

# The kinshipsymbols package\*

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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

<b>1</b>	<b>Introduction</b>	<b>2</b>
<b>2</b>	<b>Implementation</b>	<b>5</b>
2.1	Dependencies . . . . .	5
2.2	Initializing variables, modify depending on options . . . . .	5
2.3	Commands for math operators . . . . .	8
2.4	Genotypes . . . . .	9
2.5	Ancestral allele frequencies . . . . .	9
2.6	Wright's $F_{ST}$ . . . . .	10
2.7	Inbreeding coefficients . . . . .	10
2.8	Kinship coefficients . . . . .	11
2.9	Review of previous work . . . . .	12
2.10	Convergence arrows . . . . .	13
2.11	$F_{ST}$ estimators for independent subpopulations . . . . .	14
2.12	Estimators based on the standard kinship . . . . .	14
2.13	New kinship and $F_{ST}$ estimators . . . . .	16
2.14	Estimates from Beagle . . . . .	17
2.15	Cartoon genotype matrix . . . . .	17
<b>3</b>	<b>Acknowledgments</b>	<b>18</b>

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\*This document corresponds to kinshipsymbols v1.0, dated 2019/02/01.

Command	Symbol	Description
<code>\xij</code>	$x_{ij}$	Genotype
<code>\pit</code>	$p_i^T$	Ancestral allele frequency
<code>\pith</code>	$\hat{p}_i^T$	Sample $p_i^T$ estimator
<code>\kt</code>	$\varphi_{jk}^T$	Kinship coefficient
<code>\ft</code>	$f_j^T$	Inbreeding coefficient
<code>\Fst</code>	$F_{ST}$	(Wright's) Fixation index

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

Command	Symbol	Description
<code>\f{A}{B}</code>	$f_B^A$	Inbreeding of pop. $B$ relative to pop. $A$
<code>\fl</code>	$f_j^{L_j}$	Local inbreeding coefficient
<code>\fs</code>	$f_{L_j}^T$	Structural inbreeding coefficient
<code>\kl</code>	$\varphi_{jk}^{L_{jk}}$	Local kinship coefficient
<code>\ks</code>	$f_{L_{jk}}^T$	Structural kinship coefficient
<code>\fpw</code>	$f_{L_j}^{L_{jk}}$	Individual pairwise $F_{ST}$ component
<code>\mav</code>	$p(1-p)^T$	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 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  $\varphi_{jk}^T$ , but `\kt[l]` produces  $\varphi_{jl}^T$ . 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
<code>\ktHatNamed{example}</code>	$\hat{\varphi}_{jk}^{T,\text{example}}$	Named kinship estimator
<code>\ftHatNamed{example}</code>	$\hat{f}_j^{T,\text{example}}$	Named inbreeding estimator
<code>\ktHat</code>	$\hat{\varphi}_{jk}^{T,\text{std}}$	Standard kinship estimator
<code>\ftHat</code>	$\hat{f}_j^{T,\text{std}}$	Standard inbreeding estimator (I)
<code>\ftHatII</code>	$\hat{f}_j^{T,\text{stdII}}$	Alternate inbreeding estimator (II)
<code>\ftHatIII</code>	$\hat{f}_j^{T,\text{stdIII}}$	Alternate inbreeding estimator (III)
<code>\ktHatPreadj</code>	$\hat{\varphi}_{jk}^{T,\text{preadj}}$	Preadjusted kinship estimator
<code>\ktHatPreadjMin</code>	$\hat{\varphi}_{\min}^{T,\text{preadj}}$	Asymptotic minimum value of $\hat{\varphi}_{jk}^{T,\text{preadj}}$
<code>\ktHatNew</code>	$\hat{\varphi}_{jk}^{T,\text{new}}$	New kinship estimator
<code>\ftHatNew</code>	$\hat{f}_j^{T,\text{new}}$	New inbreeding estimator
<code>\klHatBeagle</code>	$\hat{\varphi}_{jk}^{L_{jk},\text{beagle}}$	Beagle-based kinship estimator
<code>\flHatBeagle</code>	$\hat{f}_j^{L_j,\text{beagle}}$	Beagle-based inbreeding estimator
<code>\Amin</code>	$A_{\text{Emin}}$	Asymptotic minimum value of $A_{jk}$
<code>\AminHat</code>	$\hat{A}_{\text{Emin}}$	Estimator of $A_{\text{Emin}}$

Table 3: Commands for miscellaneous kinship and inbreeding estimators.

