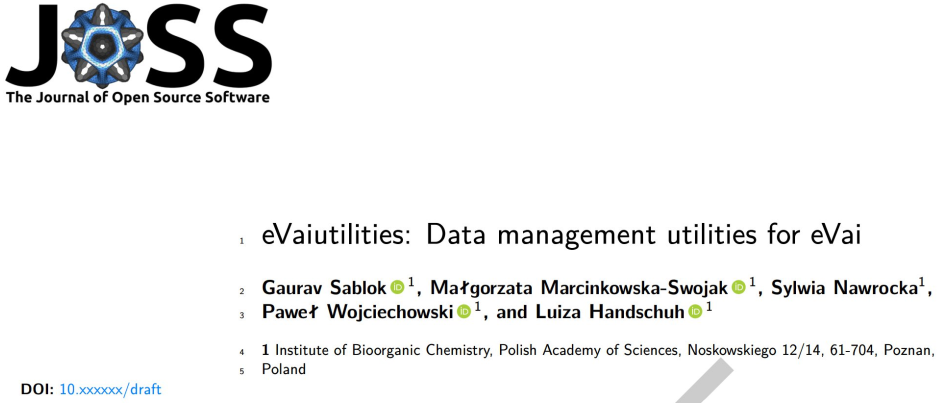
Instytut Chemii Bioorganicznej Polskiej Akademii Nauk



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eVaiutilities: Data management utilities for eVai

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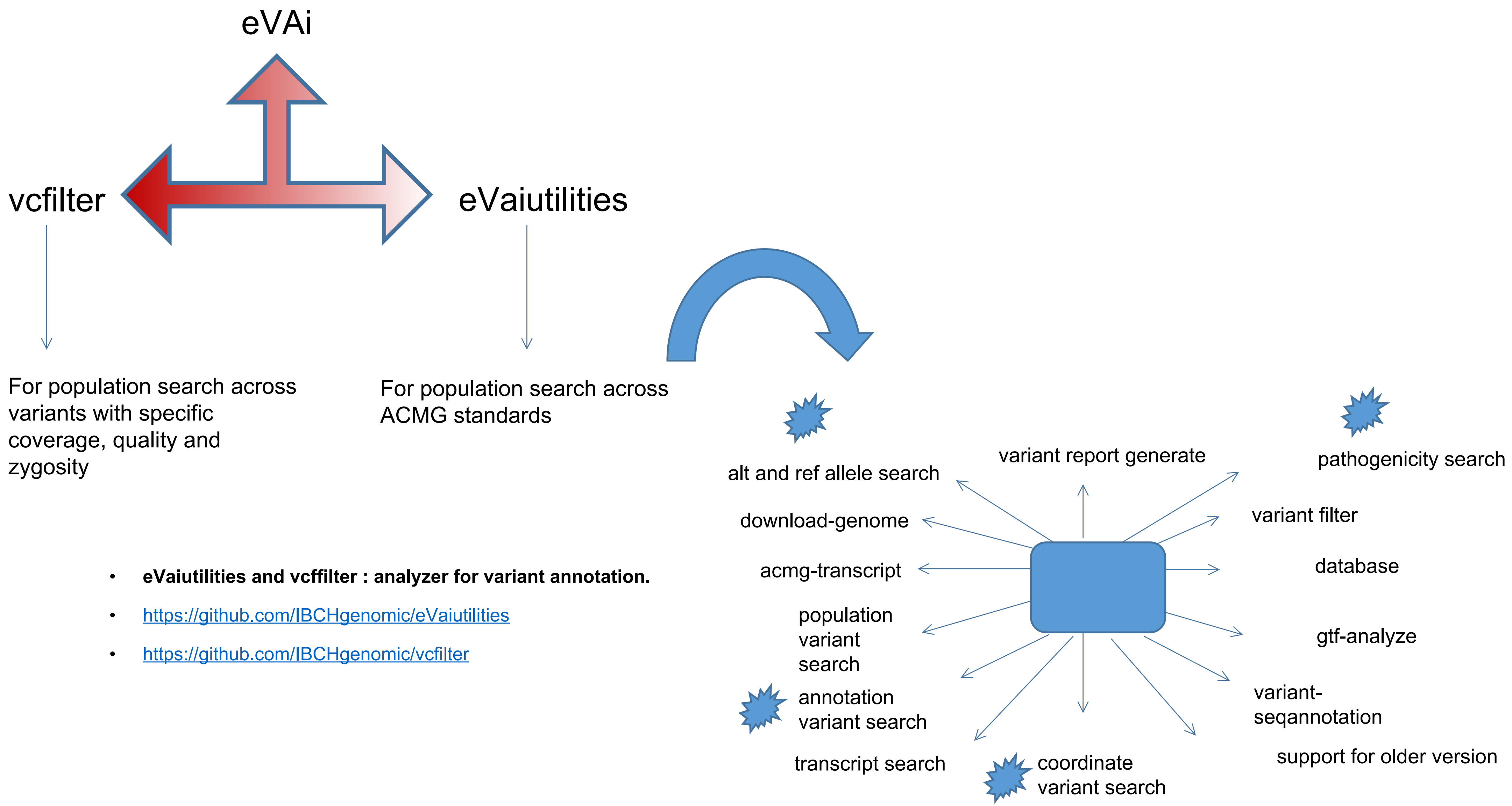
Funded by ABM project: Development of a universal fast-response platform, based on RNA technology, ensuring the national drug and epidemiological safety. 2021/ABM/05/00004-00

