

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).

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*This document corresponds to kinshipsymbols v1.04, dated 2024/02/15.

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>	φ_{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>	$f_j^{L_j^T}$	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>	$\overline{p(1-p)}^T$	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 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{\dots}\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[1]` 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:

- 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

Command	Symbol	Description
<code>\ktHat</code>	$\hat{\varphi}_{jk}^T$	Unnamed kinship estimator
<code>\ftHat</code>	\hat{f}_j^T	Unnamed inbreeding estimator
<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>\ktHatStd</code>	$\hat{\varphi}_{jk}^{T,\text{std}}$	Standard kinship estimator
<code>\ftHatStd</code>	$\hat{f}_j^{T,\text{std}}$	Standard inbreeding estimator (I)
<code>\ftHatStdII</code>	$\hat{f}_j^{T,\text{stdII}}$	Alternate inbreeding estimator (II)
<code>\ftHatStdIII</code>	$\hat{f}_j^{T,\text{stdIII}}$	Alternate inbreeding estimator (III)
<code>\ktHatNew</code>	$\hat{\varphi}_{jk}^{T,\text{new}}$	New kinship estimator
<code>\ktHatNewMin</code>	$\hat{\varphi}_{\min}^{T,\text{new}}$	Estimator of the asymptotic minimum $\hat{\varphi}_{jk}^{T,\text{new}}$
<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>\Ajk</code>	A_{jk}	New kinship-related statistic
<code>\AMinHat</code>	\hat{A}_{\min}	Estimator of the asymptotic minimum A_{jk}

Table 3: Commands for miscellaneous kinship and inbreeding estimators.

Command	Symbol	Description
<code>\FstHatSample</code>	$\hat{F}_{\text{ST},i}^{\text{sample}}$	Sample F_{ST} estimator (one locus)
<code>\FstHat</code>	\hat{F}_{ST}	Unnamed F_{ST} estimator
<code>\FstHatNamed{example}</code>	$\hat{F}_{\text{ST}}^{\text{example}}$	Named F_{ST} estimator
<code>\FstHatWc</code>	$\hat{F}_{\text{ST}}^{\text{WC}}$	Weir-Cockerham F_{ST} estimator
<code>\FstHatHudson</code>	$\hat{F}_{\text{ST}}^{\text{Hudson}}$	Hudson Pairwise F_{ST} estimator
<code>\FstHatHudsonK</code>	$\hat{F}_{\text{ST}}^{\text{HudsonK}}$	Generalized Hudson F_{ST} estimator
<code>\FstHatIs</code>	$\hat{F}_{\text{ST}}^{\text{indep}}$	Asymptotic F_{ST} estimator for indep. subpops.
<code>\FstHatStd</code>	$\hat{F}_{\text{ST}}^{\text{std}}$	Standard F_{ST} estimator (based on $\hat{\varphi}_{jk}^{T,\text{std}}$)
<code>\FstHatStdPrime</code>	\hat{F}_{ST}'	Standard F_{ST} estimator adjusted 1
<code>\FstHatStdPrimeDb1</code>	\hat{F}_{ST}''	Standard F_{ST} estimator adjusted 2
<code>\FstHatNew</code>	$\hat{F}_{\text{ST}}^{\text{new}}$	New F_{ST} estimator

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

Command	Symbol	Description
<code>\Fit</code>	F_{IT}	Wright's total inbreeding
<code>\Fis</code>	F_{IS}	Wright's local inbreeding
<code>\Gst</code>	G_{ST}	Nei's genetic diversity measure
<code>\GstPrime</code>	G'_{ST}	Normalized G_{ST}
<code>\Rst</code>	R_{ST}	F_{ST} estimator for microsatellites
<code>\PhiSt</code>	ϕ_{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>	$\xrightarrow{\text{a.s.}}_{m \rightarrow \infty}$	Almost sure convergence as m goes to ∞
<code>\toN</code>	$\xrightarrow{n \rightarrow \infty}$	Limit as n goes to ∞
<code>\toasNM</code>	$\xrightarrow{\text{a.s.}}_{n, m \rightarrow \infty}$	Almost sure convergence as both m and n go to ∞

Table 7: Commands for math convergence arrows.

