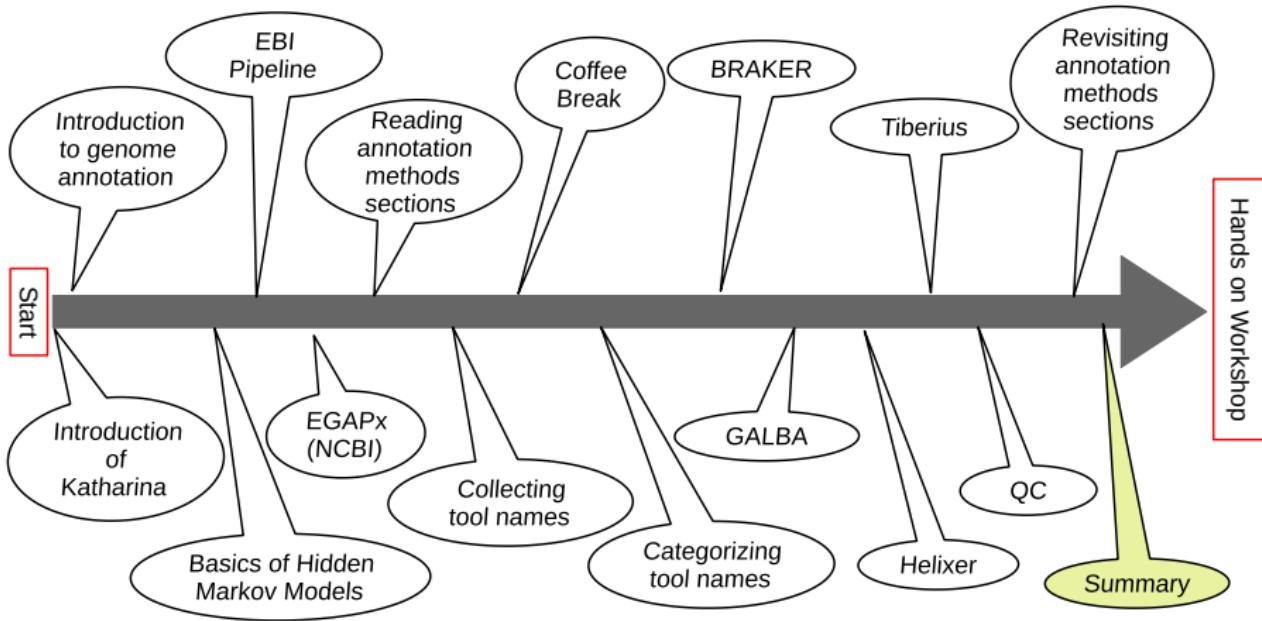
Annotation of Protein Coding Genes



Revisiting annotation methods sections

Your tasks

- 1 Read your methods snippet, again
- 2 Use our categorized tool name board at
<https://shorturl.at/uA0Tg> if you are still unsure what a tool does
- 3 Ask if you remain unsure what a method is good for
- 4 Fill the poll on Wooclap



Most important stuff on genome annotation

- structural genome annotation in eukaryotes is hard
- Hidden Markov Models are essential
- evidence helps a lot
- majority of genomes is annotated by large centers
- popular community annotation pipelines:
 - ① BRAKER
 - ② GALBA
 - ③ (EGAPx may become popular)
- deep learning is changing the field
 - ① Helixer (careful with accuracy)
 - ② Tiberius (only for two clades)
- "looking nice" is not always "correct"
- BUSCO completeness is widely used
- OMArk might be more appropriate
- high marker gene detection rate \neq high accuracy

