# GenomeChronicler: The Personal Genome Project UK Genomic Report Generator Pipeline

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**Abstract**

In recent years, there has been a significant increase in whole genome sequencing data of individual genomes produced by research projects as well as direct to consumer service providers. While many of these sources provide their users with an interpretation of the data, there is a lack of free, open tools for generating similar reports exploring the data in an easy to understand manner.

GenomeChronicler was written as part of the Personal Genome Project UK (PGP-UK) to address this need. PGP-UK provides genomic, transcriptomic, epigenomic and self-reported phenotypic data under an open-access model with full ethical approval. As a result, the reports generated by GenomeChronicler are intended for research purposes only and include information relating to potentially beneficial and potentially harmful variants, but without clinical curation.

GenomeChronicler can be used with data from whole genome or whole exome sequencing producing a genome report containing information on variant statistics, ancestry and known associated phenotypic traits. Example reports are available from the PGP-UK data page (personalgenomes.org.uk/data).

The objective of this method is to leverage on existing resources to find known phenotypes associated with the genotypes detected in each sample. The provided trait data is based primarily upon information available in SNPedia, but also collates data from ClinVar, GETevidence and gnomAD to provide additional details on potential health implications, presence of genotype in other PGP participants and population frequency of each genotype.

The whole pipeline is self-contained, and runs without internet connection, making it a good choice for privacy conscious projects that can run GenomeChronicler within their off-line safe-haven

environments. GenomeChronicler can be run for one sample at a time, or in parallel making use of the nextflow workflow manager.

The source code is available from GitHub (https://github.com/PGP-UK/GenomeChronicler), container recipes are available for Docker and Singularity, as well as a pre-built container from SingularityHub (https://singularity-hub.org/collections/3664) enabling easy deployment in a variety of settings. Users without access to computational resources to run GenomeChronicler can access the software from the Lifebit CloudOS platform (https://cloudos.lifebit.ai) enabling the production of reports and variant calls from raw sequencing data in a scalable fashion.

## 1 Introduction

The publication of the first draft human genome sequence ('Initial Sequencing and Analysis of the Human Genome' 2001) brought along the promise of a revolution in how we see ourselves as individuals and how future medical care should take into account our genetic background. Almost ten years later, the perspective of widespread personal genomics was still to be achieved (Venter 2010).

There is now a wide range of clinical and non-clinical genetic tests that are routinely employed to detect individuals' carrier status for certain disease genes or particular mutations of clinical relevance. Many more associations between genotype and phenotype have been highlighted by research, sometimes with uncertain clinical relevance or simply describing personal traits like eye color (Pontikos et al. 2017; Kuleshov et al. 2019).

Over the past few years we have seen a dramatic reduction of the cost to sequence the full human genome. This reduction in cost enables many more projects to start using whole genome sequencing (WGS) approaches, as well as the marked rise in the number of personal genomes being sequenced.

Personal genomics is very much part of the public consciousness as can be seen by the rampant rise of direct to consumer (DTC) genomic analysis offerings on the market. In this context it is unsurprising that the analysis of one's own genome provides a valuable educational opportunity (Salari et al. 2013; Linderman et al. 2018) as well as increases participant engagement as part of biomedical trials (Sanderson et al. 2016).

The personal genome project is one of the initiatives enabled by the increased popularity of whole genome sequencing and its lowering costs. The global PGP network currently consists of 5 projects spread around the world, managed independently but joined by a common goal of providing open access data containing genomic, environmental and trait information (https://www.personalgenomes.org/).

Data analysis within PGP-UK poses interesting ethical challenges, as all the data and genome reports are intended to become freely and openly available on the World Wide Web. However, until completion and approval of the reports, the data must be treated as confidential private information. Prior to enrollment, all participants are well informed and tested for their understanding of the potential risks of participating in a project of this nature. Upon receipt of their report, participants have three options. First, they can trigger the release of their report and data themselves by selecting the 'release immediately' option in their personal accounts. To date, 67% of participants have selected this release option. Second, they can withdraw from the study in which case no release occurs and all data will be deleted. This option has never been selected by any participant. Third, the participants default to a cool-off period of four weeks to explore their data and reports and to seek all

the required clarifications. If neither option one or two are selected by the end of the cool-off period, the data and reports will be released automatically.