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

Table 4: Commands for miscellaneous  $F_{\text{ST}}$  estimators.

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

Table 5: Commands for historical quantities in statistical genetics.

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

Table 6: Commands for math operators.

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

Table 7: Commands for math convergence arrows.

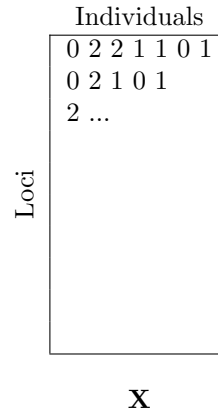


Figure 1: The cartoon genotype matrix generated by `\sampleGenMat`

- 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 ( $x_{ij}$ ) 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 ( $\varphi_{jk}^T$ ) 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 ( $p_i^T, \hat{p}_i^T, f_j^T, f_{L_j}^T, \varphi_{jk}^T, f_{L_{jk}}^T, \hat{\varphi}_{jk}^{T,\text{std}}, \hat{f}_j^{T,\text{std}}, \hat{f}_j^{T,\text{stdII}}, \hat{f}_j^{T,\text{stdIII}}, \hat{\varphi}_{jk}^{T,\text{preadj}}, \hat{\varphi}_{\min}^{T,\text{preadj}}, \hat{\varphi}_{jk}^{T,\text{new}}, \hat{f}_j^{T,\text{new}}$ , 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.

