The **kinshipsymbols** package[*]

Alejandro Ochoa
`https://ochoalab.github.io/`

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Abstract

This package defines consistent mathematical symbols for statistical genetics, particularly relating to the kinship model and F_{ST}. In addition to providing a long list of symbols, the package has two options that alter the behavior of some of the most common symbols. Option `color` highlights genotypes (blue), kinship coefficients (dark green), and the standard ancestral allele frequency estimator (red), which is useful for Beamer presentations. Option `noT` removes the ancestral population T superscript from all symbols that contain it (for simpler presentations).

Contents

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[*]This document corresponds to **kinshipsymbols** v1.06, dated 2025/12/11.

Command	Symbol	Description
`\xij`	x_{ij}	Genotype
`\x`	$\mathbf{x}_i$	Genotype vector
`\X`	$\mathbf{X}$	Genotype matrix
`\pit`	p_i^T	Ancestral allele frequency
`\pith`	$\hat{p}_i^T$	Sample p_i^T estimator
`\kt`	φ_{jk}^T	Kinship coefficient
`\kinMat`	$\mathbf{\Phi}^T$	Kinship matrix
`\ft`	f_j^T	Inbreeding coefficient
`\Fst`	F_{ST}	(Wright's) Fixation index

Table 1: Commands for the most common statistical genetics quantities.

Command	Symbol	Description
`\f{A}{B}`	f_B^A	Inbreeding of pop. B relative to pop. A
`\fl`	$f_j^{L_j}$	Local inbreeding coefficient
`\fs`	$f_{L_j}^T$	Structural inbreeding coefficient
`\kl`	$\varphi_{jk}^{L_{jk}}$	Local kinship coefficient
`\ks`	$f_{L_{jk}}^T$	Structural kinship coefficient
`\fpw`	$f_{L_j}^{L_{jk}}$	Individual pairwise F_{ST} component
`\mav`	$\overline{p(1-p)}^T$	Mean ancestral variance

Table 2: Commands for more rare statistical genetics quantities.

1 Introduction

This package provides macros for many common symbols involving the genotypes, kinship coefficients, and F_{ST}. Each of Tables 1 to 5 and 8 pairs a command to its symbol and its common description in the field. Note that these symbols work even when not in math mode, so it is not necessary to write `$\Fst$` inline, `\Fst` works! This is achieved through use of `\ensuremath{...}\xspace` in each of these definitions.

Some of these symbols accept arguments for limited flexibility. For example, `\xij` produces x_{ij}, but `\xij[k]` produces x_{ik}. Similarly, `\kt` produces φ_{jk}^T, but `\kt[l]` produces φ_{jl}^T. See the implementation section below for details for each command.

Additionally, Tables 6 and 7 lists some math operators and convergence arrows defined by this package (absent in `amsmath`). These commands do require math mode to work.

Lastly, the package provides `\sampleGenMat`, which generates the cartoon genotype table shown in Fig. 1. Note that this technically generates a "tabular" table. It is meant to be used in Beamer presentations, but works in standard documents too.

The effects of the package options `color` and `noT` are visualized in Figs. 2 to 5. Each of those figures generated the symbols with a particular combination of options:

Command	Symbol	Description
`\ktHat`	$\hat{\varphi}_{jk}^{T}$	Unnamed kinship estimator
`\kinMatHat`	$\hat{\boldsymbol{\Phi}}^{T}$	Unnamed kinship matrix estimator
`\ftHat`	$\hat{f}_{j}^{T}$	Unnamed inbreeding estimator
`\ktHatNamed{example}`	$\hat{\varphi}_{jk}^{T,\mathrm{example}}$	Named kinship estimator
`\ftHatNamed{example}`	$\hat{f}_{j}^{T,\mathrm{example}}$	Named inbreeding estimator
`\ktHatStd`	$\hat{\varphi}_{jk}^{T,\mathrm{std}}$	Standard kinship estimator
`\ftHatStd`	$\hat{f}_{j}^{T,\mathrm{std}}$	Standard inbreeding estimator (I)
`\ftHatStdII`	$\hat{f}_{j}^{T,\mathrm{stdII}}$	Alternate inbreeding estimator (II)
`\ftHatStdIII`	$\hat{f}_{j}^{T,\mathrm{stdIII}}$	Alternate inbreeding estimator (III)
`\ktHatNew`	$\hat{\varphi}_{jk}^{T,\mathrm{new}}$	New kinship estimator
`\ktHatNewMin`	$\hat{\varphi}_{\min}^{T,\mathrm{new}}$	Estimator of the asymptotic minimum $\hat{\varphi}_{jk}^{T,\mathrm{new}}$
`\ftHatNew`	$\hat{f}_{j}^{T,\mathrm{new}}$	New inbreeding estimator
`\klHatBeagle`	$\hat{\varphi}_{jk}^{L_{jk},\mathrm{beagle}}$	Beagle-based kinship estimator
`\flHatBeagle`	$\hat{f}_{j}^{L_{j},\mathrm{beagle}}$	Beagle-based inbreeding estimator
`\Ajk`	A_{jk}	New kinship-related statistic
`\AMinHat`	$\hat{A}_{\min}$	Estimator of the asymptotic minimum A_{jk}

Table 3: Commands for miscelaneous kinship and inbreeding estimators.

Command	Symbol	Description
`\FstHatSample`	$\hat{F}_{\mathrm{ST},i}^{\mathrm{sample}}$	Sample F_{ST} estimator (one locus)
`\FstHat`	$\hat{F}_{\mathrm{ST}}$	Unnamed F_{ST} estimator
`\FstHatNamed{example}`	$\hat{F}_{\mathrm{ST}}^{\mathrm{example}}$	Named F_{ST} estimator
`\FstHatWc`	$\hat{F}_{\mathrm{ST}}^{\mathrm{WC}}$	Weir-Cockerham F_{ST} estimator
`\FstHatHudson`	$\hat{F}_{\mathrm{ST}}^{\mathrm{Hudson}}$	Hudson Pairwise F_{ST} estimator
`\FstHatHudsonK`	$\hat{F}_{\mathrm{ST}}^{\mathrm{HudsonK}}$	Generalized Hudson F_{ST} estimator
`\FstHatIs`	$\hat{F}_{\mathrm{ST}}^{\mathrm{indep}}$	Asymptotic F_{ST} estimator for indep. subpops.
`\FstHatStd`	$\hat{F}_{\mathrm{ST}}^{\mathrm{std}}$	Standard F_{ST} estimator (based on $\hat{\varphi}_{jk}^{T,\mathrm{std}}$)
`\FstHatStdPrime`	$\hat{F}_{\mathrm{ST}}'$	Standard F_{ST} estimator adjusted 1
`\FstHatStdPrimeDbl`	$\hat{F}_{\mathrm{ST}}''$	Standard F_{ST} estimator adjusted 2
`\FstHatNew`	$\hat{F}_{\mathrm{ST}}^{\mathrm{new}}$	New F_{ST} estimator

Table 4: Commands for miscelaneous F_{ST} estimators.