There are several resources aimed at users of DTC genetic testing companies on the internet including Promethease and Genomelink ('Promethease' 2019; 'Genomelink | Upload Raw DNA Data for Free Analysis On 25 Traits' 2019). There are some other tools with a focus on clinical aspects or particular diseases (Nakken et al. 2018), as well as academic databases containing genotypes of other individuals (Greshake et al. 2014), pharmacogenomic information (Klein and Ritchie 2018) or genotype to phenotype links (Ramos et al. 2014; Pontikos et al. 2017; Kuleshov et al. 2019) that can be useful for the interpretation of personal genomes. Many of these are linked into resources like SNPedia (Cariaso and Lennon 2012), allowing a wide range of exploration options for the known associations of each genotype from multiple perspectives.

Surprisingly, we found no pre-existing solution that would allow the annotation and evaluation of variants on the whole genome level, assessment of ancestry and more fine-grained analysis of variants that have been previously associated with specific phenotypes. In particular one that could be run locally ensuring full control of the data before the results are scrutinized and approved.

GenomeChronicler represents, to the best of our knowledge, the first pipeline that can be run off-line or in the cloud, to generate personal genomics reports that are not limited to disease only, from whole genome or whole exome sequencing data.

GenomeChronicler contains a database of positions of interest for ancestry or phenotype. The genotype at each of these positions is inferred from the user provided data that has been mapped to the human genome. These genotypes are then compared to local versions of a series of publicly available resources to infer ancestry and likely phenotypes for each individual participant. These results are then presented as a PDF document containing hyperlinks where more information about each variant and phenotype can be found. A visual representation of the pipeline and its underlying resources is shown in Figure 1.

This pipeline will continue to be developed and used to generate genome reports by PGP-UK (Beck et al. 2018). We envision this project will also be useful to other research endeavors that want to provide personal genomes information to their participants to increase engagement; e.g. to altruistic individuals who have obtained their whole genome sequencing data from a DTC or health care provider and are looking for an ethics-approved framework to share their data;

## 2 Materials and Methods

### 2.1 Data Preprocessing Requirements

The GenomeChronicler pipeline was designed to run downstream of a standardised germline variant calling pipeline. GenomeChronicler requires a pre-processed BAM file and optionally, the summary HTML report produced by the Ensembl Variant Effect Predictor (McLaren et al. 2016).

GenomeChronicler can be run with any variant caller provided that the reference dataset is matched to the reference genome used (the included GenomeChronicler databases currently use GRCh38). It is also imperative that the BAM or CRAM files used have had their duplicates removed and quality recalibrated prior to being used for GenomeChronicler.

To simplify this entire process and to make the tool more accessible to users who may not know how to run a germline variant calling pipeline, GenomeChronicler can also be run in a fully automated mode where the germline variant calling pipeline is also run and the whole process is managed by the nextflow workflow management system. In this scenario, GenomeChronicler uses the Sarek pipeline (Garcia et al. 2018) to process raw FASTQ files in a manner that follows the GATK variant calling best practices guidelines (Van der Auwera et al. 2013). Manual inspection of the initial quality control steps of Sarek is recommended prior to perusing the final results.

The combined version of Sarek + GenomeChronicler written using the nextflow workflow manager (Di Tommaso et al. 2017) is available both on Github (https://github.com/PGP-UK/GenomeChronicler-Sarek-nf) and on Lifebit CloudOS.

## 2.2 Ancestry Inference

We infer an individuals' ancestry through a Principal Components Analysis (PCA) which is a widely used approach for identifying ancestry difference among individuals (Novembre et al. 2008).
For each sample of interest, we merged the genotypes with a reference dataset consisting of genotypes from the 1000 genomes project samples (The 1000 Genomes Project Consortium 2015), containing individuals from 26 different worldwide populations and applying PCA on the merged genotype matrix.
Prior to merging data was filtered to keep only unrelated samples. In order to avoid strand issues when merging the datasets, all ambiguous (A/T and C/G) SNPs were removed, as well as non-biallelic SNPs, SNPs with >5% of missing data, rare variants (MAF < 0.05) and SNPs out of Hardy-Weinberg equilibrium (pval < 0.0001). From the remaining SNPs, a subset of unlinked SNPs are selected by pruning those with r2 > 0.1 using 100-SNP windows shifted at 5-SNP intervals.
These genotypes are used to run PCA based on the variance-standarized relationship matrix, selecting 20 as the number of PCs to be extracted. We then project the data over the first 3 principal components to identify clusters of populations and highlight the sample of unknown ancestry on the resulting plot.
Here, we used PLINK (Purcell et al. 2007) to process the genotype data and the R Statistical Computing platform for plotting the final PCA figures to illustrate the ancestry of each sample. An example of the distribution of the reference samples on the PCA is show in Figure 2.