## 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

```

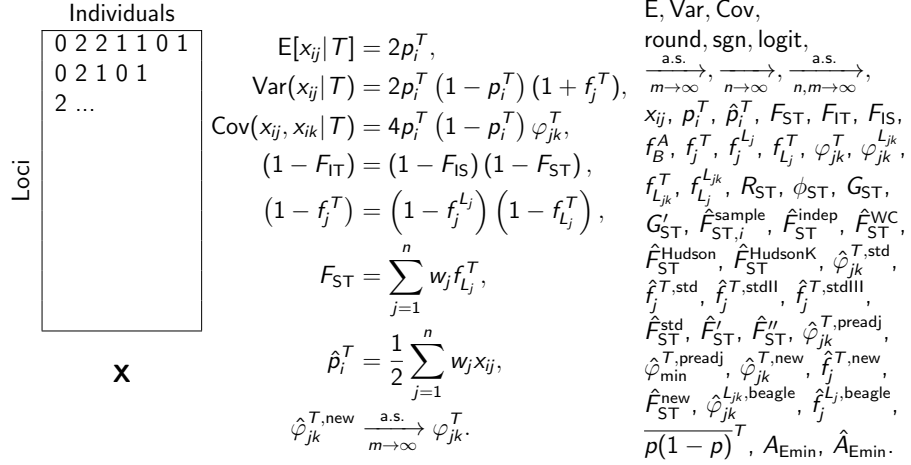


Figure 2: The vanilla version of the symbols (no colors and no omission of ancestral population  $T$  in superscripts)

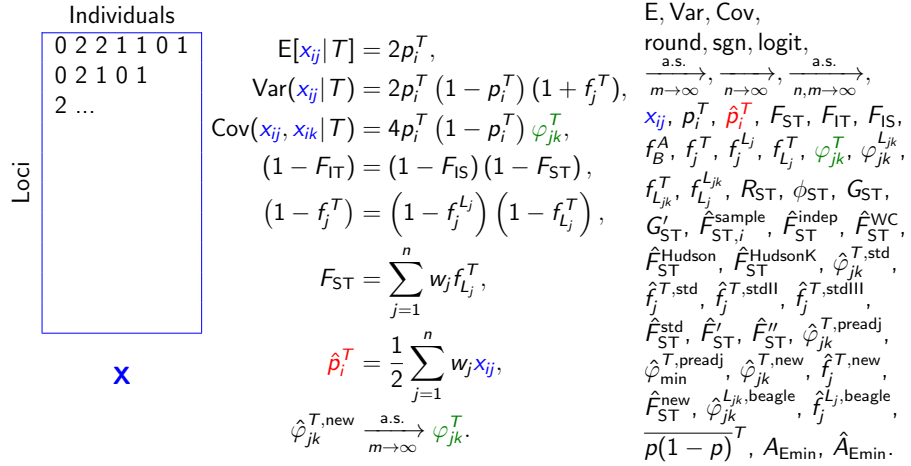


Figure 3: The color version of the symbols (with no omission of ancestral population  $T$  in superscripts)

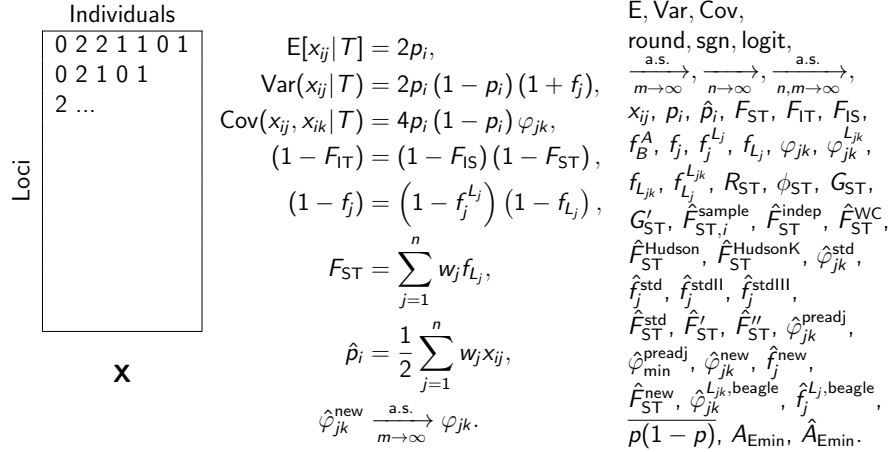


Figure 4: The noT version of the symbols (no color, with omission of ancestral population  $T$  in superscripts as appropriate)

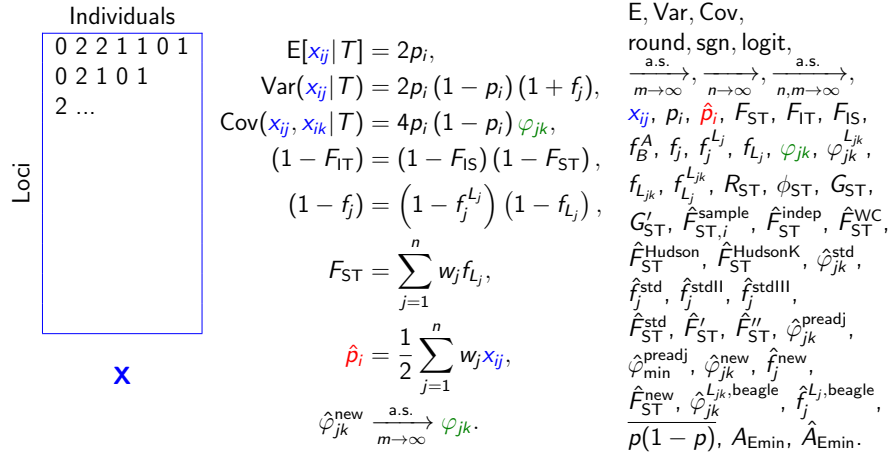


Figure 5: The color,noT version of the symbols (with color and omission of ancestral population  $T$  in superscripts as appropriate)

**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}`

`\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 }%
```

## 2.5 Ancestral allele frequencies

`\pit`  $p_i^T$ : The ancestral allele frequency at 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.

```

36 \newcommand{\pit}{%
37   \ensuremath{%
38     p_i\kinshipsymbols@T%
39   }%
40   \xspace%
41 }%
```