Command	Symbol	Description
`\Fit`	F_{IT}	Wright's total inbreeding
`\Fis`	F_{IS}	Wright's local inbreeding
`\Gst`	G_{ST}	Nei's genetic diversity measure
`\GstPrime`	G_{ST}'	Normalized G_{ST}
`\Rst`	R_{ST}	F_{ST} estimator for microsatellites
`\PhiSt`	ϕ_{ST}	AMOVA-based differentiation measure

Table 5: Commands for historical quantities in statistical genetics.

Command	Symbol	Description
\E	E	Expectation
\Var	Var	Variance
\Cov	Cov	Covariance
\round	round	Rounding function
\sgn	sgn	Sign function
\logit	logit	Logit function

Table 6: Commands for math operators.

Command	Symbol	Description
\toas	$\xrightarrow[m\to\infty]{\text{a.s.}}$	Almost sure convergence as m goes to ∞
\toN	$\xrightarrow[n\to\infty]{}$	Limit as n goes to ∞
\toasNM	$\xrightarrow[n,m\to\infty]{\text{a.s.}}$	Almost sure convergence as both m and n go to ∞

Table 7: Commands for math convergence arrows.

Command	Symbol	Description
\srmsdp	SRMSD_p	Signed root mean square deviation for null p-values
\aucpr	AUC_{PR}	Area under the precision-recall curve

Table 8: Commands for miscelaneous measures.
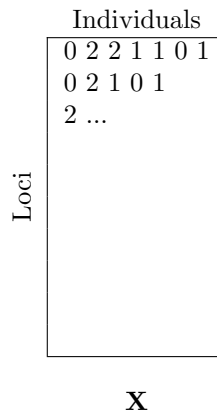
Figure 1: The cartoon genotype matrix generated by \sampleGenMat

Individuals

$$
\begin{array}{l}
0\ 2\ 2\ 1\ 1\ 0\ 1 \\
0\ 2\ 1\ 0\ 1 \\
2\ ...
\end{array}
$$

Loci

X

$$E[x_{ij}\,|\,T] = 2p_i^T,$$
$$\mathrm{Var}(x_{ij}\,|\,T) = 2p_i^T\left(1 - p_i^T\right)\left(1 + f_j^T\right),$$
$$\mathrm{Cov}(x_{ij}, x_{ik}\,|\,T) = 4p_i^T\left(1 - p_i^T\right)\varphi_{jk}^T,$$
$$(1 - F_{\mathsf{IT}}) = (1 - F_{\mathsf{IS}})\,(1 - F_{\mathsf{ST}}),$$
$$\left(1 - f_j^T\right) = \left(1 - f_j^{L_j}\right)\left(1 - f_{L_j}^T\right),$$
$$F_{\mathsf{ST}} = \sum_{j=1}^{n} w_j f_{L_j}^T,$$
$$\hat{p}_i^T = \frac{1}{2}\sum_{j=1}^{n} w_j x_{ij},$$
$$\hat{\varphi}_{jk}^{T,\mathrm{new}} \xrightarrow[m\to\infty]{\text{a.s.}} \varphi_{jk}^T.$$

E, Var, Cov, round, sgn, logit, $\xrightarrow[m\to\infty]{\text{a.s.}}$, $\xrightarrow[n\to\infty]{}$, $\xrightarrow[n,m\to\infty]{\text{a.s.}}$, x_{ij}, $\mathbf{x}_i$, $\mathbf{X}$, p_i^T, $\hat{p}_i^T$, F_{ST}, F_{IT}, F_{IS}, f_B^A, f_j^T, $f_j^{L_j}$, $f_{L_j}^T$, φ_{jk}^T, $\boldsymbol{\Phi}^T$, $\varphi_{jk}^{L_{jk}}$, $f_{L_{jk}}^T$, $f_{L_j}^{L_{jk}}$, R_{ST}, ϕ_{ST}, G_{ST}, G'_{ST}, $\hat{F}_{\mathsf{ST},i}^{\mathrm{sample}}$, $\hat{F}_{\mathsf{ST}}$, $\hat{F}_{\mathsf{ST}}^{\mathrm{indep}}$, $\hat{F}_{\mathsf{ST}}^{\mathsf{WC}}$, $\hat{F}_{\mathsf{ST}}^{\mathsf{Hudson}}$, $\hat{F}_{\mathsf{ST}}^{\mathsf{HudsonK}}$, $\hat{\varphi}_{jk}^T$, $\hat{\boldsymbol{\Phi}}^T$, $\hat{f}_j^T$, $\hat{\varphi}_{jk}^{T,\mathrm{std}}$, $\hat{f}_j^{T,\mathrm{std}}$, $\hat{f}_j^{T,\mathrm{stdII}}$, $\hat{f}_j^{T,\mathrm{stdIII}}$, $\hat{F}_{\mathsf{ST}}^{\mathrm{std}}$, $\hat{F}'_{\mathsf{ST}}$, $\hat{F}''_{\mathsf{ST}}$, $\hat{\varphi}_{jk}^{T,\mathrm{new}}$, $\hat{\varphi}_{\min}^{T,\mathrm{new}}$, $\hat{f}_j^{T,\mathrm{new}}$, $\hat{F}_{\mathsf{ST}}^{\mathrm{new}}$, $\hat{\varphi}_{jk}^{L_{jk},\mathrm{beagle}}$, $\hat{f}_j^{L_j,\mathrm{beagle}}$, $\overline{p(1-p)}^T$, A_{jk}, $\hat{A}_{\min}$, SRMSD_p, $\mathrm{AUC}_{\mathsf{PR}}$.
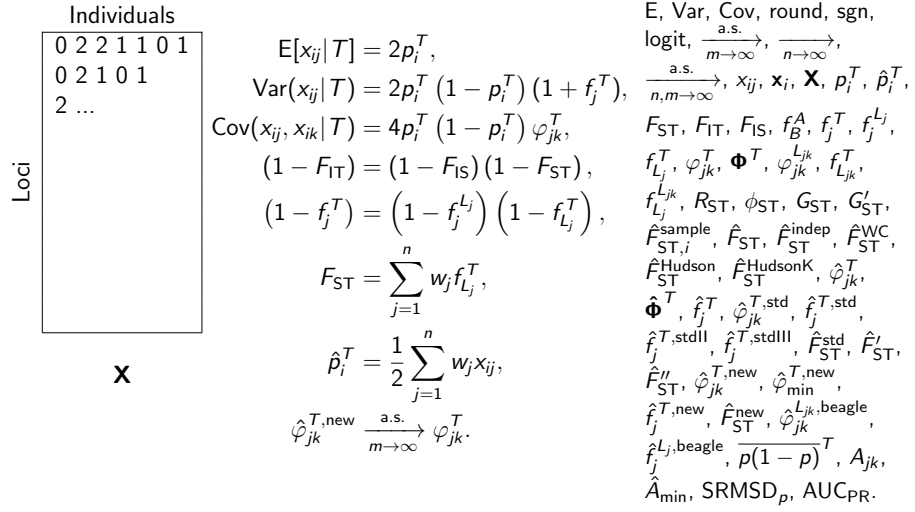
Figure 2: The vanilla version of the symbols (no colors and no omission of ancestral population T in superscripts