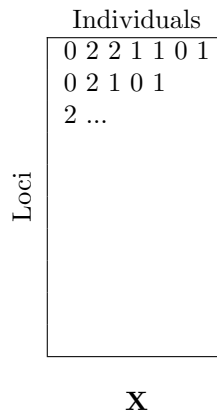


Figure 1: The cartoon genotype matrix generated by `\sampleGenMat`

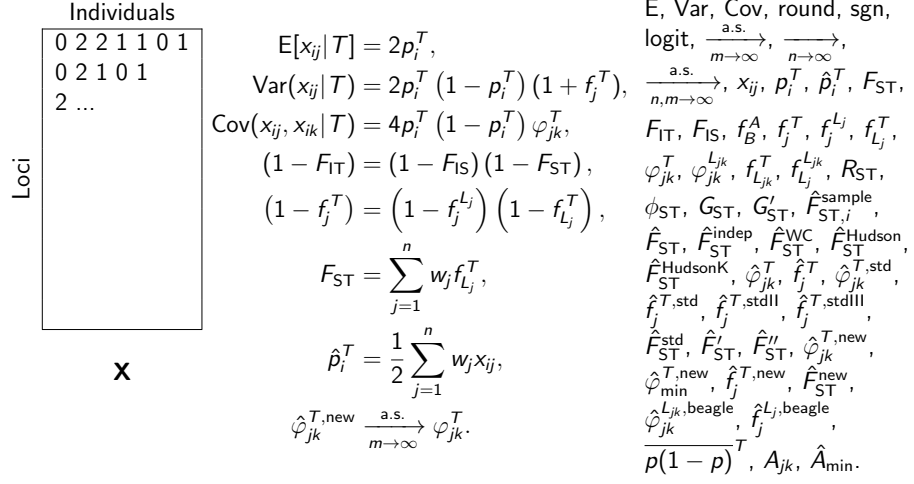


Figure 2: The vanilla version of the symbols (no colors and no omission of ancestral population T in superscripts)

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 (φ_{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 , $f_{L_j}^T$, φ_{jk}^T , $f_{L_{jk}}^T$, $\hat{\varphi}_{jk}^T$, \hat{f}_j^T , $\hat{\varphi}_{jk}^{T,\text{std}}$, $\hat{f}_j^{T,\text{std}}$, $\hat{f}_j^{T,\text{stdII}}$, $\hat{f}_j^{T,\text{stdIII}}$, $\hat{\varphi}_{jk}^{T,\text{new}}$, $\hat{\varphi}_{\min}^{T,\text{new}}$, $\hat{f}_j^{T,\text{new}}$, 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

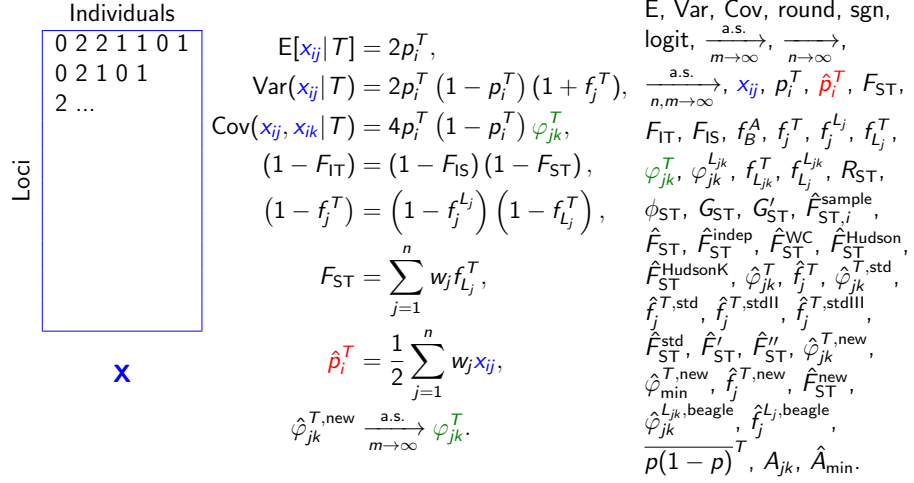


Figure 3: The color version of the symbols (with no omission of ancestral population T in superscripts)