`\pith`  $\hat{p}_i^T$ : The sample estimator of the ancestral allele frequency at 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).

```

42 \newcommand{\pith}{%
```

```

43 \ensuremath{%
44   \ifcolor \textcolor{pithColor}{ \fi%
45     \hat{p}_i\kinshipsymbols@T%
46   \ifcolor } \fi%
47 }%
48 \xspace%
49 }%

```

## 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.

```

50 \newcommand{\Fst}{%
51   \ensuremath{%
52     F_{\text{ST}}}%
53   }%
54   \xspace%
55 }%

```

`\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.

```

56 \newcommand{\Fit}{%
57   \ensuremath{%
58     F_{\text{IT}}}%
59   }%
60   \xspace%
61 }%

```

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

```

62 \newcommand{\Fis}{%
63   \ensuremath{%
64     F_{\text{IS}}}%
65   }%
66   \xspace%
67 }%

```

## 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.

```

68 \newcommand{\f}[2]{%
69   \ensuremath{%
70     f^{\#1}_{\#2}%
71   }%

```

```

72 \xspace%
73 }%

\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.
74 \newcommand{\ft}[1][j]{%
75   \ensuremath{%
76     f_{#1}\kinshipsymbols@T%
77   }%
78   \xspace%
79 }%

\fl  $f_j^{L_j}$ : The local inbreeding coefficient of individual  $j$  (default). The optional argu-
ment allows setting other individuals (\fl[k] gives  $f_k^{L_k}$  for individual  $k$ ).
80 \newcommand{\fl}[1][j]{%
81   \ensuremath{%
82     f_{#1}^{L_{#1}}%
83   }%
84   \xspace%
85 }%

\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.
86 \newcommand{\fs}[1][j]{%
87   \ensuremath{%
88     f_{L_{#1}}\kinshipsymbols@T%
89   }%
90   \xspace%
91 }%

```

## 2.8 Kinship coefficients

```

\kt  $\varphi_{jk}^T$ : The (total) kinship coefficient between the pair of individuals  $j$  and  $k$  (de-
fault). The optional argument allows setting another second individual (\kt[l]
gives  $\varphi_{jl}^T$  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).
92 \newcommand{\kt}[1][k]{%
93   \ensuremath{%
94     \ifcolor \textcolor{kinColor}{\fi%

```

```

95      \varphi_{j\#1}\kinshipsymbols@T%
96      \ifcolor } \fi%
97    }%
98    \xspace%
99 }%

\kl  $\varphi_{jk}^{L_{jk}}$ : The local kinship coefficient between the pair of individuals  $j$  and  $k$ .
100 \newcommand{\kl}{%
101   \ensuremath{%
102     \varphi_{jk}^{L_{jk}}}%
103   }%
104   \xspace%
105 }%

\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.
106 \newcommand{\ks}{%
107   \ensuremath{%
108     f_{L_{jk}}\kinshipsymbols@T}%
109   }%
110   \xspace%
111 }%

\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  $f_{L_k}^{L_{jk}}$ .
112 \newcommand{\fpw}[1][j]{%
113   \f{L_{jk}}{L_{#1}}}%
114 }%

```

## 2.9 Review of previous work

```

\Rst  $R_{ST}$ : An  $F_{ST}$  estimator developed for microsatellites.
115 \newcommand{\Rst}{%
116   \ensuremath{%
117     R_{\text{ST}}}%
118   }%
119   \xspace%
120 }%

\PhiSt  $\phi_{ST}$ : An  $F_{ST}$ -like estimate based on AMOVA.
121 \newcommand{\PhiSt}{%
122   \ensuremath{%
123     \phi_{\text{ST}}}%
124   }%

```

```

125 \xspace%
126 }%

\Gst  $G_{ST}$ : Nei's genetic diversity measure.
127 \newcommand{\Gst}{%
128 \ensuremath{%
129 G_{\text{ST}}}%
130 }%
131 \xspace%
132 }%

\GstPrime  $G'_{ST}$ : A normalized  $G_{ST}$  statistic.
133 \newcommand{\GstPrime}{%
134 \ensuremath{%
135 G_{\text{ST}}'%
136 }%
137 \xspace%
138 }%

\FstHatSample  $\hat{F}_{ST,i}^{\text{sample}}$ : A sample  $F_{ST}$  estimator for a single locus  $i$ .
139 \newcommand{\FstHatSample}{%
140 \ensuremath{%
141 \hat{F}_{\text{ST},i}^{\text{sample}}}%
142 }%
143 \xspace%
144 }%