- Fig. 2: `\usepackage{kinshipsymbols}` "vanilla" version (no options). This version shows symbols completely (without omitting the ancestral population T from superscripts) and without color.

- Fig. 3: `\usepackage[color]{kinshipsymbols}` version. Same as the vanilla version except a few common symbols gain colors:

  - The genotypes (x_{ij}, $\mathbf{x}_i$, $\mathbf{X}$) become blue (and also the cartoon genotype matrix drawn by `\sampleGenMat`). Highlighted since this is the observed data from which inferences are drawn.

  - The kinship coefficients (φ_{jk}^T, $\boldsymbol{\Phi}^T$) become dark green. Highlighted since these are the main unknown parameters we wish to estimate.

  - The standard ancestral allele frequency estimator ($\hat{p}_i^T$) becomes red. Highlighted since this is a particularly problematic estimator that leads to biases in common approaches.

- Fig. 4: `\usepackage[noT]{kinshipsymbols}` version. Same as the vanilla version except the ancestral population T is omitted in the superscript of several symbols (p_i^T, $\hat{p}_i^T$, f_j^T, $f_{L_j}^T$, φ_{jk}^T, $\boldsymbol{\Phi}^T$, $\hat{\boldsymbol{\Phi}}^T$, $f_{L_{jk}}^T$, $\hat{\varphi}_{jk}^T$, $\hat{f}_j^T$, $\hat{\varphi}_{jk}^{T,\mathrm{std}}$, $\hat{f}_j^{T,\mathrm{std}}$, $\hat{f}_j^{T,\mathrm{stdII}}$, $\hat{f}_j^{T,\mathrm{stdIII}}$, $\hat{\varphi}_{jk}^{T,\mathrm{new}}$, $\hat{\varphi}_{\min}^{T,\mathrm{new}}$, $\hat{f}_j^{T,\mathrm{new}}$, and $\overline{p(1-p)}^T$). This option is provided to simplify the heavy notation in a context where T is implicit or fixed.

- Fig. 5: `\usepackage[color,noT]{kinshipsymbols}` version. A straightforward combination of the color and noT options described above.
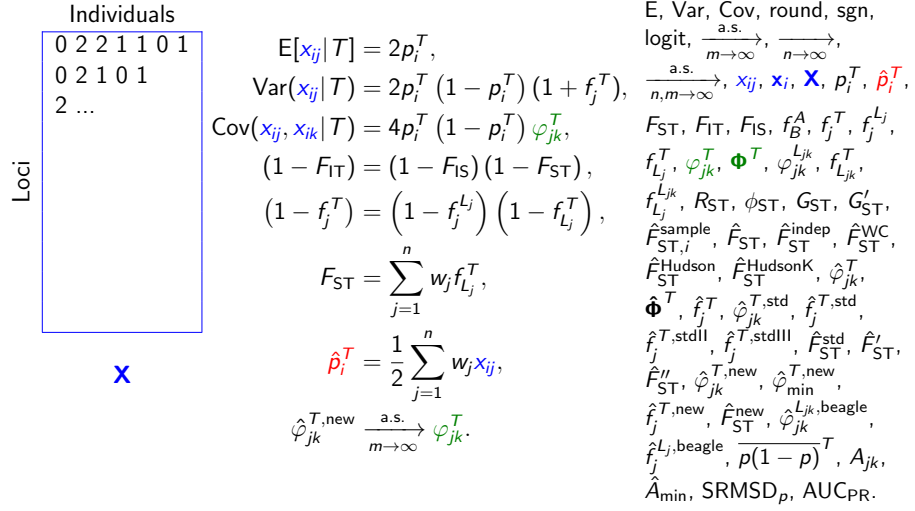
5

Figure 3: The `color` version of the symbols (with no omission of ancestral population T in superscripts
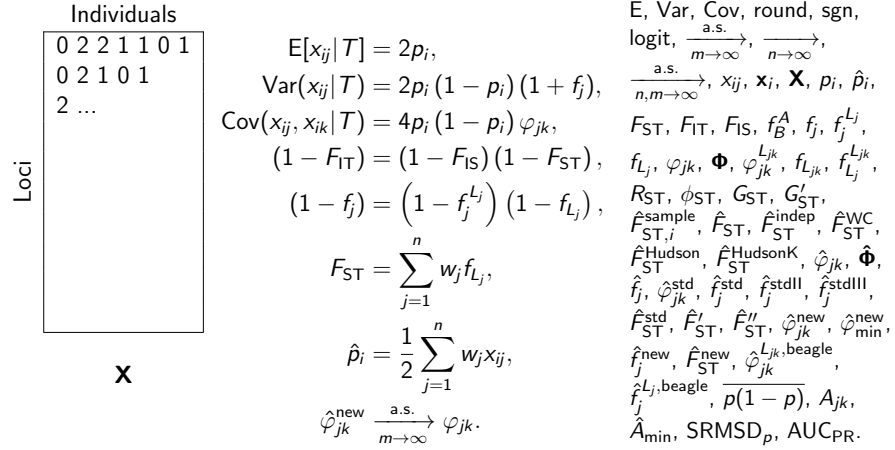

