VARIANTPLANER

QUERING MANY VARIANT WITHOUT CLUSTER

Pierre Marijon, Sacha Schutz

GCS SeqOIA

September 20, 2023

SEQOIA

1082 Prescribers / **40** Prescription assistant

SEQOIA LBM Médecine génomique

Biologist in charge – Pierre BLANC

SEQOIA GEN Médecine génomique

Pierre BLANC

Wet-Lab - Logistics, Reception, Extraction, STHD (Integragen)

SEQOIA IT Médecine génomique

Alban LERMINE

Dry Lab - Bioinformatics

SEQOIA LMG Médecine génomique

Pierre BLANC, Boris KEREN, Jennifer WONG
Damien VASSEUR, Emmanuelle CLAPPIER,

Interpretation of exams
190 Biologists

Accreditation ISO 15189 (GC07 & GS07) cofrac filed on October 2021

Agreements

16 agreements with non-GCS establishments

GCS SeqOIA

ASSISTANCE PUBLIQUE HÔPITAUX DE PARIS

institutCurie

GUSTAVE ROUSSY CANCER CAMPUS GRAND PARIS

SAKE: SEQOIA DATA LAKE

Which sample has:

- denovo variant in these gene/region

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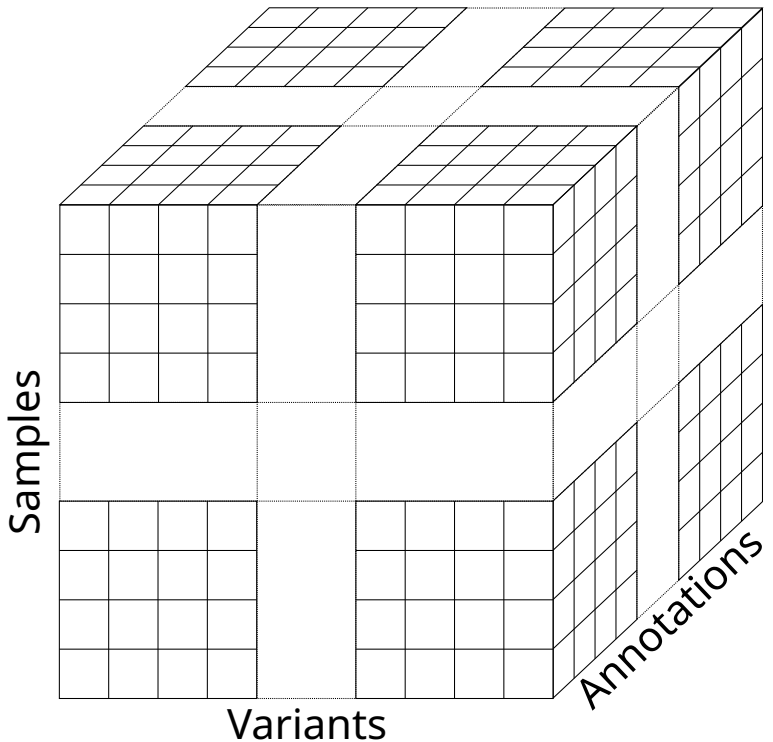

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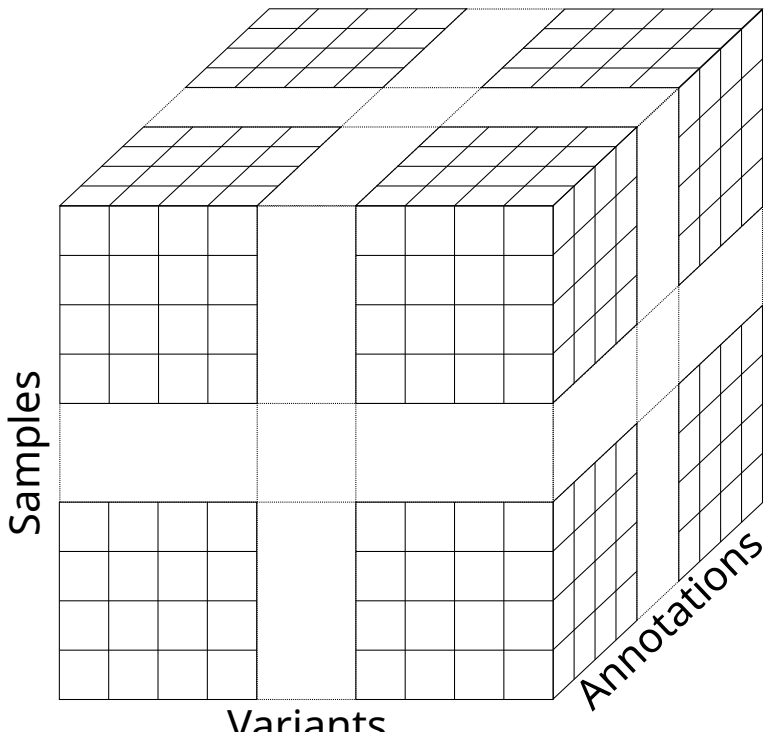