```

## 2.10 Convergence arrows

```

\toas  $\xrightarrow[m \rightarrow \infty]{\text{a.s.}}$ : Almost sure convergence as  $m$  goes to  $\infty$ .
145 \newcommand{\toas}{%
146 \xrightarrow[m \rightarrow \infty]{\text{a.s.}}%
147 }%

\toN  $\xrightarrow[n \rightarrow \infty]{}:$  The limit as  $n$  goes to  $\infty$ . Optional argument changes the variable name
( $\$ \toN[m] \$$  gives  $\xrightarrow[m \rightarrow \infty]{}).$ 
148 \newcommand{\toN}[1][n]{%
149 \xrightarrow[#1 \rightarrow \infty]{}%
150 }%

\toasNM  $\xrightarrow[n,m \rightarrow \infty]{\text{a.s.}}$ : Almost sure convergence as both  $n$  and  $m$  go to  $\infty$ .
151 \newcommand{\toasNM}{%
152 \xrightarrow[n,m \rightarrow \infty]{\text{a.s.}}%
153 }%

```

## 2.11 $F_{ST}$ estimators for independent subpopulations

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

```

154 \newcommand{\FstHatNamed}[1]{%
155   \ensuremath{%
156     \hat{F}_{\text{ST}}^{\text{\#1}}%
157   }%
158   \xspace%
159 }%

```

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

```

160 \newcommand{\FstHatIs}{\FstHatNamed{indep}}

```

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

```

161 \newcommand{\FstHatWc}{\FstHatNamed{WC}}

```

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

```

162 \newcommand{\FstHatHudson}{\FstHatNamed{Hudson}}

```

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

```

163 \newcommand{\FstHatHudsonK}{\FstHatNamed{HudsonK}}

```

## 2.12 Estimators based on the standard kinship

`\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[1]{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.

```

164 \newcommand{\ktHatNamed}[2][k]{%
165   \ensuremath{%
166     \hat{\varphi}_{\text{\#1}}^{\text{kinshipsymbols@Ts\#2}}%
167   }%
168   \xspace%
169 }%

```

`\ktHat`  $\hat{\varphi}_{jk}^{T,\text{std}}$ : Standard kinship estimator for individuals  $j$  and  $k$  (default). The optional argument allows setting another second individual (`\ktHat[1]` 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.

```

170 \newcommand{\ktHat}[1][k]{\ktHatNamed[\#1]{std}}

```

`\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.

```
171 \newcommand{\ftHatNamed}[2][j]{%
172   \ensuremath{%
173     \hat{f}_{\text{#1}}^{\text{kinshipsymbols@Ts\text{#2}}}%
174   }%
175   \xspace%
176 }
```

`\ftHat`  $\hat{f}_j^{T,\text{std}}$ : 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.

```
177 \newcommand{\ftHat}{\ftHatNamed{std}}
```

`\ftHatII`  $\hat{f}_j^{T,\text{stdII}}$ : 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.

```
178 \newcommand{\ftHatII}{\ftHatNamed{stdII}}
```

`\ftHatIII`  $\hat{f}_j^{T,\text{stdIII}}$ : 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.

```
179 \newcommand{\ftHatIII}{\ftHatNamed{stdIII}}
```

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

```
180 \newcommand{\FstHat}{\FstHatNamed{std}}
```

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

```
181 \newcommand{\FstHatPrime}{%
182   \ensuremath{%
183     \hat{F}_{\text{ST}}'%
184   }%
185   \xspace%
186 }
```

`\FstHatPrimeDb1`  $\hat{F}_{\text{ST}}''$ : Standard  $F_{\text{ST}}$  estimator adjusted 2.

```
187 \newcommand{\FstHatPrimeDb1}{%
188   \ensuremath{%
189     \hat{F}_{\text{ST}}''%
190   }%
191   \xspace%
192 }
```