Figure 4: The `noT` version of the symbols (no color, with omission of ancestral population T in superscripts as appropriate
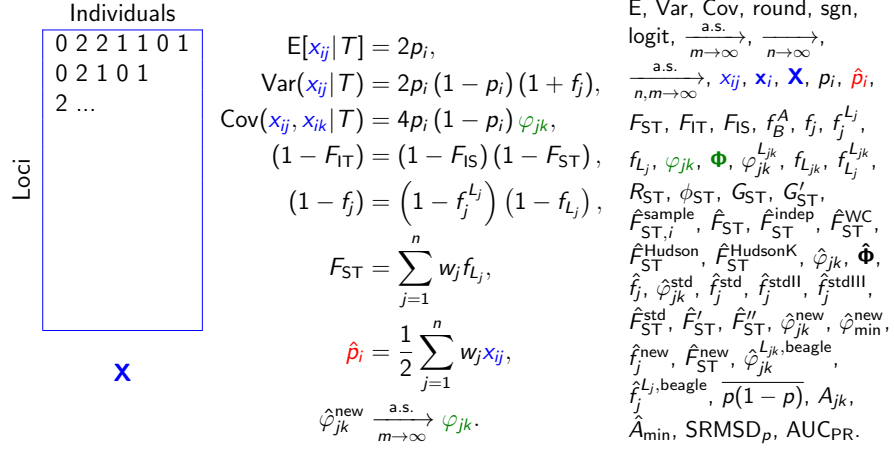
Figure 5: The `color,noT` version of the symbols (with color and omission of ancestral population T in superscripts as appropriate

Individuals

```
0 2 2 1 1 0 1
0 2 1 0 1
2 ...
```

Loci

$\mathbf{X}$

$$E[x_{ij}|T] = 2p_i,$$
$$\mathrm{Var}(x_{ij}|T) = 2p_i(1-p_i)(1+f_j),$$
$$\mathrm{Cov}(x_{ij}, x_{ik}|T) = 4p_i(1-p_i)\,\varphi_{jk},$$
$$(1-F_{\mathrm{IT}}) = (1-F_{\mathrm{IS}})(1-F_{\mathrm{ST}}),$$
$$(1-f_j) = \left(1-f_j^{L_j}\right)(1-f_{L_j}),$$
$$F_{\mathrm{ST}} = \sum_{j=1}^{n} w_j f_{L_j},$$
$$\hat{p}_i = \frac{1}{2}\sum_{j=1}^{n} w_j x_{ij},$$
$$\hat{\varphi}_{jk}^{\mathrm{new}} \xrightarrow[m\to\infty]{\mathrm{a.s.}} \varphi_{jk}.$$

E, Var, Cov, round, sgn, logit, $\xrightarrow[m\to\infty]{\mathrm{a.s.}}$, $\xrightarrow[n\to\infty]{}$, $\xrightarrow[n,m\to\infty]{\mathrm{a.s.}}$, x_{ij}, $\mathbf{x}_i$, $\mathbf{X}$, p_i, $\hat{p}_i$, F_{ST}, F_{IT}, F_{IS}, f_B^A, f_j, $f_j^{L_j}$, f_{L_j}, φ_{jk}, $\mathbf{\Phi}$, $\varphi_{jk}^{L_{jk}}$, $f_{L_{jk}}$, $f_{L_j}^{L_{jk}}$, R_{ST}, ϕ_{ST}, G_{ST}, G'_{ST}, $\hat{F}_{\mathrm{ST},i}^{\mathrm{sample}}$, $\hat{F}_{\mathrm{ST}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{indep}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{WC}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{Hudson}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{HudsonK}}$, $\hat{\varphi}_{jk}$, $\hat{\mathbf{\Phi}}$, $\hat{f}_j$, $\hat{\varphi}_{jk}^{\mathrm{std}}$, $\hat{f}_j^{\mathrm{std}}$, $\hat{f}_j^{\mathrm{stdII}}$, $\hat{f}_j^{\mathrm{stdIII}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{std}}$, $\hat{F}'_{\mathrm{ST}}$, $\hat{F}''_{\mathrm{ST}}$, $\hat{\varphi}_{jk}^{\mathrm{new}}$, $\hat{\varphi}_{\min}^{\mathrm{new}}$, $\hat{f}_j^{\mathrm{new}}$, $\hat{F}_{\mathrm{ST}}^{\mathrm{new}}$, $\hat{\varphi}_{jk}^{L_{jk},\mathrm{beagle}}$, $\hat{f}_j^{L_j,\mathrm{beagle}}$, $\overline{p(1-p)}$, A_{jk}, $\hat{A}_{\min}$, SRMSD_p, $\mathrm{AUC}_{\mathrm{PR}}$.

2 Implementation

2.1 Dependencies

This package requires `amsmath` to define the various math symbols and operators, `xspace` to allow inline math symbols to have appropriate spacings when used outside math mode, `xcolor` for color management and tricks, and `colortbl` and `multirow` for the cartoon genotype matrix.

```
1 \RequirePackage{amsmath}
2 \RequirePackage{xspace}
3 \RequirePackage{xcolor}
4 \RequirePackage{colortbl}
5 \RequirePackage{multirow}
```

2.2 Initializing variables, modify depending on options

Then we define the special colors we want to use (in a way that is easy to tweak later if needed).