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Matrix size:

September 1st values

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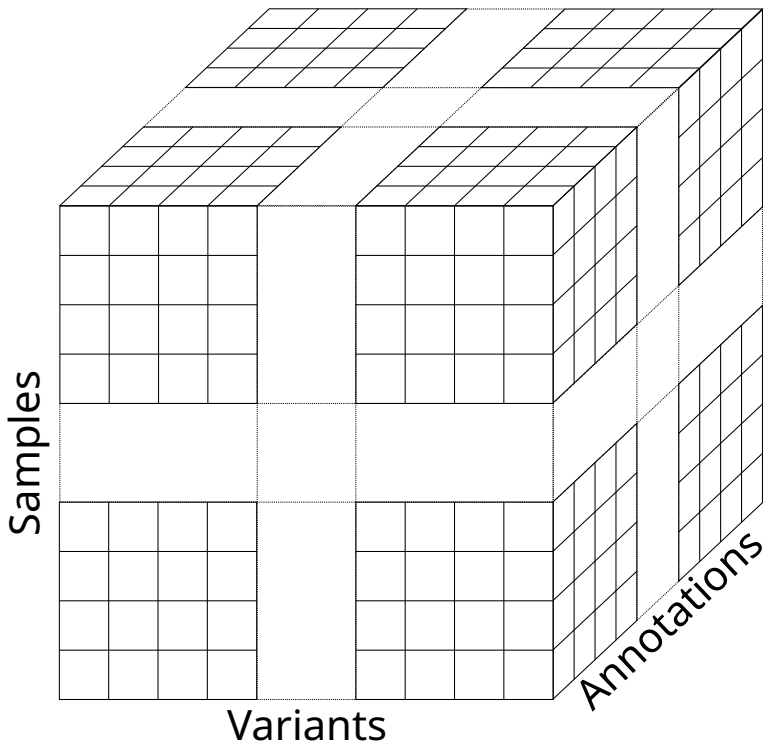

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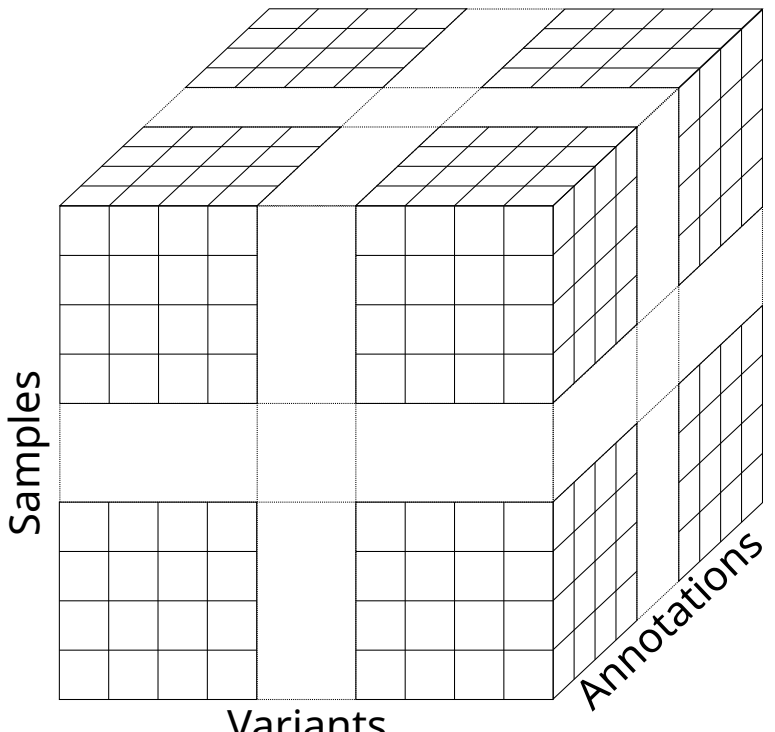