## 2.13 New kinship and $F_{ST}$ estimators

`\ktHatPreadj`  $\hat{\varphi}_{jk}^{T, \text{preadj}}$ : Preadjusted kinship estimator for the pair of individuals  $j$  and  $k$  (default). The optional argument allows setting another second individual (`\ktHatPreadj[1]` gives  $\hat{\varphi}_{jl}^{T, \text{preadj}}$  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.

```
193 \newcommand{\ktHatPreadj}[1][k]{\ktHatNamed[#1]{preadj}}
```

`\ktHatPreadjMin`  $\hat{\varphi}_{\min}^{T, \text{preadj}}$ : Minimum value of  $\hat{\varphi}_{jk}^{T, \text{preadj}}$  across pairs of individuals and in the limit of infinite loci.

```
194 \newcommand{\ktHatPreadjMin}{%
195   \ensuremath{%
196     \hat{\varphi}_{\text{min}}\kinshipsymbols@Ts{preadj}%
197   }%
198   \xspace%
199 }
```

`\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[1]` 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.

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

`\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.

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

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

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

`\AMin`  $A_{\text{Emin}}$ : Minimum value of the expectation of the  $A_{jk}$  statistics across all pairs of individuals.

```
203 \newcommand{\AMin}{%
204   \ensuremath{%
205     A_{\text{Emin}}%
206   }%
207   \xspace%
208 }
```

`\AMinHat`  $\hat{A}_{\text{Emin}}$ : Estimator of  $A_{\text{Emin}}$ .

```
209 \newcommand{\AMinHat}{%
```



```

210 \ensuremath{%
211   \hat{A}_{\text{Emin}}}%
212 }%
213 \xspace%
214 }%

```

`\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.

```

215 \newcommand{\mav}{%
216   \ensuremath{%
217     \overline{p(1-p)}}\kinshipsymbols@T%
218   }%
219   \xspace%
220 }%

```

## 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  $k$ .

```

221 \newcommand{\klHatBeagle}{%
222   \ensuremath{%
223     \hat{\varphi}_{jk}^{L_{jk}, \text{beagle}}}%
224   }%
225   \xspace%
226 }%

```

`\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  $k$ ).

```

227 \newcommand{\flHatBeagle}[1][j]{%
228   \ensuremath{%
229     \hat{f}_{\#1}^{L_{\#1}, \text{beagle}}}%
230   }%
231   \xspace%
232 }%

```

## 2.15 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>

```

233 % after package colortbl is loaded
234 \makeatletter
235 \@ifclassloaded{beamer}{%

```

```

236 \patchcmd\@cline
237     {\arrayrulewidth\hfill}% search
238     {\arrayrulewidth\hfill\kern\z@}% replace
239     {}% success
240     {\errmessage{Patching \string\@cline\space failed}}% failure
241 }{%
242 % nothing to do here?
243 }
244 \makeatother

```

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

```

245 \newcommand{\sampleGenMat}{%
246 \begin{tabular}{cc}%
247 & Individuals \\%
248 \ifcolor \arrayrulecolor{genColor} \fi% % gets applied to whole table
249 \cline{2-2}%
250 \multirow{10}{*}{\rotatebox[origin=c]{90}{Loci}}%
251 & \multicolumn{1}{|l|}{0 2 2 1 1 0 1} \\%
252 & \multicolumn{1}{|l|}{0 2 1 0 1 } \\%
253 & \multicolumn{1}{|l|}{2 ...} \\%
254 & \multicolumn{1}{|l|}{ } \\%
255 & \multicolumn{1}{|l|}{ } \\%
256 & \multicolumn{1}{|l|}{ } \\%
257 & \multicolumn{1}{|l|}{ } \\%
258 & \multicolumn{1}{|l|}{ } \\%
259 & \multicolumn{1}{|l|}{ } \\%
260 & \multicolumn{1}{|l|}{ } \\%
261 \cline{2-2}%
262 & \\%
263 & $\mathbf{X}$
264 \ifcolor \textcolor{genColor}{ } \fi%
265 X
266 \ifcolor } \fi%
267 }$ \\%
268 \end{tabular}%
269 }%

```

### 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 L<sup>A</sup>T<sub>E</sub>X package.

## Change History

v1.0

General: Initial version . . . . . 1

## Index

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.