Key Features:

- RUST, Conda ,Asynchronous, SQLITE
- Population scale analysis
- Stats features for variants
- Variant summary for easy annotation.
- Annotate variant



eVAi

vcfilter

eVaiutilities

For population search across variants with specific coverage, quality and zygosity

For population search across ACMG standards

- **eVaiutilities and vcffilter : analyzer for variant annotation.**
- https://github.com/IBCHgenomic/eVaiutilities
- https://github.com/IBCHgenomic/vcfilter

alt and ref allele search

variant report generate

pathogenicity search

download-genome

variant filter

acmg-transcript

database

population variant search

gtf-analyze

annotation variant search

variant-seqannotation

transcript search

coordinate variant search

support for older version

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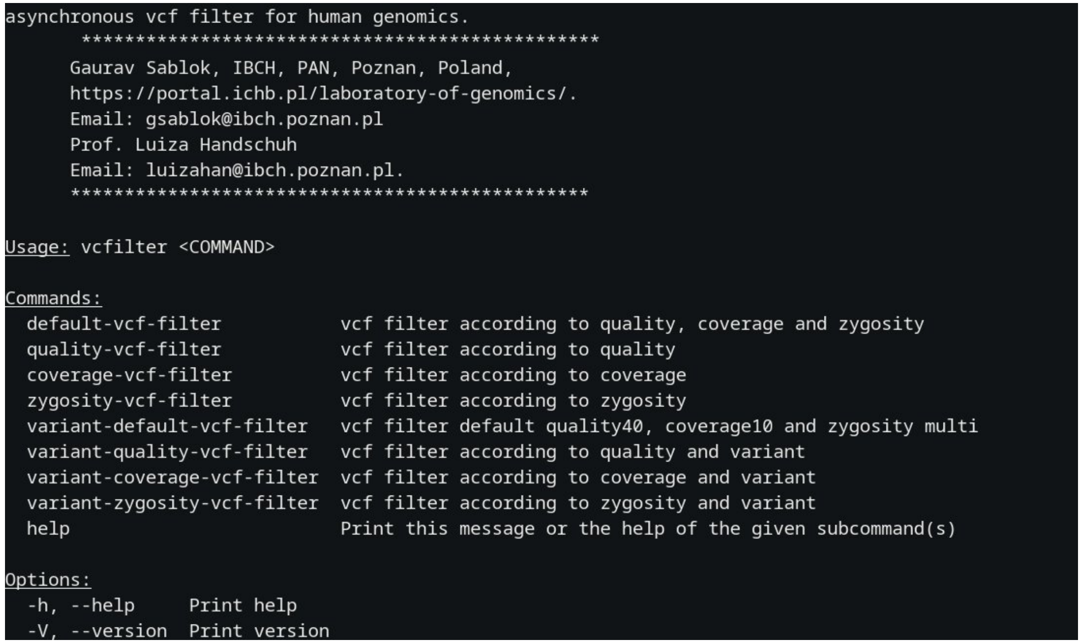

```
asynchronous vcf filter for human genomics.
       ************************************************
      Gaurav Sablok, IBCH, PAN, Poznan, Poland,
      https://portal.ichb.pl/laboratory-of-genomics/.
      Email: gsablok@ibch.poznan.pl
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      Email: luizahan@ibch.poznan.pl.
      ************************************************

Usage: vcfilter <COMMAND>

Commands:
  default-vcf-filter           vcf filter according to quality, coverage and zygosity
  quality-vcf-filter           vcf filter according to quality
  coverage-vcf-filter          vcf filter according to coverage
  zygosity-vcf-filter          vcf filter according to zygosity
  variant-default-vcf-filter   vcf filter default quality40, coverage10 and zygosity multi
  variant-quality-vcf-filter   vcf filter according to quality and variant
  variant-coverage-vcf-filter  vcf filter according to coverage and variant
  variant-zygosity-vcf-filter  vcf filter according to zygosity and variant
  help                         Print this message or the help of the given subcommand(s)

Options:
  -h, --help     Print help
  -V, --version  Print version
```
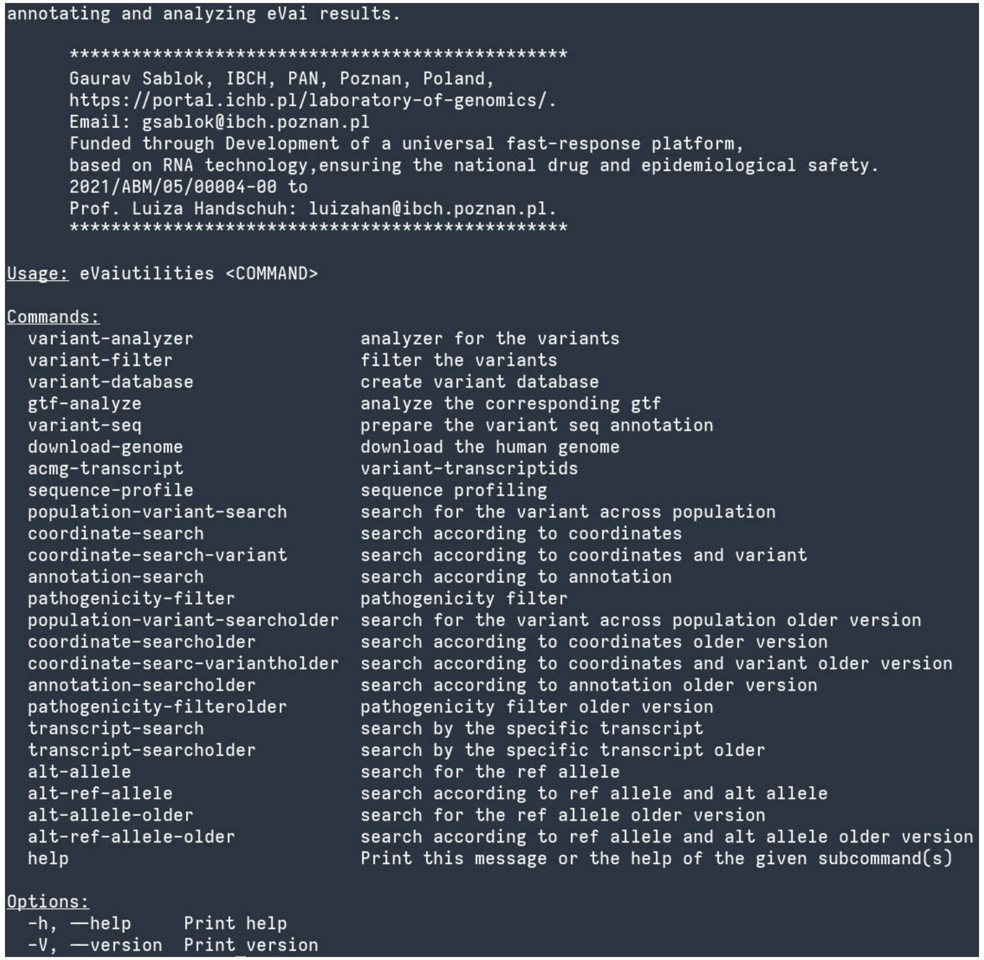