## 2.3 Linked Databases

### 2.3.1 **SNPedia**

SNPedia is a large public repository of manually added as well as automatically mined genotype to phenotype links sourced from existing literature. SNPedia (Cariaso and Lennon 2012) is the core resource behind the phenotype tables in GenomeChronicler; it not only provides annotations for single-gene phenotypes, but also for a few phenotypes involving multiple loci referred to as genosets in the produced reports.

### 2.3.2 **ClinVar**

ClinVar (Landrum and Kattman 2018) is a database hosted by the NCBI that focuses exclusive of variants related to health that has been running since 2013. In comparison to SNPedia, ClinVar is a much smaller database that is closely linked to the clinical relevance of each variant. ClinVar is curated more strictly with clinical review – something that is not available for the other data sources used by GenomeChronicler.

#### 2.3.3 **GETevidence**

GETevidence was developed as part of the Personal Genome Project Harvard (Mao et al. 2016) to showcase the variants present within its participants and to allow manual annotation and interpretations of the results. For some of the genotypes present, it also contains manual annotations that have been added by the users or curation team. GETevidence allow individuals to compare their genotypes against those from other personal genomes available within the Harvard project.

#### 2.3.4 **gnomAD**

Spanning several human populations, the Genome Aggregation Database (gnomAD) (Karczewski et al. 2019) aggregates data from multiple sources to produce an atlas of variation across the human genome. Extensively annotated and now covering most of the latest assembly of the human genome, these links enable easy access to information such as allele frequencies for the genotype across different populations around the world, as well as some annotation context for each variant, regarding potential effect on genes if relevant and how selection forces are constraining the genomic region.

### 2.4 Database Updates

The underlying databases required to run GenomeChronicler are provided within the package. A set of scripts to regenerate these SQLite databases is also provided within the source code. When the databases are generated, a set of positions of the interest is compiled so that when genotyping is performed only relevant positions are computed to save computational time.

SNPedia provides an API to query its records in a systematic way. The other linked databases provide regular dumps of the whole dataset, enabling easy assessment for which dbSNP rs identifiers are represented within the full database. The use of rs identifiers and genotypes to link between the different databases enables an unambiguous way to compare information between different resources.

### 2.5 Genotype assessment and reporting

In many scenarios, during normal genomics data processing, only VCF files are produced, which do not include any information regarding the positions of the genome that match the reference sequence. These become indistinguishable from positions in the genome where there is no read coverage.

To ensure comparable results between runs, the genotype information (gVCF) is computed, following GATK best practices, during each run of GenomeChronicler. To reduce the computational burden of computing genotypes, only a subset of genomic positions that we know are meaningful, from the ancestry and phenotype databases, are computed thus saving computational time and storage space.

### 2.6 The Genome Report Template

GenomeChronicler is a multistep modular approach in which the final report is only compiled as the very last step, integrating data from all previous steps. To give users the possibility of fully customising the report layout and the amount and content of extra information provided in each report, GenomeChronicler uses a template file written in the LaTeX typesetting language. This can be modified to better suit the user, for example: To include project branding and introductory texts to put the report into perspective; To integrate more analyses from other pipelines ran independently from GenomeChronicler provided the results are in a format that can be typeset using LaTeX and are

present in predefined locations that can be sourced from the template file; To deactivate certain sections of the report that are not relevant; Or simply to modify the structure of the report produced.

## 2.7 Output Files

The main output of the GenomeChronicler pipeline is a full report in PDF format, containing information from all sections of the pipeline that have run as set by the LaTeX template provided when running the script. Additionally an Excel file containing the genotype phenotype link information, and all corresponding hyperlinks is also produced, allowing the user to reorder and/or filter out results as they see fit in a familiar environment. While most intermediate files are automatically removed at the end of the GenomeChronicler run, the original PDF version of the ancestry PCA plot is retained, as well as a file containing the sample name within the results directory to ease automation and a log file containing output produced whilst running GenomeChronicler.