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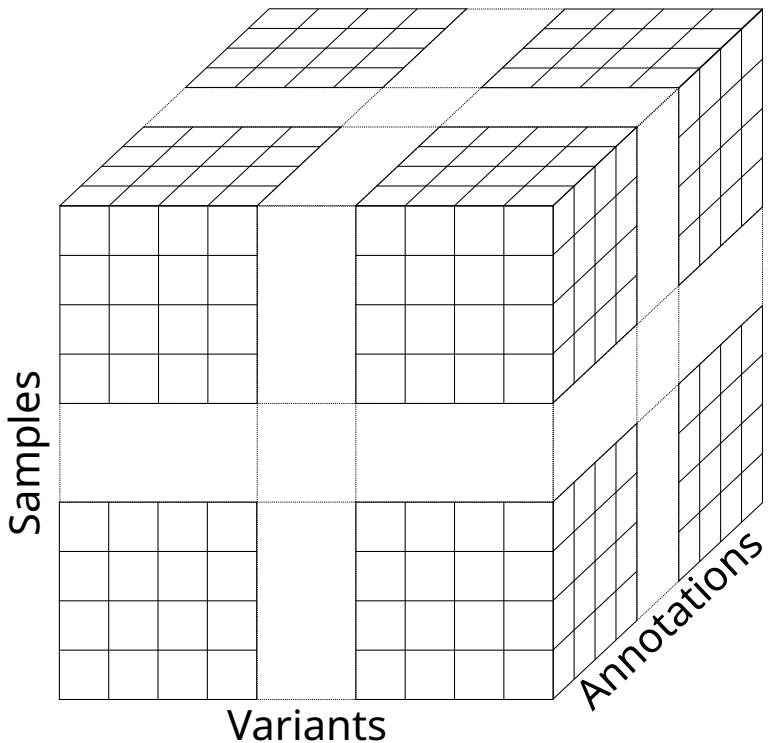

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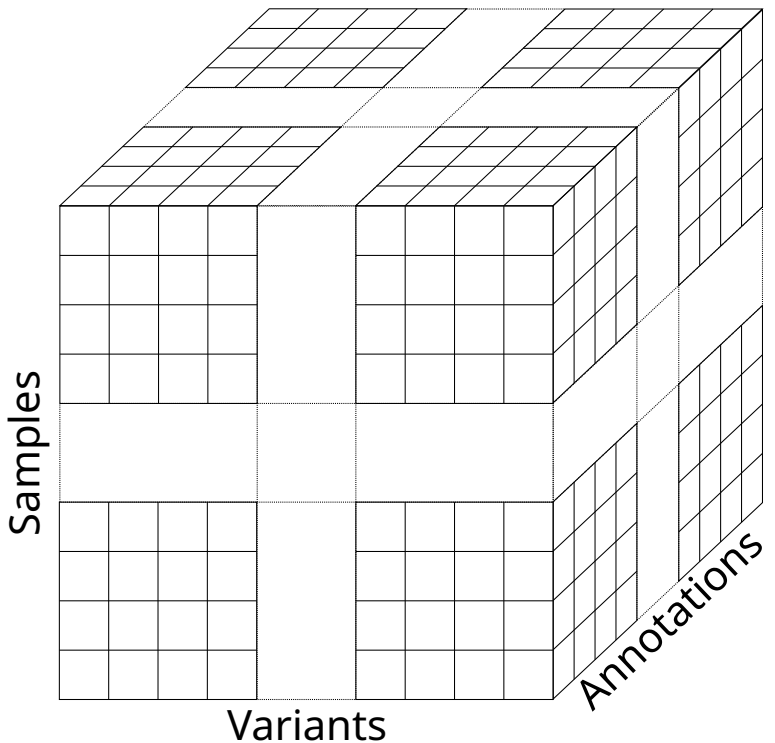

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- sparse matrix: 98.5 % variants have 0/0 genotype

September 1st values

SAKE: SEQOIA DATA LAKE

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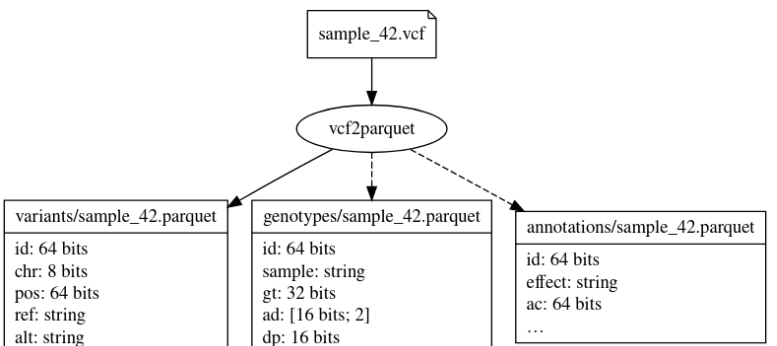
VariantPlaner

- Part of the generalisable SAKE generation pipeline
- Python module and command line
- Based on pola-rs