`\ifcolor` LaTeX boolean for whether color option is on or off.

```
6 \newif\ifcolor%
7 \colorfalse% default is false
```

`genColor` The hardcoded "genotype color" is blue, applied if the `color` package option is set.

```
8 \colorlet{genColor}{blue}
```

`kinColor` The hardcoded "kinship color" is a dark green, applied if the `color` package option is set.

```
9 \colorlet{kinColor}{green!50!black}
```

pithColor   The hardcoded "\pith color" is red, applied if the `color` package option is set.

```
10 \colorlet{pithColor}{red}
```

We also define two tricky commands to handle the ancestra population T superscript that we want to optionally omit. Note that these are internal commands not meant to be used directly outside the package.

\kinshipsymbols@T   This is a basic superscript T that becomes blank if the `noT` package option is set.

```
11 \newcommand{\kinshipsymbols@T}{^T}
```

\kinshipsymbols@Ts   This is a second superscript T which takes a mandatory argument that is shown next to it as text. Only the T becomes blank if the `noT` package option is set (the argument is shown alone as a text superscript in that case).

```
12 \newcommand{\kinshipsymbols@Ts}[1]{^{T,\text{#1}}}
```

This turns on colors if the `color` package option is set.

```
13 \DeclareOption{color}{
14   \colortrue
15 }
```

Similarly, this updates the commands to omit the T superscript if the `noT` package option is set. Note that the second command still emits the additional text passed as argument in the superscript.

```
16 \DeclareOption{noT}{
17   \renewcommand{\kinshipsymbols@T}{}
18   \renewcommand{\kinshipsymbols@Ts}[1]{^{\text{#1}}}
19 }
```

This creates a warning if any additional options are passed, then processes the options.

```
20 \DeclareOption*{\PackageWarning{examplepackage}{Unknown '\CurrentOption'}}
21 \ProcessOptions\relax
```

2.3   Commands for math operators

Here we define some trivial widely-used operators, which are not specific to statistical genetics but which are absent from the standard `amsmath` package.

\E   Expectation of a random variable.

```
22 \DeclareMathOperator{\E}{E}
```

\Var   Variance of a random variable.

```
23 \DeclareMathOperator{\Var}{Var}
```

\Cov   Covariance of a random variable.

```
24 \DeclareMathOperator{\Cov}{Cov}
```

\round   The rounding function.

```
25 \DeclareMathOperator{\round}{round}
```

8

\sgn The sign function.

```
26 \DeclareMathOperator{\sgn}{sgn}
```

\logit The logit function.

```
27 \DeclareMathOperator{\logit}{logit}
```

2.4 Genotypes

\xij x_{ij}: Genotype variable at locus i of individual j (default). The optional argument allows setting other individuals (\xij[k] gives x_{ik} for individual k). If the package option `color` is passed, then this symbol turns the color `genColor` (default blue).

```
28 \newcommand{\xij}[1][j]{%
29   \ensuremath{%
30     \ifcolor \textcolor{genColor}{ \fi%
31       x_{i#1}%
32     \ifcolor } \fi%
33   }%
34   \xspace%
35 }%
```

\x $\mathbf{x}_i$: Genotype vector at locus i (default). The optional argument allows setting other loci (\x[i'] gives $\mathbf{x}_{i'}$ for locus i'). If the package option `color` is passed, then this symbol turns the color `genColor` (default blue).

```
36 \newcommand{\x}[1][i]{%
37   \ensuremath{%
38     \ifcolor \textcolor{genColor}{ \fi%
39       \mathbf{x}_{#1}%
40     \ifcolor } \fi%
41   }%
42   \xspace%
43 }%
```

\X $\mathbf{X}$: Genotype matrix. If the package option `color` is passed, then this symbol turns the color `genColor` (default blue).

```
44 \newcommand{\X}{%
45   \ensuremath{%
46     \ifcolor \textcolor{genColor}{ \fi%
47       \mathbf{X}%
48     \ifcolor } \fi%
49   }%
50   \xspace%
51 }%
```

2.5 Ancestral allele frequencies

\pit p_i^T: The ancestral allele frequency at locus i (default). The optional argument allows setting other loci (\pit[i'] gives $p_{i'}^T$ for locus i'). This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
52 \newcommand{\pit}[1][i]{%
53   \ensuremath{%
54     p_{#1}\kinshipsymbols@T%
```

```
55   }%
56   \xspace%
57 }%
```

`\pith` $\hat{p}_i^T$: The sample estimator of the ancestral allele frequency at locus i (default). The optional argument allows setting other loci (`\pith[i']` gives $\hat{p}_{i'}^T$ for locus i'). The parameter being estimated has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed. If the package option `color` is passed, then this symbol turns the color `pithColor` (default red).

```
58 \newcommand{\pith}[1][i]{%
59   \ensuremath{%
60     \ifcolor \textcolor{pithColor}{ \fi%
61       \hat{p}_{#1}\kinshipsymbols@T%
62     \ifcolor } \fi%
63   }%
64   \xspace%
65 }%
```

2.6 Wright's F_{ST}

`\Fst` F_{ST}: Wright's Fixation index. Although the T in the subscript technically refers to the ancestral population T, in this case it is never omitted (even if the package option `noT` is passed) to always match the more traditional and highly recognizable notation.

```
66 \newcommand{\Fst}{%
67   \ensuremath{%
68     F_{\text{ST}}%
69   }%
70   \xspace%
71 }%
```

`\Fit` F_{IT}: Wright's total inbreeding coefficient. Although the T in the subscript technically refers to the ancestral population T, in this case it is never omitted (even if the package option `noT` is passed) to always match the more traditional and highly recognizable notation.

```
72 \newcommand{\Fit}{%
73   \ensuremath{%
74     F_{\text{IT}}%
75   }%
76   \xspace%
77 }%
```

`\Fis` F_{IS}: Wright's local inbreeding coefficient.

```
78 \newcommand{\Fis}{%
79   \ensuremath{%
80     F_{\text{IS}}%
81   }%
82   \xspace%
83 }%
```

2.7 Inbreeding coefficients

`\f` f_B^A: The inbreeding coefficient (of F_{ST}) of population B relative to an ancestral population A. Note that this command has two mandatory arguments.

