



# PLINKR

## Work with PLINK and PLINK2 from R

### Why use plinkr?

- Easy install
- Convert data
- Uniform interface
- Safety
- Simulate data
- Compare PLINK versions
- Teaching
- Tidyverse style
- Vignettes with PLINK tutorials

```
remotes::install_github(
  "richelbilderbeek/plinkr"
)
```



### Use any PLINK version

PLINK v1.7

PLINK v1.9

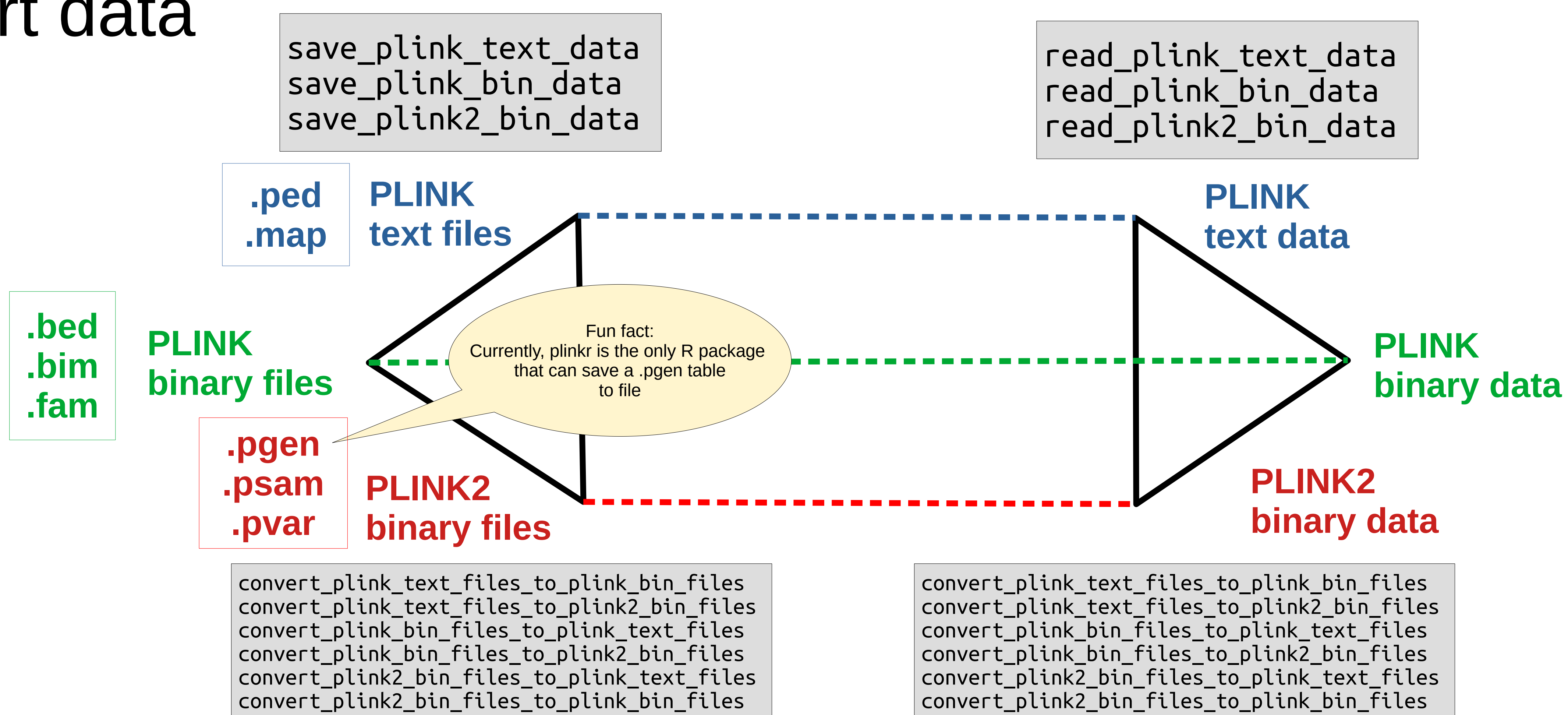
install\_plinks()

PLINK v2.0

Also known as  
PLINK 2

```
run_plink(
  args = "--help",
  plink_options = create_plink_v2_0_options()
)
```

### Convert data



### Uniform interface

Function name	Data
	Parameters
	PLINK version

```
assoc(
  data = [...],
  assoc_params = create_assoc_params([...]),
  plink_options = [...]
)
```

### Safety

- Type-safe interface
- Checks flags
- Checks data
- Checks files

Not all commands accept covariates, and PLINK will not always give you an error or warning.

```
run_plink(
  args = c("--assoc", "--covar", [...])
)
```

### Simulate data

- Additive traits
- Dominant traits
- Tri/quad-allelic traits
- Polygenic traits
- Rare traits
- Your custom traits

```
create_demo_assoc_params(
  n_individuals = [...],
  trait = create_random_case_control_trait(
    n_snps = [...],
    mafs = 0.05
  )
)
```

### Compare versions

Data type	PLINK version	t (sec)
PLINK text files	1.7	29
PLINK text files	1.9	4
PLINK binary files	1.7	25
PLINK binary files	1.9	4
PLINK2 binary files	2	2

```
compare_assoc_qt_speed(
  n_individuals = 1000,
  n_phenotypes = 100,
  n_snps_per_phenotype = 100
)
```

