Abracadabra

Finding genetic mutations in Go



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Mendelics

- Mendelics is a genomic analysis lab from São Paulo, Brazil.
- We do genetic tests, trying to find mutations that explain diseases on our patients so that they can get treatment.

Abracadabra

- Each patient has thousands of mutations.
- We needed a fast and accurate way to point out which ones caused diseases.
- Abracadabra is built in Go and uses Random Forests to solve that problem.

The beginning

- CEO, a neurologist, started programming by himself.
- He chose Go almost an accident.
- A prototype was built despite the lack of experience.

The monolith



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Learning Go

- No one on the team had experience with Go before.
- In just a few weeks we were able to get a good grasp of the language and started becoming productive.
- Great documentation.

Growing pains

- Bad habits from other languages.
- We loaded the whole genome in memory, it wasn't a good implementation at first
 - 3+ billion bases (ACTG)
 - 3 gigabases == gigabytes
- go tool pprof to the rescue



Moving forward

- The new language was no longer an issue
- In less than a month we could focus on our real issues:
 - bioinformatics, genetics and machine learning

Open source: github.com/mendelics/vcf

type SVType

type Variant

o func (i SVType) String() string

func (v *Variant) String() string

GoDoc	Home	Index	About	Search
vef: aithub	.com/meno	delics/vcf		Index Examples Files
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packa	age v	cf		
import "gi	thub.com/	mendelic	s/vcf"	
Package vo	f provides a	n API for p	parsing genomic data compliant with the Variant	Call Format 4.2 Specification
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Example				
Example Index				

Machine Learning in Go

- RandomForests™
- github.com/ryanbressler/CloudForest

CloudForest



Google Group

Fast, flexible, multi-threaded ensembles of decision trees for machine learning in pure Go (golang).

Machine Learning in Go

- Trial and error
- CloudForest is powerful



Machine Learning in Go

- Over 90% accuracy
- Predicting a mutation is benign is much more precise. Thousands of mutations are filtered, avoiding waste of time from our geneticists.

Today

- Every patient goes through Abracadabra.
- More than two years in production, users refuse to go back.
- Moving towards TensorFlow.

Today

HERANÇA COMPATÍVEL

HERANÇA INCOMPATÍVEL

VARIANTES NÃO RELEVANTES

BUSCA DE GENES

1 - BRCA2 (Breast Cancer 2, Early Onset)

IGV

READS

PUBMED

2

REMOVER DO LAUDO

[612555] Familial Breast-Ovarian Cancer (BROVCA2) | Herança: monoallelic

[613029] Glioma Susceptibility (GLM3) | Herança: monoallelic

[613347] Pancreatic Cancer | Herança: monoallelic

[114480] Breast Cancer | Herança: monoallelic [155255] Medulloblastoma (MDB) | Herança: monoallelic

[605724] Fanconi Anemia (FANCD1) | Herança: biallelic

Variante	UCSC	IGV	Cópias	Efeito	MAF	Clinvar	PubMed	Predição	Consenso	Qual.	Validação
Chr13:32,905,109-32,905,110 Ref: AT (2bp) Alt: A	UCSC	IGV	1	Frameshift p.Phe246Leu fs*5 AA 246/3418, Exon 9/27 ENST00000380152	0.000000			Deletério	pathogenic 😝		i

What Go made possible

- Simple enough for a physician to start.
- Powerful enough to do machine learning in production.
- Most of our problems solved in the stdlib.
- All of that built in Brazil.

GopherCon Brasil - gopherconbr.org/en



Thanks



twitter.com/vdemario

github.com/vdemario