```
84 \newcommand{\f}[2]{%
85   \ensuremath{%
86     f^{#1}_{#2}%
87   }%
88   \xspace%
89 }%
```

`\ft` f_j^T: The (total) inbreeding coefficient of individual j (default). The optional argument allows setting other individuals (`\ft[k]` gives f_k^T for individual k). This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
90 \newcommand{\ft}[1][j]{%
91   \ensuremath{%
92     f_{#1}\kinshipsymbols@T%
93   }%
94   \xspace%
95 }%
```

`\fl` $f_j^{L_j}$: The local inbreeding coefficient of individual j (default). The optional argument allows setting other individuals (`\fl[k]` gives $f_k^{L_k}$ for individual k).

```
96  \newcommand{\fl}[1][j]{%
97    \ensuremath{%
98      f_{#1}^{L_{#1}}%
99    }%
100   \xspace%
101 }%
```

`\fs` $f_{L_j}^T$: The structural inbreeding coefficient of individual j (default). The optional argument allows setting other individuals (`\fs[k]` gives $f_{L_k}^T$ for individual k). This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
102 \newcommand{\fs}[1][j]{%
103   \ensuremath{%
104     f_{L_{#1}}\kinshipsymbols@T%
105   }%
106   \xspace%
107 }%
```

2.8 Kinship coefficients

`\kt` φ_{jk}^T: The (total) kinship coefficient between the pair of individuals j and k (default). The optional argument allows setting another second individual (`\kt[l]` gives φ_{jl}^T for a second individual l). This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed. If the package option `color` is passed, then this symbol turns the color `kinColor` (default dark green).

```
108 \newcommand{\kt}[1][k]{%
109   \ensuremath{%
110     \ifcolor \textcolor{kinColor}{ \fi%
111       \varphi_{j#1}\kinshipsymbols@T%
112     \ifcolor } \fi%
113   }%
114   \xspace%
115 }%
```

\kinMat $\boldsymbol{\Phi}^T$: The matrix of (total) kinship coefficients between every pair of individuals. This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed. If the package option `color` is passed, then this symbol turns the color `kinColor` (default dark green).

```
116 \newcommand{\kinMat}{%
117   \ensuremath{%
118     \ifcolor \textcolor{kinColor}{ \fi%
119       \boldsymbol{\Phi}\kinshipsymbols@T%
120     \ifcolor } \fi%
121   }%
122   \xspace%
123 }%
```

\kl $\varphi_{jk}^{L_{jk}}$: The local kinship coefficient between the pair of individuals j and k.

```
124 \newcommand{\kl}{%
125   \ensuremath{%
126     \varphi_{jk}^{L_{jk}}%
127   }%
128   \xspace%
129 }%
```

\ks $f_{L_{jk}}^T$: The structural kinship coefficient between the pair of individuals j and k. This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
130 \newcommand{\ks}{%
131   \ensuremath{%
132     f_{L_{jk}}\kinshipsymbols@T%
133   }%
134   \xspace%
135 }%
```

\fpw $f_{L_j}^{L_{jk}}$: A component of the pairwise F_{ST} between a pair of individuals j and k (default). The optional argument changes the individual in the subscript only (so \fpw[k] gives $f_{L_k}^{L_{jk}}$, and is obviously intended to be used for k only). Note that the actual pairwise F_{ST} between j and k is given by the average of $f_{L_j}^{L_{jk}}$ and $f_{L_k}^{L_{jk}}$.

```
136 \newcommand{\fpw}[1][j]{%
137   \f{L_{jk}}{L_{#1}}%
138 }%
```

2.9 Review of previous work

\Rst R_{ST}: An F_{ST} estimator developed for microsatellites.

```
139 \newcommand{\Rst}{%
140   \ensuremath{%
141     R_{\text{ST}}%
142   }%
143   \xspace%
144 }%
```

\PhiSt ϕ_{ST}: An F_{ST}-like estimate based on AMOVA.

```
145 \newcommand{\PhiSt}{%
146   \ensuremath{%
147     \phi_{\text{ST}}%
148   }%
149   \xspace%
150 }%
```

\Gst G_{ST}: Nei's genetic diversity measure.

```
151 \newcommand{\Gst}{%
152   \ensuremath{%
153     G_{\text{ST}}%
154   }%
155   \xspace%
156 }%
```

\GstPrime G'_{ST}: A normalized G_{ST} statistic.

```
157 \newcommand{\GstPrime}{%
158   \ensuremath{%
159     G_{\text{ST}}'%
160   }%
161   \xspace%
162 }%
```

\FstHatSample $\hat{F}_{\text{ST},i}^{\text{sample}}$: A sample F_{ST} estimator for a single locus i.

```
163 \newcommand{\FstHatSample}{%
164   \ensuremath{%
165     \hat{F}_{\text{ST},i}^{\text{sample}}%
166   }%
167   \xspace%
168 }%
```

2.10 Convergence arrows

\toas $\xrightarrow[m\to\infty]{\text{a.s.}}$: Almost sure convergence as m goes to ∞. Optional argument changes the variable name ($\toas[n]$ gives $\xrightarrow[n\to\infty]{\text{a.s.}}$).

```
169 \newcommand{\toas}[1][m]{%
170   \xrightarrow[#1 \rightarrow \infty]{\text{a.s.}}
171 }%
```

\toN $\xrightarrow[n\to\infty]{}$: The limit as n goes to ∞. Optional argument changes the variable name ($\toN[m]$ gives $\xrightarrow[m\to\infty]{}$).

13

```
172 \newcommand{\toN}[1][n]{%
173   \xrightarrow[#1 \rightarrow \infty]{}%
174 }%
```

$\toasNM$ $\xrightarrow[n,m\to\infty]{\text{a.s.}}$: Almost sure convergence as both n and m go to ∞.

```
175 \newcommand{\toasNM}{%
176   \xrightarrow[n,m \rightarrow \infty]{\text{a.s.}}%
177 }%
```

2.11 F_{ST} estimators for independent subpopulations

$\FstHat$ $\hat{F}_{\text{ST}}$: Unnamed F_{ST} estimator.

```
178 \newcommand{\FstHat}{%
179   \ensuremath{%
180     \hat{F}_{\text{ST}}%
181   }%
182   \xspace%
183 }%
```

$\FstHatNamed$ $\hat{F}_{\text{ST}}^{\text{example}}$: Base command for a named F_{ST} estimator. Takes on one mandatory argument—the name of the estimator—which is rendered as text.

```
184 \newcommand{\FstHatNamed}[1]{%
185   \ensuremath{%
186     \hat{F}_{\text{ST}}^{\text{#1}}%
187   }%
188   \xspace%
189 }%
```