## 2.8 Accessing GenomeChronicler

Just like the PGP-UK data, all the code for GenomeChronicler is freely available. To make it easier to implement, several options are available to remove the need for installing dependencies and underlying packages, or even the need to own computer hardware capable of handling the processing of a human genome. The range of options available is detailed below and illustrated in Figure 1.

### 2.8.1 **Running GenomeChronicler Locally**

#### 2.8.1.1 From the available source code

The source code for GenomeChronicler is available on GitHub at https://github.com/PGP-UK/GenomeChronicler. The pre-compiled accessory databases are available as links within a setup script that will help download all the required information.

GenomeChronicler has a series of dependencies including LaTeX, R and Perl. The provided Singularity recipe file can act as a useful list of required packages, in particular for those installing it on a Debian/Ubuntu based system.

#### 2.8.1.2 Using a pre-compiled container

For those that have access to a machine where the Singularity (Kurtzer, Sochat, and Bauer 2017) container solution is installed, a container with all dependencies pre-installed and ready to use can be obtained from SingularityHub (Sochat, Prybol, and Kurtzer 2017). This can be performed by running the command: `singularity pull shub://PGP-UK/GenomeChronicler`.

Once downloaded, the main script (GenomeChronicler_mainDruid.pl) can be run with the desired data and options to produce genome reports.

### 2.8.2 **Running GenomeChronicler on Cloud**

To enable reproducible, massively parallel, cloud native analyses, GenomeChronicler has also been implemented as a Nextflow pipeline. The implementation abstracts the installation overhead from the end user, as all the dependencies are already available via pre-built containers, integrated seamlessly in the Nextflow pipeline. The source code for this implementation is available on GitHub at https://github.com/PGP-UK/GenomeChronicler-nf, as a standalone nextflow process. To provide an end-to-end FASTQ to PGP-UK reports pipeline, we also implemented an integration of

GenomeChronicler, with a curated and widely used by the bioinformatics community pipeline, namely Sarek (Garcia et al. 2018; Ewels et al. 2019). This PGP-UK implementation of Sarek is available on GitHub at https://github.com/PGP-UK/GenomeChronicler-Sarek-nf. The aforementioned pipeline, is available in the collection of curated pipelines on the Lifebit CloudOS platform (https://cloudos.lifebit.ai/app/home). Lifebit CloudOS enables users without any prior cloud computing knowledge to deploy analysis in the Cloud. In order to run the pipeline the user only needs to specify input files, desired parameters and select resources from an intuitive graphical user interface. After the completion of the analysis on Lifebit CloudOS, the user has a permanent shareable live link that includes performance and file metadata, the associated github repository revision and also links to the generated results. The relevant analysis page can be used to repeat the exact same analysis. The analysis page for the PGP-UK user with id uk35C650 can be accessed in the following permalink https://cloudos.lifebit.ai/public/jobs/5e3582dae3474100f4665c7a. Each analysis can have different privacy settings allowing the user to choose if the results are publicly visible, making it easier for sharing, or private use, thus maintaining data confidentiality.

## 3 Results

The main resulting document is a multipage PDF file containing sections relating to variants of unknown significance, ancestry estimation (as exemplified in Figure 2) and variants with an associated phenotype, separated by either potentially beneficial or potentially harmful as well as phenotypes affected by multiple variants, referred to as genosets.

To date, more than one hundred such reports have been produced and made available available as part of the PGP-UK (Beck et al. 2018) and are publicly available in the projects open access data page (https://www.personalgenomes.org.uk/data). This collection contributes to the educational potential of the project as a whole. On one hand it allows participants of PGP-UK and other users of the GenomeChronicler tool to compare their genome report results to those of other individuals. On the other hand, it allows individuals that are interested in the subject but did not have their genome sequenced to explore what a personal genome looks like.

Methods such as GenomeChronicler also allow other research projects in possession of sequencing data collected from a single individual to easily produce genome reports, customisable with static text providing information about the project that can be other to the template file, or even the addition of links to other databases that are relevant.

## 4 Conclusions

Here we present GenomeChronicler, a computational pipeline to produce genome reports including variant calling summary data, ancestry inference, and phenotype annotation from genotype data for personal genomics data obtained through whole genome or whole exome sequencing.