<b>A</b>		
\AMin . . . . .	<u>203</u>	
\AMinHat . . . . .	<u>209</u>	
<b>C</b>		
\colorfalse . . . . .	7	
\colortrue . . . . .	14	
\Cov . . . . .	<u>24</u>	
<b>E</b>		
\E . . . . .	<u>22</u>	
<b>F</b>		
\f . . . . .	<u>68</u> , 113	
\fi . . . . .	30, 32, 44, 46,	
	94, 96, 248, 264, 266	
\Fis . . . . .	<u>62</u>	
\Fit . . . . .	<u>56</u>	
\fl . . . . .	<u>80</u>	
\flHatBeagle . . . . .	<u>227</u>	
\fpw . . . . .	<u>112</u>	
\fs . . . . .	<u>86</u>	
\Fst . . . . .	<u>50</u>	
\FstHat . . . . .	<u>180</u>	
\FstHatHudson . . . . .	<u>162</u>	
\FstHatHudsonK . . . . .	<u>163</u>	
\FstHatIs . . . . .	<u>160</u>	
\FstHatNamed . . . . .	<u>154</u> ,	
	160–163, 180, 202	
\FstHatNew . . . . .	<u>202</u>	
\FstHatPrime . . . . .	<u>181</u>	
\FstHatPrimeDbl . . . . .	<u>187</u>	
\FstHatSample . . . . .	<u>139</u>	
\FstHatWc . . . . .	<u>161</u>	
\ft . . . . .	<u>74</u>	
\ftHat . . . . .	<u>177</u>	
\ftHatII . . . . .	<u>178</u>	
\ftHatIII . . . . .	<u>179</u>	
\ftHatNamed . . . . .		
	. <u>171</u> , 177–179, 201	
\ftHatNew . . . . .	<u>201</u>	
<b>G</b>		
\genColor . . . . .	<u>8</u>	
\Gst . . . . .	<u>127</u>	
\GstPrime . . . . .	<u>133</u>	
<b>I</b>		
\ifcolor . . . . .		
	6, 30, 32, 44, 46,	
	94, 96, 248, 264, 266	
<b>K</b>		
\kinColor . . . . .	<u>9</u>	
\kinshipsymbols@T . . . . .		
	. <u>11</u> , 17, 38, 45,	
	76, 88, 95, 108, 217	
\kinshipsymbols@Ts . . . . .		
	<u>12</u> , 18, 166, 173, 196	
\kl . . . . .	<u>100</u>	
\klHatBeagle . . . . .	<u>221</u>	
\ks . . . . .	<u>106</u>	
\kt . . . . .	<u>92</u>	
\ktHat . . . . .	<u>170</u>	
\ktHatNamed . . . . .		
	. <u>164</u> , 170, 193, 200	
\ktHatNew . . . . .	<u>200</u>	
\ktHatPreadj . . . . .	<u>193</u>	
\ktHatPreadjMin . . . . .	<u>194</u>	
<b>L</b>		
\logit . . . . .	<u>27</u>	
<b>M</b>		
\mav . . . . .	<u>215</u>	
<b>N</b>		
\newif . . . . .	<u>6</u>	
<b>P</b>		
\PhiSt . . . . .	<u>121</u>	
\pit . . . . .	<u>36</u>	
\pith . . . . .	<u>42</u>	
\pithColor . . . . .	<u>10</u>	
<b>R</b>		
\round . . . . .	<u>25</u>	
\Rst . . . . .	<u>115</u>	
<b>S</b>		
\sampleGenMat . . . . .	<u>245</u>	
\sgn . . . . .	<u>26</u>	
<b>T</b>		
\toas . . . . .	<u>145</u>	
\toasNM . . . . .	<u>151</u>	
\toN . . . . .	<u>148</u>	
<b>V</b>		
\Var . . . . .	<u>23</u>	
<b>X</b>		
\xij . . . . .	<u>28</u>	