$\FstHatIs$ $\hat{F}_{\text{ST}}^{\text{indep}}$: Asymptotic F_{ST} estimator for independent subpopulations.

```
190 \newcommand{\FstHatIs}{\FstHatNamed{indep}}
```

$\FstHatWc$ $\hat{F}_{\text{ST}}^{\text{WC}}$: Weir-Cockerham F_{ST} estimator.

```
191 \newcommand{\FstHatWc}{\FstHatNamed{WC}}
```

$\FstHatHudson$ $\hat{F}_{\text{ST}}^{\text{Hudson}}$: Hudson pairwise F_{ST} estimator.

```
192 \newcommand{\FstHatHudson}{\FstHatNamed{Hudson}}
```

$\FstHatHudsonK$ $\hat{F}_{\text{ST}}^{\text{HudsonK}}$: Generalized Hudson F_{ST} estimator (for K subpopulations).

```
193 \newcommand{\FstHatHudsonK}{\FstHatNamed{HudsonK}}
```

2.12 Estimators based on the standard kinship

$\ktHat$ $\hat{\varphi}_{jk}^{T}$: An unnamed kinship estimator for individuals j and k (default). The optional argument allows setting another second individual ($\ktHat[l]$ gives $\hat{\varphi}_{jl}^{T}$ for a second individual l). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option noT is passed.

```
194 \newcommand{\ktHat}[1][k]{%
195   \ensuremath{%
196     \hat{\varphi}_{j#1}\kinshipsymbols@T%
197   }%
198   \xspace%
199 }%
```

14

\ktHatNamed $\hat{\varphi}_{jk}^{T,\text{example}}$: A generic named kinship estimator for individuals j and k (default). Mandatory argument is the name, rendered as text. The optional argument allows setting another second individual (`\ktHatNamed[l]{example}` gives $\hat{\varphi}_{jl}^{T,\text{example}}$ for a second individual l). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
200 \newcommand{\ktHatNamed}[2][k]{%
201   \ensuremath{%
202     \hat{\varphi}_{j#1}\kinshipsymbols@Ts{#2}%
203   }%
204   \xspace%
205 }%
```

\kinMatHat $\hat{\boldsymbol{\Phi}}^{T}$: The unnamed (total) kinship matrix estimator between every pair of individuals. This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
206 \newcommand{\kinMatHat}{%
207   \ensuremath{%
208     \boldsymbol{\hat{\Phi}}\kinshipsymbols@T%
209   }%
210   \xspace%
211 }%
```

\ktHatStd $\hat{\varphi}_{jk}^{T,\text{std}}$: Standard kinship estimator for individuals j and k (default). The optional argument allows setting another second individual (`\ktHatStd[l]` gives $\hat{\varphi}_{jl}^{T,\text{std}}$ for a second individual l). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
212 \newcommand{\ktHatStd}[1][k]{\ktHatNamed[#1]{std}}
```

\ftHat $\hat{f}_{j}^{T}$: Unnamed inbreeding coefficient estimator for individual j (default). The optional argument allows setting another individual (`\ftHat[k]` gives $\hat{f}_{k}^{T}$ for individual k). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
213 \newcommand{\ftHat}[1][j]{%
214   \ensuremath{%
215     \hat{f}_{#1}\kinshipsymbols@T%
216   }%
217   \xspace%
218 }%
```

\ftHatNamed $\hat{f}_{j}^{T,\text{example}}$: Named inbreeding coefficient estimator for individual j (default). Mandatory argument is the name, rendered as text. The optional argument allows setting another individual (`\ftHatNamed[k]{example}` gives $\hat{f}_{k}^{T,\text{example}}$ for individual k). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
219 \newcommand{\ftHatNamed}[2][j]{%
220   \ensuremath{%
```

```
221          \hat{f}_{#1}\kinshipsymbols@Ts{#2}%
222     }%
223     \xspace%
224 }%
```

$\ftHatStd$ $\hat{f}_j^{T,\text{std}}$: Standard inbreeding coefficient estimator (I) for individual j. The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option noT is passed.

```
225 \newcommand{\ftHatStd}{\ftHatNamed{std}}
```

$\ftHatStdII$ $\hat{f}_j^{T,\text{stdII}}$: Alternate inbreeding coefficient estimator (II) for individual j. The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option noT is passed.

```
226 \newcommand{\ftHatStdII}{\ftHatNamed{stdII}}
```

$\ftHatStdIII$ $\hat{f}_j^{T,\text{stdIII}}$: Alternate inbreeding coefficient estimator (III) for individual j. The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option noT is passed.

```
227 \newcommand{\ftHatStdIII}{\ftHatNamed{stdIII}}
```

$\FstHatStd$ $\hat{F}_{\text{ST}}^{\text{std}}$: Standard F_{ST} estimator (based on the standard kinship estimator).

```
228 \newcommand{\FstHatStd}{\FstHatNamed{std}}
```

$\FstHatStdPrime$ $\hat{F}_{\text{ST}}'$: Standard F_{ST} estimator adjusted 1.

```
229 \newcommand{\FstHatStdPrime}{%
230     \ensuremath{%
231         \hat{F}_{\text{ST}}'%
232     }%
233     \xspace%
234 }%
```

$\FstHatStdPrimeDbl$ $\hat{F}_{\text{ST}}''$: Standard F_{ST} estimator adjusted 2.

```
235 \newcommand{\FstHatStdPrimeDbl}{%
236     \ensuremath{%
237         \hat{F}_{\text{ST}}''%
238     }%
239     \xspace%
240 }%
```

2.13 New kinship and F_{ST} estimators

$\ktHatNew$ $\hat{\varphi}_{jk}^{T,\text{new}}$: New kinship estimator for the pair of individuals j and k (default). The optional argument allows setting another second individual ($\ktHatNew[l]$ gives $\hat{\varphi}_{jl}^{T,\text{new}}$ for a second individual l). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option noT is passed.