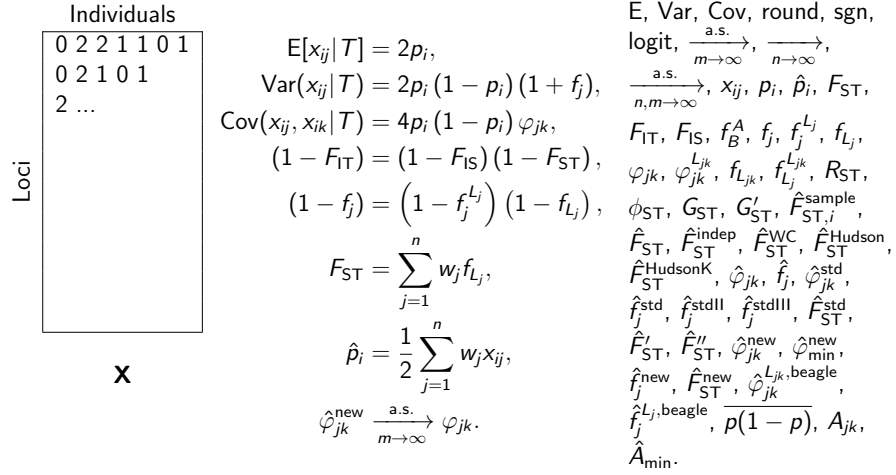


Figure 4: The noT version of the symbols (no color, with omission of ancestral population T in superscripts as appropriate)

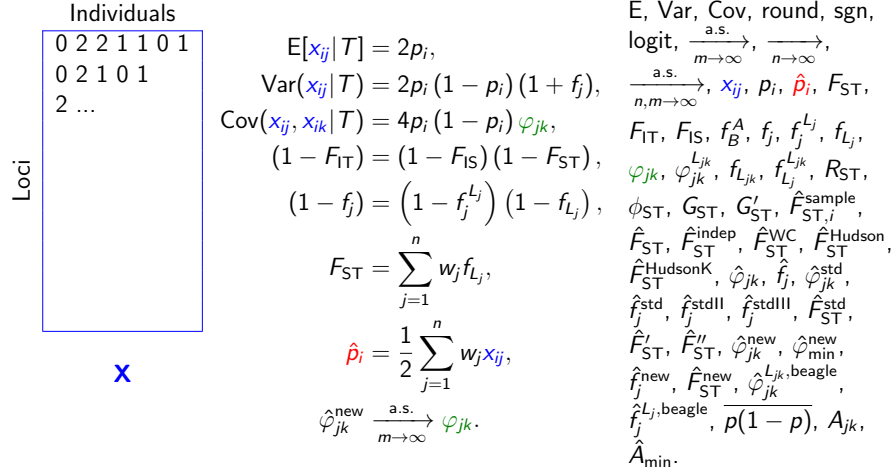


Figure 5: The `color,noT` version of the symbols (with color and omission of ancestral population T in superscripts as appropriate)

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}{\textsuperscript{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]{\text{\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 argument 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` 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).

```

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` ϕ_{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 ∞ . Optional argument changes the variable name (`\toas[n]` gives $\xrightarrow[n \rightarrow \infty]{\text{a.s.}}$).

```

145 \newcommand{\toas}[1][m]{%
146   \xrightarrow[#1]{\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]{\text{a.s.}}
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]{\text{a.s.}}
153 }%
```

2.11 F_{ST} estimators for independent subpopulations

```

\FstHat  $\hat{F}_{ST}$ : Unnamed  $F_{ST}$  estimator.
154 \newcommand{\FstHat}{%
155   \ensuremath{%
156     \hat{F}_{\text{ST}}
157   }%
158   \xspace%
159 }%

\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.
160 \newcommand{\FstHatNamed}[1]{%
161   \ensuremath{%
162     \hat{F}_{\text{ST}}^{\text{\#1}}
163   }%
164   \xspace%
165 }%

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

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

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

\FstHatHudsonK  $\hat{F}_{ST}^{\text{HudsonK}}$ : Generalized Hudson  $F_{ST}$  estimator (for  $K$  subpopulations).
169 \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**[1] 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.
- ```

170 \newcommand{\ktHat}[1][k]{%
171 \ensuremath{%
172 \hat{\varphi}_{#1}\kinshipsymbols@T%
173 }%
174 \xspace%
175 }%
```
- \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.
- ```

176 \newcommand{\ktHatNamed}[2][k]{%
177   \ensuremath{%
178     \hat{\varphi}_{#1}\kinshipsymbols@Ts{#2}%
179   }%
180   \xspace%
181 }%
```
- \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**[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.
- ```

182 \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.
- ```

183 \newcommand{\ftHat}[1][j]{%
184   \ensuremath{%
185     \hat{f}_{#1}\kinshipsymbols@T%
186   }%
187   \xspace%
188 }%
```
- \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.

