

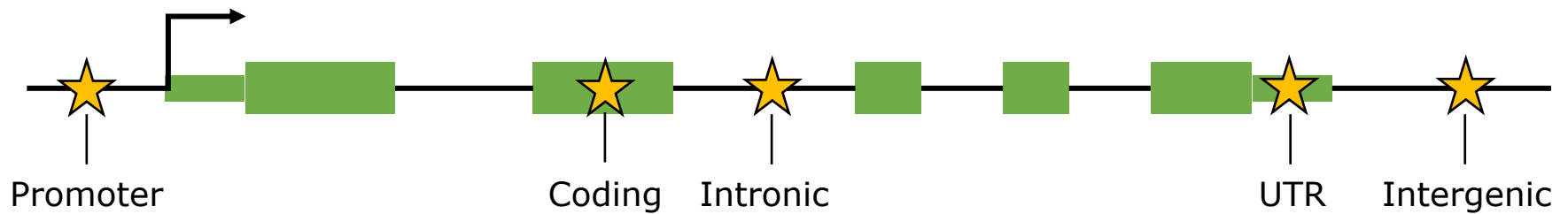
# NGS - variant analysis

Variant annotation

# Variant annotation

**Functional annotation:** relative to genomic features (often genes)

- Coding regions
- Promoter regions



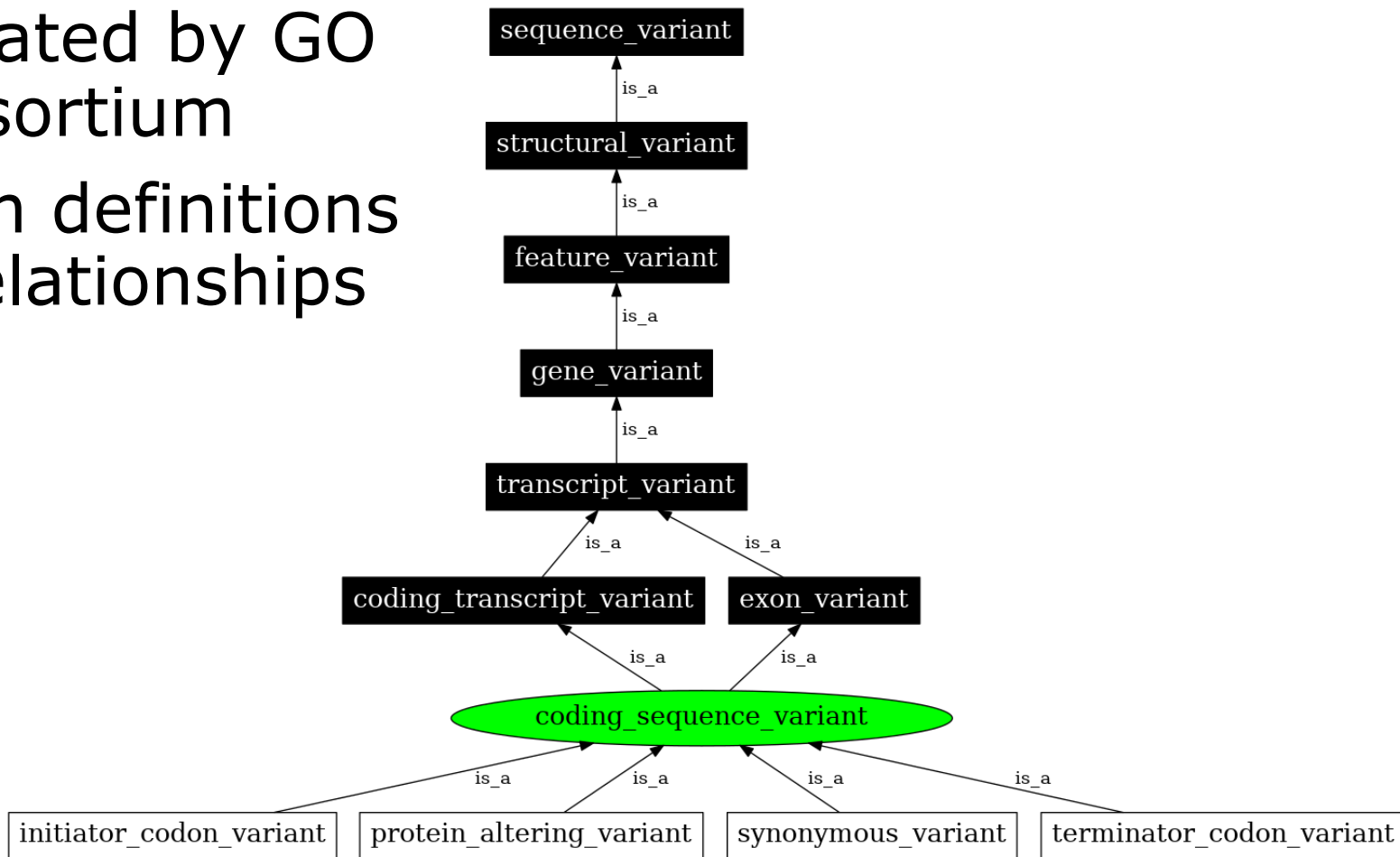
# Coding variants

GCA AGA GAT AAT TGT TGG CAA  
Ala Arg Asp Asn Cys Trp Gln

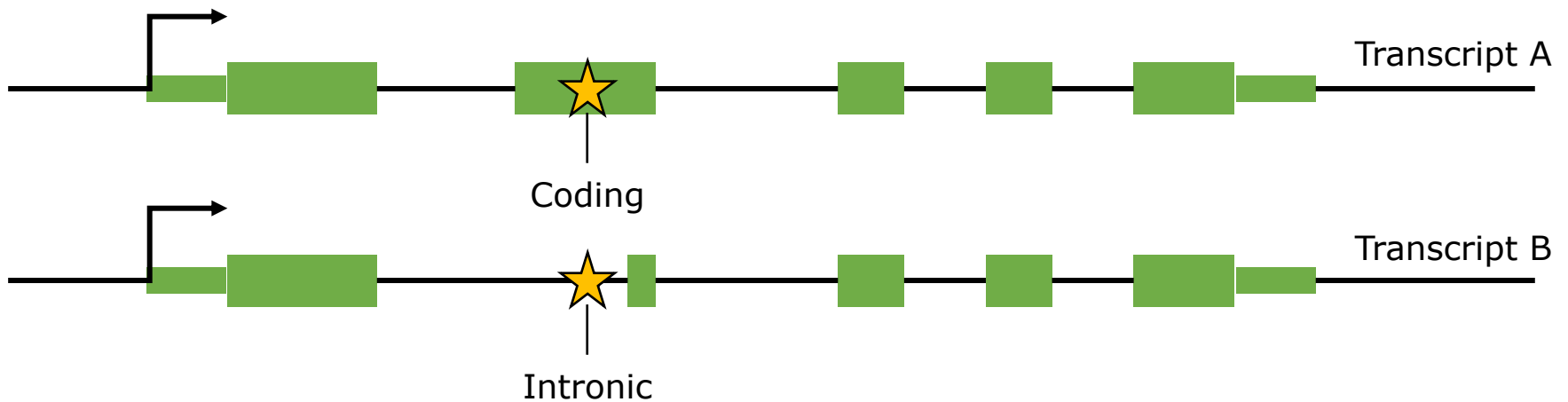
synonymous missense frameshift  
| stop gained |  
GCA AGG GAT AAA TGA TG- C AA  
Ala Arg Asp Lys \* Cys

# Sequence ontology

- Initiated by GO consortium
- Term definitions + relationships






# Isoforms




- Most genes have multiple isoforms
- Annotation for all isoforms?
- Single annotation/variant:
  - Effect with most impact
  - Most relevant transcript, e.g. based on ensembl [transcript tags](#)

# Functional annotation tools

Web interface	Command line tool
 <ul style="list-style-type: none"><li>• Point-and-click interface</li><li>• Suits smaller volumes of data</li></ul> <p><a href="#">Documentation</a></p>	 <ul style="list-style-type: none"><li>• More options and flexibility</li><li>• For large volumes of data</li></ul> <p><a href="#">Documentation</a></p>
	<p><a href="#">Clone from GitHub</a></p> <p><a href="#">Download (zip)</a></p> <p><a href="#">Pull Docker image from DockerHub</a></p>

<https://www.ensembl.org/info/docs/tools/vep/index.html>



Command line:  
<https://annovar.openbioinformatics.org/>

Web-based:  
<https://wannovar.wglab.org/>

## Snpeff

Genetic variant annotation and functional effect prediction toolbox. It annotates and predicts the effects of genetic variants on genes and proteins (such as amino acid changes).

Features:

- Supports over **38,000 genomes**.

# Effect prediction scores

- One “high impact” mutation is not the other
- Prediction of effect based on e.g.:
  - Comparative genomics (conserved regions)
  - Protein structure/biochemistry
  - Experimental function (e.g. eQTL)
- For human genome many databases available, e.g.:
  - [dbNSFP](#)
  - [MutationTaster](#)