User interface of vcfilter



```
annotating and analyzing eVai results.

      ************************************************
      Gaurav Sablok, IBCH, PAN, Poznan, Poland,
      https://portal.ichb.pl/laboratory-of-genomics/.
      Email: gsablok@ibch.poznan.pl
      Funded through Development of a universal fast-response platform,
      based on RNA technology,ensuring the national drug and epidemiological safety.
      2021/ABM/05/00004-00 to
      Prof. Luiza Handschuh: luizahan@ibch.poznan.pl.
      ************************************************

Usage: eVaiutilities <COMMAND>

Commands:
  variant-analyzer                analyzer for the variants
  variant-filter                  filter the variants
  variant-database                create variant database
  gtf-analyze                     analyze the corresponding gtf
  variant-seq                     prepare the variant seq annotation
  download-genome                 download the human genome
  acmg-transcript                 variant-transcriptids
  sequence-profile                sequence profiling
  population-variant-search       search for the variant across population
  coordinate-search               search according to coordinates
  coordinate-search-variant       search according to coordinates and variant
  annotation-search               search according to annotation
  pathogenicity-filter            pathogenicity filter
  population-variant-searcholder  search for the variant across population older version
  coordinate-searcholder          search according to coordinates older version
  coordinate-searc-variantholder  search according to coordinates and variant older version
  annotation-searcholder          search according to annotation older version
  pathogenicity-filterolder       pathogenicity filter older version
  transcript-search               search by the specific transcript
  transcript-searcholder          search by the specific transcript older
  alt-allele                      search for the ref allele
  alt-ref-allele                  search according to ref allele and alt allele
  alt-allele-older                search for the ref allele older version
  alt-ref-allele-older            search according to ref allele and alt allele older version
  help                            Print this message or the help of the given subcommand(s)

Options:
  -h, —help     Print help
  -V, —version  Print version
```

User interface of eVai-analyzer