The pipeline is modular, fully open source, and available as containers and on the Lifebit CloudOS computing platform, enabling easy integration with other projects, regardless of computational resources available and bioinformatics expertise.

This work was developed as part of PGP-UK, and incorporates feedback from early participants to improve the usefulness of the reports produced, and of participant engagement. It is designed to be easily expandable, adaptable to other contexts and most of all, suit projects with a wide range of ethical requirements, from those that need the data to be processed inside a safe-haven environment to those that process all the data in the public domain.

Future directions for this work will include the integration of other omics data types that are produced within PGP-UK, as well as potentially expanding the databases that are linked by default when running the pipeline.

We hope that GenomeChronicler will be useful to other projects and interested individuals. As it is open source, the pipeline can easily adapt custom templates to satisfy any curiosity-driven analyses and increase the level of genomic understanding in general. It can also be of interest to educational groups such as Open Humans (Greshake Tzovaras et al. 2019). Open Humans (https://www.openhumans.org/) is a vibrant community of researchers, patients, data and citizen scientists who want to learn more about themselves.

## 5 Conflict of Interest

Pablo P. Prieto is CTO of Lifebit and Christina Chatzipantsiou is an employee of Lifebit. All other authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

## 6 Author Contributions

J.A.G.-A. led the development and implementation of the method and wrote the manuscript with input from all authors. J.A.G.-A., L.C. contributed computer code. C.C. contributed the nextflow and Lifebit CloudOS integrations with support from P.P.P.. J.A.G.-A., L.C., I.M., A.P.W., S.E., JH., O.C. and S.B. contributed to the conceptual development of the method and usability. All authors read and approved the manuscript.

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## 9 Data Availability Statement

The datasets analyzed and used for the development of the approach here described are deposited at the European Nucleotide Archive (ENA) hosted by the EMBL-EBI under the umbrella accession PRJEB24961. [https://www.ebi.ac.uk/ena/data/view/PRJEB24961]. The PGP-UK pilot data was described in a data descriptor published in Scientific Data (Chervova et al. 2019). The source code for the software is deposited and maintained in GitHub and available at [https://github.com/PGP-UK/GenomeChronicler]. The nextflow integrated version is available at [https://github.com/PGP-UK/GenomeChronicler-nf] and finally, the version also containing the Sarek variant calling pipeline is available at [https://github.com/PGP-UK/GenomeChronicler-Sarek-nf]. Reports generated using

this approach for PGP-UK samples are archived in the PGP-UK data page https://www.personalgenomes.org.uk/data.

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## 11 Figure Legends

Figure 1: Flow Diagram of GenomeChronicler processing pipeline, illustrating the multiple entry points for the pipeline, resources integrated by default and generated outcomes. Either entry point of the pipeline can be run locally in a single machine, as a nextflow workflow or in the Cloud. All source code and integrations are freely available in their respective GitHub repositories. The stand-alone GenomeChronicler is available at (https://github.com/PGP-UK/GenomeChronicler), the integration of GenomeChronicler with nextflow is available at (https://github.com/PGP-UK/GenomeChronicler-nf) and the combined GenomeChronicler with Sarek variant calling is available at (https://github.com/PGP-UK/GenomeChronicler-Sarek-nf). The recipe files for the Docker and Singularity containers are available within the respective GitHub repositories. The resource logos are reproduced from the respective resource websites and remain copyright of their original owner.

Figure2: Example Ancestry PCA plot containing the current reference data from the 1000 genomes project used by GenomeChronicler, with shaded areas broadly illustrating the origin of the populations represented.

