# Package 'kgp'

December 21, 2022
Type Package
Title 1000 Genomes Project Metadata
Version 1.1.1
<b>Description</b> Metadata about populations and data about samples from the 1000 Genomes Project, including the 2,504 samples sequenced for the Phase 3 release and the expanded collection of 3,202 samples with 602 additional trios. The data is described in Auton et al. (2015) <doi:10.1038 nature15393=""> and Byrska-Bishop et al. (2022) <doi:10.1016 j.cell.2022.08.004="">, and raw data is available at <a href="http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/">http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/</a>&gt;. See Turner (2022) <doi:10.48550 arxiv.2210.00539=""> for more details.</doi:10.48550></doi:10.1016></doi:10.1038>
<pre>URL https://github.com/stephenturner/kgp,</pre>
https://stephenturner.github.io/kgp/
<b>License</b> Apache License (>= 2)
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NeedsCompilation no
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1000 Genomes, SGDP, HGDP, and GGVP metadata

#### **Description**

Population metadata from 212 populations from the 1000 Genomes Project (kgp), Simons Genome Diversity Project (sgdp), Human Genome Diversity Project (hgdp), and Gambian Genome Variation Project (ggvp).

### Usage

allmeta

#### **Format**

A tibble with 212 rows and 8 columns:

pop Short population code

reg Short region code

population Long population description

region Long region description

regcolor Color for plotting this region on a map

lat Population latitude

**Ing** Population longitude

**dataset** Which dataset (kgp = 1000 Genomes Project; ggvp = Gambian Genome Variation Project; hgdp = Human Genome Diversity Project; Simons Genome Diversity Project).

#### References

Byrska-Bishop, Marta, et al. "High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios." Cell 185.18 (2022): 3426-3440.

1000 Genomes Project Consortium. "A global reference for human genetic variation." Nature 526.7571 (2015): 68.

Clarke, Laura, et al. "The international Genome sample resource (IGSR): A worldwide collection of genome variation incorporating the 1000 Genomes Project data." Nucleic acids research 45.D1 (2017): D854-D859.

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kgp3

1000 Genomes Project sample data (Phase 3)

## Description

Sample, pedigree, and population data for 2,504 samples in the Phase 3 release of the 1000 Genomes Project data.

## Usage

kgp3

#### **Format**

A tibble with 2504 rows and 10 columns:

```
fid Family ID

id Individual ID

pid Paternal ID

mid Maternal ID

sex Sex (1=Male, 2=Female)

sexf Sex as a factor

pop Short population code

reg Short region code
```

population Long population description

region Long region description

## **Source**

```
http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/
```

#### References

Byrska-Bishop, Marta, et al. "High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios." Cell 185.18 (2022): 3426-3440.

1000 Genomes Project Consortium. "A global reference for human genetic variation." Nature 526.7571 (2015): 68.

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kgpe

1000 Genomes Project sample data (Expanded)

## **Description**

Sample, pedigree, and population data for 3,202 samples in the expanded 1000 Genomes Project data.

## Usage

kgpe

#### **Format**

```
A tibble with 3202 rows and 11 columns:
```

fid Family ID

id Individual ID

pid Paternal ID

mid Maternal ID

sex Sex (1=Male, 2=Female)

sexf Sex as a factor

pop Short population code

reg Short region code

population Long population description

region Long region description

phase3 Logical; indicates whether this sample is included in the Phase 3 release data

#### **Source**

```
http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/
```

#### References

Byrska-Bishop, Marta, et al. "High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios." Cell 185.18 (2022): 3426-3440.

1000 Genomes Project Consortium. "A global reference for human genetic variation." Nature 526.7571 (2015): 68.

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kgpmeta

1000 Genomes Project population metadata

## Description

Population metadata from 26 populations across five continental regions.

## Usage

kgpmeta

#### **Format**

A tibble with 26 rows and 7 columns:

pop Short population code

reg Short region code

population Long population description

region Long region description

regcolor Color for plotting this region on a map

lat Population latitude

Ing Population longitude

## Source

```
http://ftp.1000genomes.ebi.ac.uk/vol1/ftp/
```

### References

Byrska-Bishop, Marta, et al. "High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios." Cell 185.18 (2022): 3426-3440.

1000 Genomes Project Consortium. "A global reference for human genetic variation." Nature 526.7571 (2015): 68.

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