```
241 \newcommand{\ktHatNew}[1][k]{\ktHatNamed[#1]{new}}
```

\ktHatNewMin $\hat{\varphi}_{\min}^{T,\text{new}}$: Estimator of the limit of the minimum value of the expectation of $\hat{\varphi}_{jk}^{T,\text{new}}$ across all pairs of individuals. The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
242 \newcommand{\ktHatNewMin}{%
243   \ensuremath{%
244     \hat{\varphi}_{\text{min}}\kinshipsymbols@Ts{new}%
245   }%
246   \xspace%
247 }%
```

\ftHatNew $\hat{f}_j^{T,\text{new}}$: New inbreeding estimator for individual j (default). The optional argument allows setting other individuals (`\ftHatNew[k]` gives $\hat{f}_k^{T,\text{new}}$ for individual k). The estimated parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
248 \newcommand{\ftHatNew}[1][j]{\ftHatNamed[#1]{new}}
```

\FstHatNew $\hat{F}_{\text{ST}}^{\text{new}}$: New F_{ST} estimator.

```
249 \newcommand{\FstHatNew}{\FstHatNamed{new}}
```

\Ajk A_{jk}: A new statistic proportional in expectation to $\varphi_{jk}^T - 1$ for the pair of individuals j and k (default). The optional argument allows setting another second individual (`\Ajk[l]` gives A_{jl} for a second individual l).

```
250 \newcommand{\Ajk}[1][k]{%
251   \ensuremath{%
252     A_{j#1}%
253   }%
254   \xspace%
255 }%
```

\AMinHat $\hat{A}_{\min}$: Estimator of the limit of the minimum value of the expectation of A_{jk} across all pairs of individuals.

```
256 \newcommand{\AMinHat}{%
257   \ensuremath{%
258     \hat{A}_{\text{min}}%
259   }%
260   \xspace%
261 }%
```

\AAvgHat $\hat{A}_{\text{avg}}$: Estimator of the limit of the average value of the expectation of A_{jk} across all pairs of individuals.

```
262 \newcommand{\AAvgHat}{%
263   \ensuremath{%
264     \hat{A}_{\text{avg}}%
265   }%
266   \xspace%
267 }%
```

\mav $\overline{p(1-p)}^T$: Mean ancestral variance. This parameter has a value that depends on the ancestral population T, which is by default denoted in the superscript, but which gets omitted if the package option `noT` is passed.

```
268 \newcommand{\mav}{%
269    \ensuremath{%
270      \overline{p(1-p)}\kinshipsymbols@T%
271    }%
272    \xspace%
273 }%
```

2.14   Estimates from Beagle

\klHatBeagle $\hat{\varphi}_{jk}^{L_{jk},\text{beagle}}$: Local kinship estimator based on Beagle, for the pair of individuals j and k.

```
274 \newcommand{\klHatBeagle}{%
275    \ensuremath{%
276      \hat{\varphi}_{jk}^{L_{jk},\text{beagle}}}%
277    }%
278    \xspace%
279 }%
```

\flHatBeagle $\hat{f}_{j}^{L_{j},\text{beagle}}$: Local inbreeding estimator based on Beagle, for individual j (default). The optional argument allows setting other individuals (\flHatBeagle[k] gives $\hat{f}_{k}^{L_{k},\text{beagle}}$ for individual k).

```
280 \newcommand{\flHatBeagle}[1][j]{%
281    \ensuremath{%
282      \hat{f}_{#1}^{L_{#1},\text{beagle}}}%
283    }%
284    \xspace%
285 }%
```

2.15   Measures of association and related problems

\srmsdp SRMSD$_p$: The Signed Root Mean Square Deviation (SRMSD) of null p-values from their expectation that they have uniform quantiles.

```
286 \newcommand{\srmsdp}{%
287    \ensuremath{%
288      \text{SRMSD}_p%
289    }%
290    \xspace%
291 }%
```

\aucpr AUC$_{\text{PR}}$: The Area Under the Curve (AUC) for precision-recall (PR) curves, which is a proxy measure for calibrated power.

```
292 \newcommand{\aucpr}{%
293    \ensuremath{%
294      \text{AUC}_\text{PR}%
295    }%
296    \xspace%
297 }%
```

2.16   Cartoon genotype matrix

I use this cartoon genotype matrix often in Beamer presentations. Unfortunately I also use the `color` kinshipsymbols package option in my presentations,

but due to a strange bug the colors do not show up in Beamer. This solution was found online: https://tex.stackexchange.com/questions/159378/cline-disappears-in-beamer

```
298 % after package colortbl is loaded
299 \makeatletter
300 \@ifclassloaded{beamer}{%
301   \patchcmd\@cline
302     {\arrayrulewidth\hfill}% search
303     {\arrayrulewidth\hfill\kern\z@}% replace
304     {}% success
305     {\errmessage{Patching \string\@cline\space failed}}% failure
306 }{%
307   % nothing to do here?
308 }
309 \makeatother
```

\sampleGenMat This is the bulky code used to generate the cartoon genotype matrix shown in Fig. 1.

```
310 \newcommand{\sampleGenMat}{%
311   \begin{tabular}{cc}%
312     & Individuals \\%
313     \ifcolor \arrayrulecolor{genColor} \fi% % gets applied to whole table
314     \cline{2-2}%
315     \multirow{10}{*}{\rotatebox[origin=c]{90}{Loci}}%
316     & \multicolumn{1}{|l|}{0 2 2 1 1 0 1} \\%
317     & \multicolumn{1}{|l|}{0 2 1 0 1 } \\%
318     & \multicolumn{1}{|l|}{2 ...} \\%
319     & \multicolumn{1}{|l|}{ } \\%
320     & \multicolumn{1}{|l|}{ } \\%
321     & \multicolumn{1}{|l|}{ } \\%
322     & \multicolumn{1}{|l|}{ } \\%
323     & \multicolumn{1}{|l|}{ } \\%
324     & \multicolumn{1}{|l|}{ } \\%
325     & \multicolumn{1}{|l|}{ } \\%
326     \cline{2-2}%
327     & \\%
328     & \X \\%
329   \end{tabular}%
330 }%
```

3   Acknowledgments

The symbols in this package were originally designed with John D. Storey (Alex Ochoa's postdoctoral adviser and coauthor of several papers about kinship and F_{ST}).

The package was written following Scott Pakin's guide How to Package Your LaTeX package.

Change History

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Numbers written in italic refer to the page where the corresponding entry is described; numbers underlined refer to the code line of the definition; numbers in roman refer to the code lines where the entry is used.