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

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[*]This document corresponds to **kinshipsymbols** v1.01, dated 2020/03/05.

Command	Symbol	Description
\xij	x_{ij}	Genotype
\pit	p_i^T	Ancestral allele frequency
\pith	$\hat{p}_i^T$	Sample p_i^T estimator
\kt	φ_{jk}^T	Kinship coefficient
\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 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
`\ktHatNamed{example}`	$\hat{\varphi}_{jk}^{T,\text{example}}$	Named kinship estimator
`\ftHatNamed{example}`	$\hat{f}_{j}^{T,\text{example}}$	Named inbreeding estimator
`\ktHatStd`	$\hat{\varphi}_{jk}^{T,\text{std}}$	Standard kinship estimator
`\ftHatStd`	$\hat{f}_{j}^{T,\text{std}}$	Standard inbreeding estimator (I)
`\ftHatStdII`	$\hat{f}_{j}^{T,\text{stdII}}$	Alternate inbreeding estimator (II)
`\ftHatStdIII`	$\hat{f}_{j}^{T,\text{stdIII}}$	Alternate inbreeding estimator (III)
`\ktHatNew`	$\hat{\varphi}_{jk}^{T,\text{new}}$	New kinship estimator
`\ftHatNew`	$\hat{f}_{j}^{T,\text{new}}$	New inbreeding estimator
`\klHatBeagle`	$\hat{\varphi}_{jk}^{L_{jk},\text{beagle}}$	Beagle-based kinship estimator
`\flHatBeagle`	$\hat{f}_{j}^{L_{j},\text{beagle}}$	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`	$\hat{F}_{\text{ST},i}^{\text{sample}}$	Sample F_{ST} estimator (one locus)
`\FstHatNamed{example}`	$\hat{F}_{\text{ST}}^{\text{example}}$	Named F_{ST} estimator
`\FstHatWc`	$\hat{F}_{\text{ST}}^{\text{WC}}$	Weir-Cockerham F_{ST} estimator
`\FstHatHudson`	$\hat{F}_{\text{ST}}^{\text{Hudson}}$	Hudson Pairwise F_{ST} estimator
`\FstHatHudsonK`	$\hat{F}_{\text{ST}}^{\text{HudsonK}}$	Generalized Hudson F_{ST} estimator
`\FstHatIs`	$\hat{F}_{\text{ST}}^{\text{indep}}$	Asymptotic F_{ST} estimator for indep. subpops.
`\FstHatStd`	$\hat{F}_{\text{ST}}^{\text{std}}$	Standard F_{ST} estimator (based on $\hat{\varphi}_{jk}^{T,\text{std}}$)
`\FstHatStdPrime`	$\hat{F}_{\text{ST}}'$	Standard F_{ST} estimator adjusted 1
`\FstHatStdPrimeDbl`	$\hat{F}_{\text{ST}}''$	Standard F_{ST} estimator adjusted 2
`\FstHatNew`	$\hat{F}_{\text{ST}}^{\text{new}}$	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.
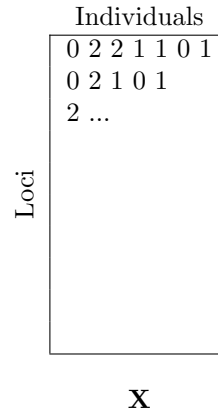