Figure 1

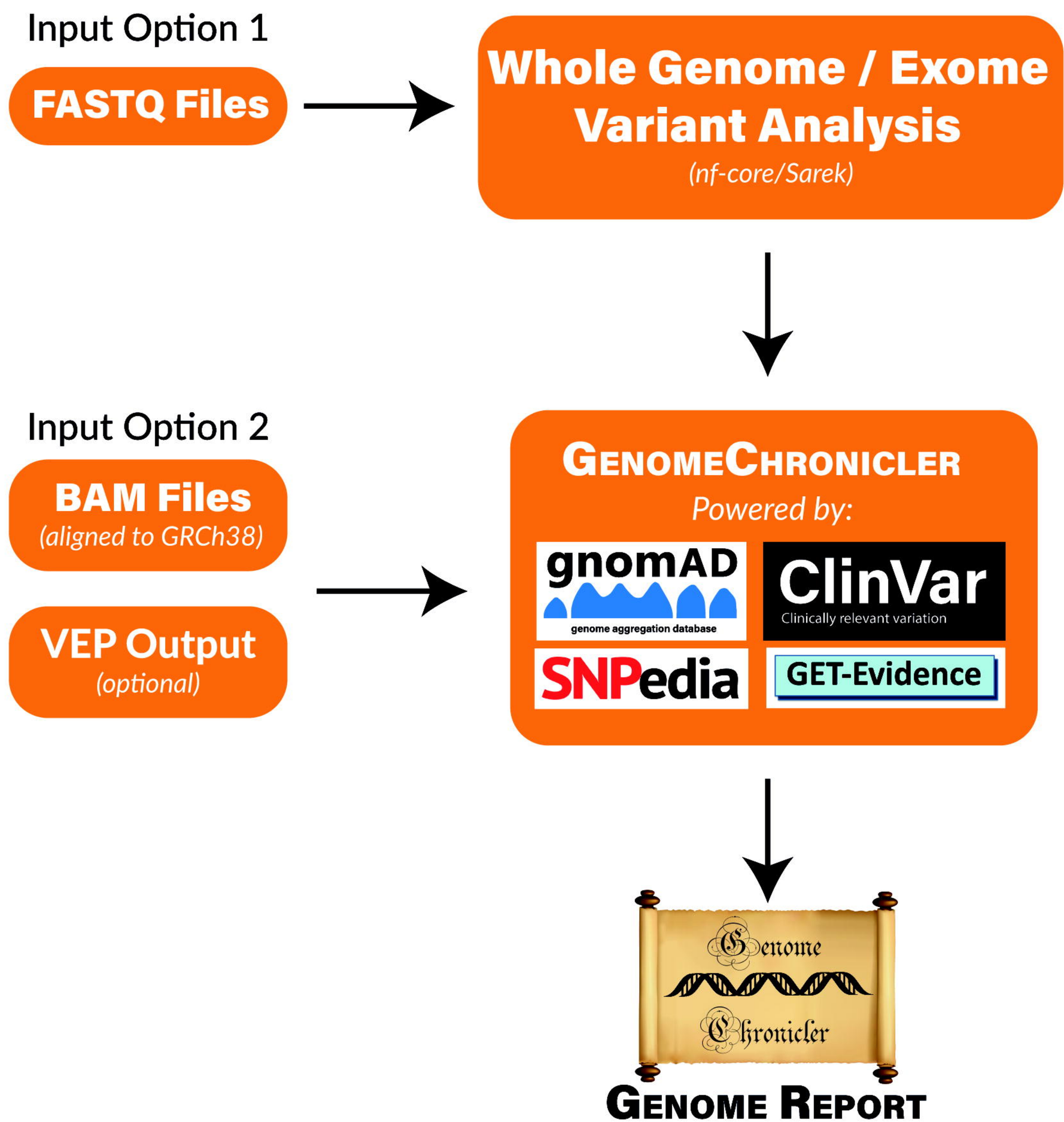
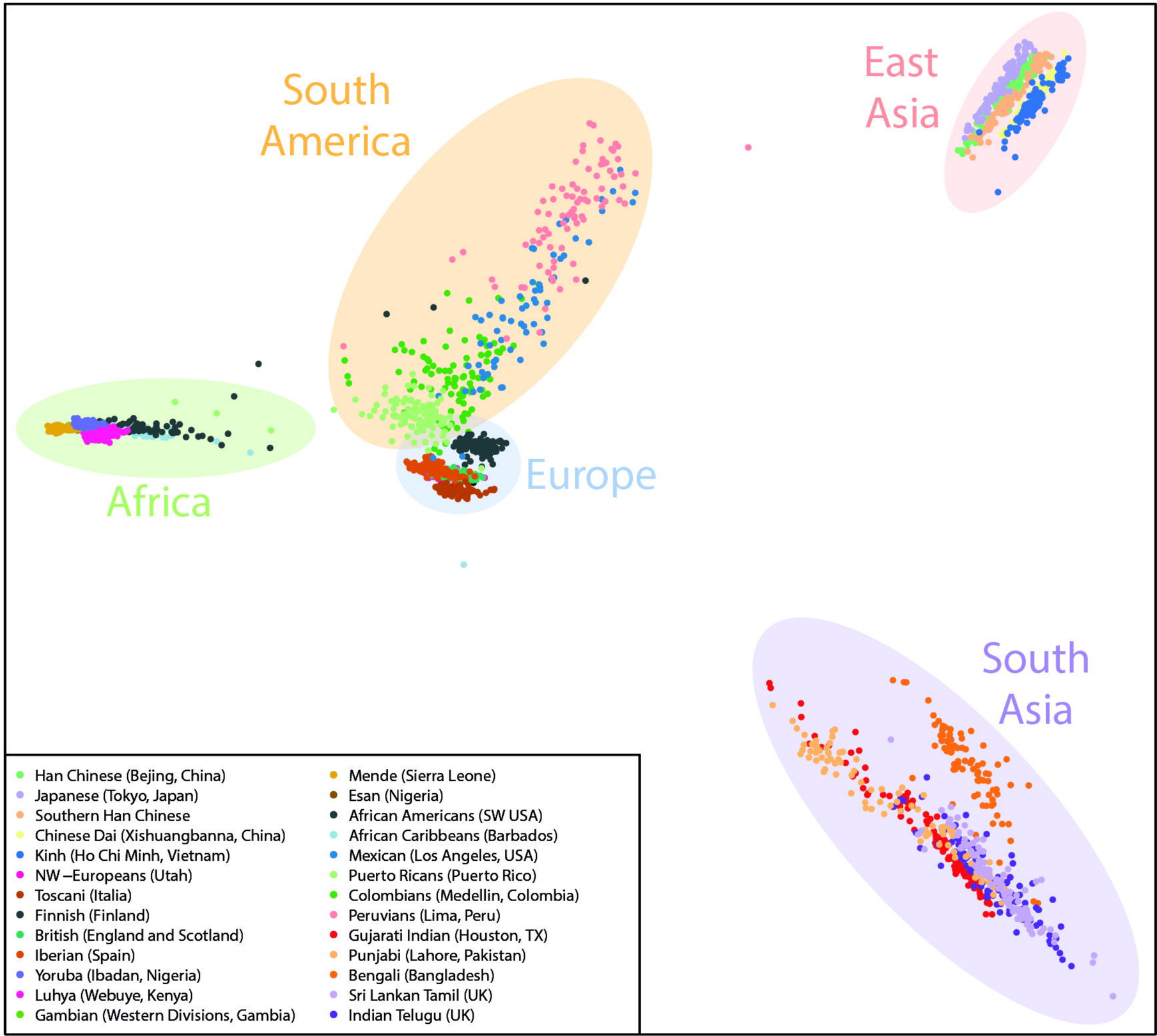