VARIANTPLANER

VCF2PARQUET



VARIANTPLANER

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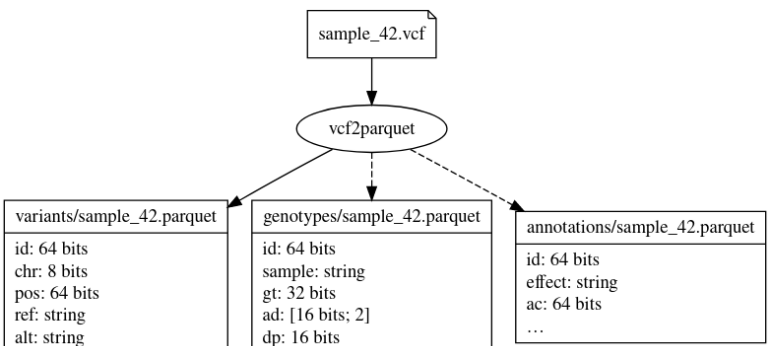

id computation:

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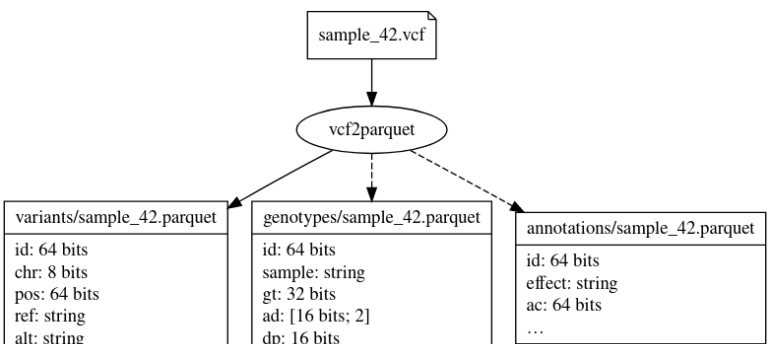

id computation:

- v0.1: hash of `chr, pos, ref, alt`
- V0.2 if $len(ref) + len(alt)$:
  - $13 \rightarrow$ perfect hash (96%)
  - $> 13 \rightarrow$ v0.1 hash

VariantPlaner

Genotype Organisation

```
variantplaner struct [-i sample/{}.parquet] genotypes -o genotypes/variants/
```

```
id_mod=0    id_mod=127  id_mod=156  id_mod=185  id_mod=213  id_mod=242  id_mod=41  id_mod=70
id_mod=1    id_mod=128  id_mod=157  id_mod=186  id_mod=214  id_mod=243  id_mod=42  id_mod=71
id_mod=10   id_mod=129  id_mod=158  id_mod=187  id_mod=215  id_mod=244  id_mod=43  id_mod=72
id_mod=100  id_mod=13   id_mod=159  id_mod=188  id_mod=216  id_mod=245  id_mod=44  id_mod=73
id_mod=101  id_mod=130  id_mod=16   id_mod=189  id_mod=217  id_mod=246  id_mod=45  id_mod=74
id_mod=102  id_mod=131  id_mod=160  id_mod=19   id_mod=218  id_mod=247  id_mod=46  id_mod=75
id_mod=103  id_mod=132  id_mod=161  id_mod=190  id_mod=219  id_mod=248  id_mod=47  id_mod=76
id_mod=104  id_mod=133  id_mod=162  id_mod=191  id_mod=22   id_mod=249  id_mod=48  id_mod=77
id_mod=105  id_mod=134  id_mod=163  id_mod=192  id_mod=220  id_mod=25   id_mod=49  id_mod=78
id_mod=106  id_mod=135  id_mod=164  id_mod=193  id_mod=221  id_mod=250  id_mod=5   id_mod=79
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```
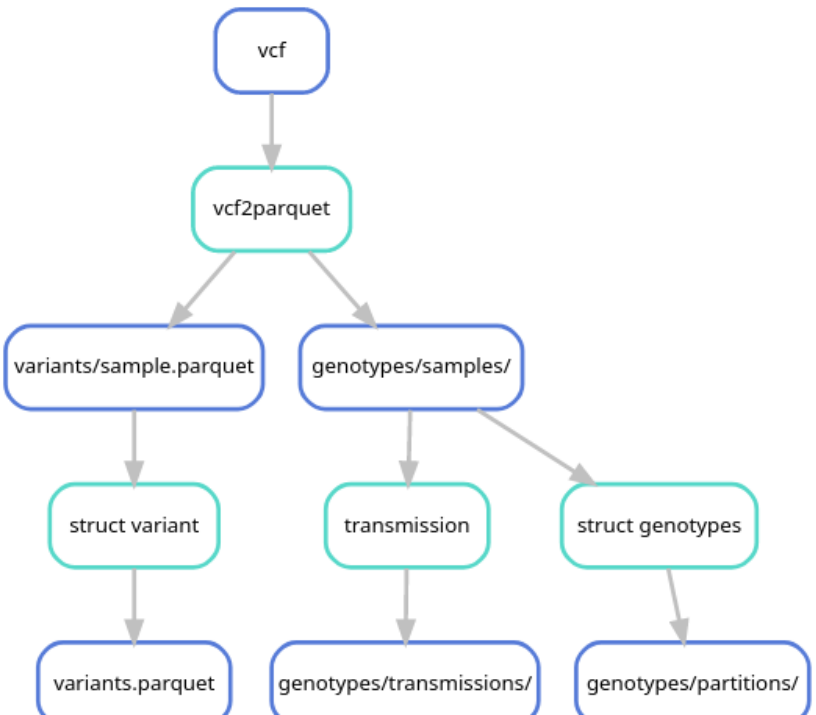