```

189 \newcommand{\ftHatNamed}[2][j]{%
190   \ensuremath{%
191     \hat{f}_{\text{#1}}\kinshipsymbols@Ts{#2}%
192   }%
193   \xspace%
194 }%

\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.
195 \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.
196 \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.
197 \newcommand{\ftHatStdIII}{\ftHatNamed{stdIII}}

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

\FstHatStdPrime  $\hat{F}_{\text{ST}}'$ : Standard  $F_{\text{ST}}$  estimator adjusted 1.
199 \newcommand{\FstHatStdPrime}{%
200   \ensuremath{%
201     \hat{F}_{\text{ST}}'%
202   }%
203   \xspace%
204 }%

\FstHatStdPrimeDbl  $\hat{F}_{\text{ST}}''$ : Standard  $F_{\text{ST}}$  estimator adjusted 2.
205 \newcommand{\FstHatStdPrimeDbl}{%
206   \ensuremath{%
207     \hat{F}_{\text{ST}}''%
208   }%
209   \xspace%
210 }%

```

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[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.

```

211 \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.

```

212 \newcommand{\ktHatNewMin}{%
213   \ensuremath{%
214     \hat{\varphi}_{\text{min}}\kinshipsymbols@Ts{new}%
215   }%
216   \xspace%
217 }%
```

`\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.

```

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

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

```

219 \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).

```

220 \newcommand{\Ajk}[1][k]{%
221   \ensuremath{%
222     A_{j\#1}%
223   }%
224   \xspace%
225 }%
```

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

```

226 \newcommand{\AMinHat}{%
227   \ensuremath{%
228     \hat{A}_{\text{min}}%
229   }%
230   \xspace%
231 }%
```

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

```

232 \newcommand{\AAvgHat}{%
233   \ensuremath{%
234     \hat{A}_{\text{avg}}%
235   }%
236   \xspace%
237 }%
```

`\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.


```

238 \newcommand{\mav}{%
239   \ensuremath{%
240     \overline{p(1-p)}}\kinshipsymbols@T%
241   }%
242   \xspace%
243 }%

```

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 .

```

244 \newcommand{\klHatBeagle}{%
245   \ensuremath{%
246     \hat{\varphi}_{jk}^{L_{jk}, \text{beagle}}}%
247   }%
248   \xspace%
249 }%

```

`\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).

```

250 \newcommand{\flHatBeagle}[1][j]{%
251   \ensuremath{%
252     \hat{f}_{\#1}^{L_{\#1}, \text{beagle}}}%
253   }%
254   \xspace%
255 }%

```

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>

```

256 % after package colortbl is loaded
257 \makeatletter
258 \@ifclassloaded{beamer}{%
259   \patchcmd\@cline
260     {\arrayrulewidth\hfill}% search
261     {\arrayrulewidth\hfill\kern\z@}% replace
262     {}% success
263     {\errmessage{Patching \string\@cline\space failed}}% failure
264 }{%
265   % nothing to do here?
266 }
267 \makeatother

```

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

```

268 \newcommand{\sampleGenMat}{%
269   \begin{tabular}{cc}%

```

```

270 & Individuals \\%
271 \ifcolor \arrayrulecolor{genColor} \fi% % gets applied to whole table
272 \cline{2-2}%
273 \multirow{10}{*}{\rotatebox[origin=c]{90}{Loci}}%
274 & \multicolumn{1}{|l|}{0 2 2 1 1 0 1} \\%
275 & \multicolumn{1}{|l|}{0 2 1 0 1 } \\%
276 & \multicolumn{1}{|l|}{2 ...} \\%
277 & \multicolumn{1}{|l|}{ } \\%
278 & \multicolumn{1}{|l|}{ } \\%
279 & \multicolumn{1}{|l|}{ } \\%
280 & \multicolumn{1}{|l|}{ } \\%
281 & \multicolumn{1}{|l|}{ } \\%
282 & \multicolumn{1}{|l|}{ } \\%
283 & \multicolumn{1}{|l|}{ } \\%
284 \cline{2-2}%
285 & \\%
286 & $\mathbf{X}$
287 \ifcolor \textcolor{genColor}{ } \fi%
288 X
289 \ifcolor } \fi%
290 }$ \\%
291 \end{tabular}%
292 }%

```

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^AT_EX package](#).

Change History

v1.00	General: Initial version 1	v1.03	General: Added unnamed \hat{F}_{ST} , $\hat{\phi}_{jk}^T$, and \hat{f}_j^T symbols (without estimator name) 1
v1.01	General: Added NEWS, README, and symbols A_{jk} , \hat{A}_{avg} , and *Std versions 1	v1.04	General: Added option to change variable name in $\frac{a.s.}{m \rightarrow \infty}$ 1
v1.02	General: Added $\hat{\phi}_{min}^{T,new}$ symbol 1		

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