Figure 1: The cartoon genotype matrix generated by \sampleGenMat

- 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 (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, $f_{L_{jk}}^T$, $\hat{\varphi}_{jk}^{T,\text{std}}$, $\hat{f}_j^{T,\text{std}}$, $\tilde{f}_j^{T,\text{stdII}}$, $\hat{f}_j^{T,\text{stdIII}}$, $\hat{\varphi}_{jk}^{T,\text{new}}$, $\hat{f}_j^{T,\text{new}}$, 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
```
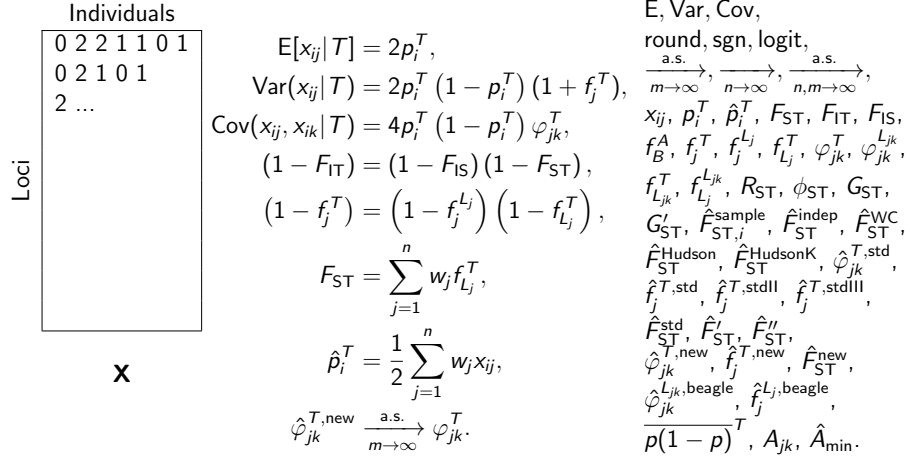
Individuals

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

Loci

$\mathbf{x}$

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

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}, 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, $\varphi_{jk}^{L_{jk}}$,
$f_{L_{jk}}^T$, $f_{L_j}^{L_{jk}}$, R_{ST}, ϕ_{ST}, G_{ST},
G'_{ST}, $\hat{F}_{\text{ST},i}^{\text{sample}}$, $\hat{F}_{\text{ST}}^{\text{indep}}$, $\hat{F}_{\text{ST}}^{\text{WC}}$,
$\hat{F}_{\text{ST}}^{\text{Hudson}}$, $\hat{F}_{\text{ST}}^{\text{HudsonK}}$, $\hat{\varphi}_{jk}^{T,\text{std}}$,
$\hat{f}_j^{T,\text{std}}$, $\hat{f}_j^{T,\text{stdII}}$, $\hat{f}_j^{T,\text{stdIII}}$,
$\hat{F}_{\text{ST}}^{\text{std}}$, $\hat{F}'_{\text{ST}}$, $\hat{F}''_{\text{ST}}$,
$\hat{\varphi}_{jk}^{T,\text{new}}$, $\hat{f}_j^{T,\text{new}}$, $\hat{F}_{\text{ST}}^{\text{new}}$,
$\hat{\varphi}_{jk}^{L_{jk},\text{beagle}}$, $\hat{f}_j^{L_j,\text{beagle}}$,
$\overline{p(1-p)}^T$, A_{jk}, $\hat{A}_{\text{min}}$.

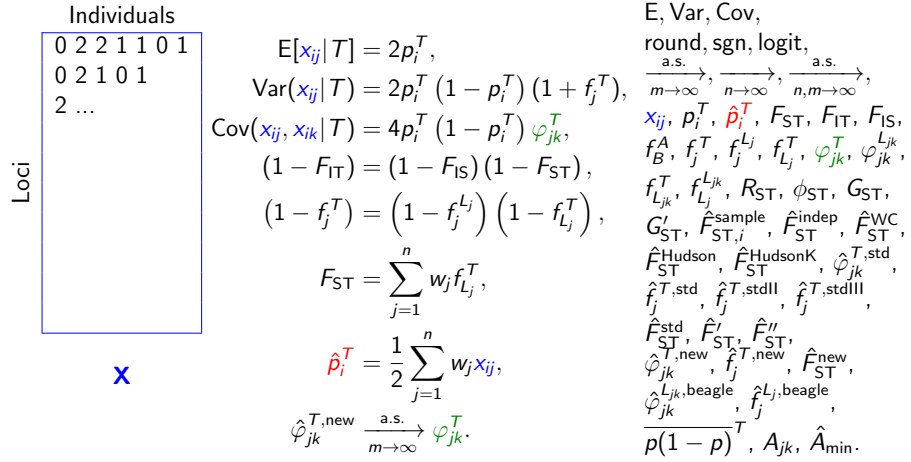Figure 2: The vanilla version of the symbols (no colors and no omission of ancestral population T in superscripts

Individuals

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

Loci

$\mathbf{x}$

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

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}, 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, $\varphi_{jk}^{L_{jk}}$,
$f_{L_{jk}}^T$, $f_{L_j}^{L_{jk}}$, R_{ST}, ϕ_{ST}, G_{ST},
G'_{ST}, $\hat{F}_{\text{ST},i}^{\text{sample}}$, $\hat{F}_{\text{ST}}^{\text{indep}}$, $\hat{F}_{\text{ST}}^{\text{WC}}$,
$\hat{F}_{\text{ST}}^{\text{Hudson}}$, $\hat{F}_{\text{ST}}^{\text{HudsonK}}$, $\hat{\varphi}_{jk}^{T,\text{std}}$,
$\hat{f}_j^{T,\text{std}}$, $\hat{f}_j^{T,\text{stdII}}$, $\hat{f}_j^{T,\text{stdIII}}$,
$\hat{F}_{\text{ST}}^{\text{std}}$, $\hat{F}'_{\text{ST}}$, $\hat{F}''_{\text{ST}}$,
$\hat{\varphi}_{jk}^{T,\text{new}}$, $\hat{f}_j^{T,\text{new}}$, $\hat{F}_{\text{ST}}^{\text{new}}$,
$\hat{\varphi}_{jk}^{L_{jk},\text{beagle}}$, $\hat{f}_j^{L_j,\text{beagle}}$,
$\overline{p(1-p)}^T$, A_{jk}, $\hat{A}_{\text{min}}$.

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

6

Individuals

| 0 2 2 1 1 0 1 |
| 0 2 1 0 1 |
| 2 ... |

Loci

X

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

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

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

Individuals

| 0 2 2 1 1 0 1 |
| 0 2 1 0 1 |
| 2 ... |

Loci

X

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

$E, \mathrm{Var}, \mathrm{Cov},$
$\mathrm{round}, \mathrm{sgn}, \mathrm{logit},$
$\xrightarrow[m\to\infty]{a.s.}, \xrightarrow[n\to\infty]{}, \xrightarrow[n,m\to\infty]{a.s.},$
$x_{ij}, p_i, \hat{p}_i, F_{ST}, F_{IT}, F_{IS},$