Input Option 1
FASTQ Files
Whole Genome / Exome Variant Analysis
(nf-core/Sarek)
Input Option 2
BAM Files
(aligned to GRCh38)
VEP Output
(optional)
GenomeChronicler
Powered by:
gnomAD
genome aggregation database
ClinVar
Clinically relevant variation
SNPedia
GET-Evidence
Genome
Chronicler
Genome Report

Figure 2


South America
East Asia
Africa
Europe
South Asia
Han Chinese (Bejing, China)
Japanese (Tokyo, Japan)
Southern Han Chinese
Chinese Dai (Xishuangbanna, China)
Kinh (Ho Chi Minh, Vietnam)
NW –Europeans (Utah)
Toscani (Italia)
Finnish (Finland)
British (England and Scotland)
Iberian (Spain)
Yoruba (Ibadan, Nigeria)
Luhya (Webuye, Kenya)
Gambian (Western Divisions, Gambia)
Mende (Sierra Leone)
Esan (Nigeria)
African Americans (SW USA)
African Caribbeans (Barbados)
Mexican (Los Angeles, USA)
Puerto Ricans (Puerto Rico)
Colombians (Medellin, Colombia)
Peruvians (Lima, Peru)
Gujarati Indian (Houston, TX)
Punjabi (Lahore, Pakistan)
Bengali (Bangladesh)
Sri Lankan Tamil (UK)
Indian Telugu (UK)