```
variantplaner transmission -i sample/42.parquet -p 42.ped -m
transmissions/42.parquet
```

id	index gt	mother gt	father gt	origin
15225413595434247130	2	0	0	200
12902036237217108692	1	1	0	110
2909135909504078072	1	0	2	102
15241688863478200138	2	3	3	233

VariantPlaner

Performance: build SAKE



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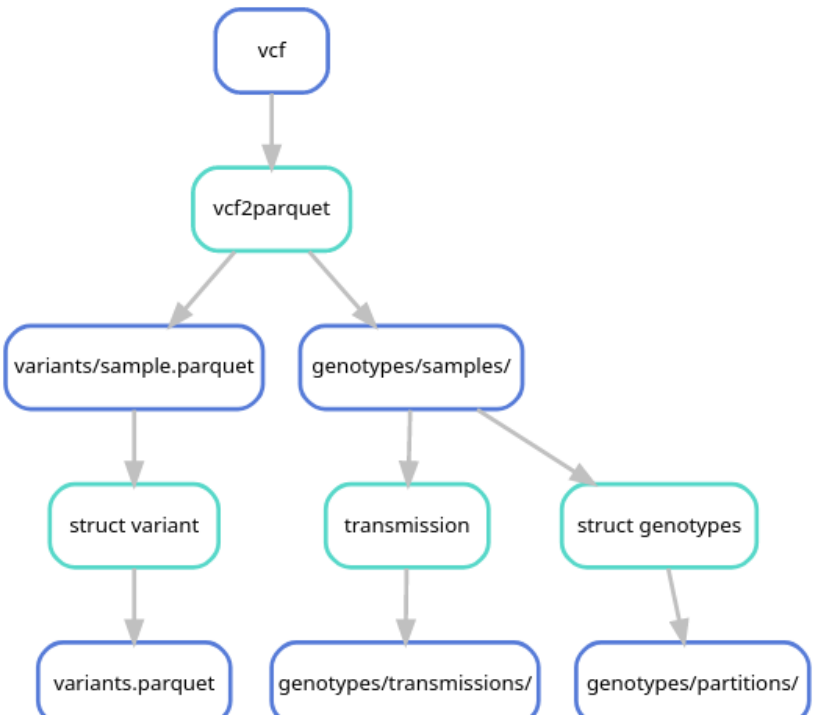

`vcf2parquet`: ~30s per sample
`struct variant`: ~4h 30m for all
`transmission`: ~50s per sample
`struct genotype`: ~2h 50m for all

VariantPlaner

Performance: interrogate SAKE

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SELECT * FROM Variants WHERE chr="MT"
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SELECT * FROM Variants as v JOIN SpliceAI as s ON v.id=s.id
JOIN Recurence as r ON v.id=r.id WHERE v.chr=13 and
v.pos > 6670360 and v.pos < 6694030 and r.ac < 10
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Around 20 minutes

```
SELECT * FROM selected_variant_and_genotypes as svg JOIN Transmission as t ON
svg.sample=t.sample WHERE origin = 200 and origin = 100
```

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Highly variable

Conclusion

VariantPlaner builds an efficient, queryable database of variants:

- With reasonable resources (190Gb of ram)
- Reduce disk usage (SAKE use 3.7Tb)
- Available as a python module and command line
- Open to suggestion and modification

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natir/variantplaner

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natir/variantplaner

"Ré-analyse périodique semi-automatisée en génétique constitutionnelle"
Friday morning at 9 hours by Alban Lermine:

REFERENCES I