$f_B^A, f_j, f_j^{L_j}, f_{L_j}, \varphi_{jk}, \varphi_{jk}^{L_{jk}},$
$f_{L_{jk}}, f_{L_j}^{L_{jk}}, R_{ST}, \phi_{ST}, G_{ST},$
$G'_{ST}, \hat{F}_{ST,i}^{sample}, \hat{F}_{ST}^{indep}, \hat{F}_{ST}^{WC},$
$\hat{F}_{ST}^{Hudson}, \hat{F}_{ST}^{HudsonK}, \hat{\varphi}_{jk}^{std},$
$\hat{f}_j^{std}, \hat{f}_j^{stdII}, \hat{f}_j^{stdIII},$
$\hat{F}_{ST}^{std}, \hat{F}'_{ST}, \hat{F}''_{ST},$
$\hat{\varphi}_{jk}^{new}, \hat{f}_j^{new}, \hat{F}_{ST}^{new},$
$\hat{\varphi}_{jk}^{L_{jk},beagle}, \hat{f}_j^{L_j,beagle},$
$\overline{p(1-p)}, A_{jk}, \hat{A}_{min}.$
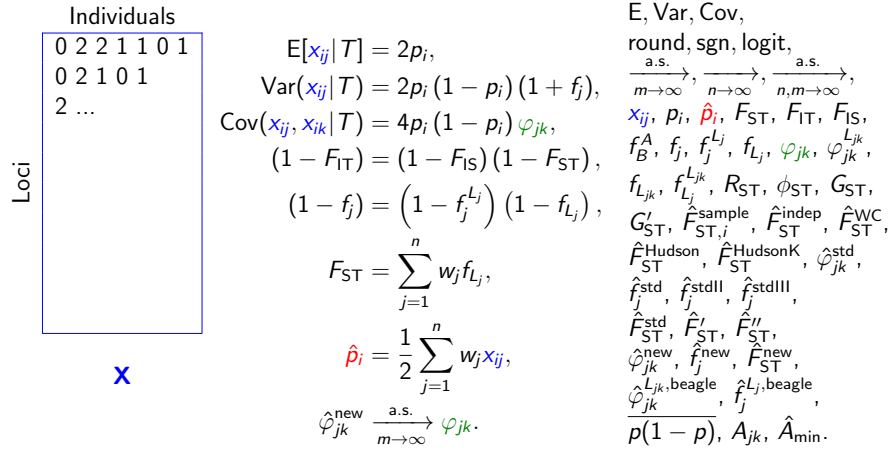
Figure 5: The `color,noT` version of the symbols (with color and omission of ancestral population T in superscripts as appropriate

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 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 $\hat{F}_{\text{ST},i}^{\text{sample}}$: 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 $\xrightarrow[m \to \infty]{\text{a.s.}}$: Almost sure convergence as m goes to ∞.

```
145 \newcommand{\toas}{%
146    \xrightarrow[m \rightarrow \infty]{\text{a.s.}}
147 }%
```

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

```
148 \newcommand{\toN}[1][n]{%
149    \xrightarrow[#1 \rightarrow \infty]{}%
150 }%
```

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

```
151 \newcommand{\toasNM}{%
152    \xrightarrow[n,m \rightarrow \infty]{\text{a.s.}}%
153 }%
```

2.11 $F_{\mathbf{ST}}$ estimators for independent subpopulations

\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.

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

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

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

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

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

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

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

\FstHatHudsonK $\hat{F}_{\text{ST}}^{\text{HudsonK}}$: 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[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.

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

\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.

```
170 \newcommand{\ktHatStd}[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}_{#1}\kinshipsymbols@Ts{#2}%
174   }%
175   \xspace%
176 }%
```

\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.

```
177 \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.

```
178 \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.

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

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

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

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

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

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

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

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.

```
193 \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.

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

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

```
195 \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).

```
196 \newcommand{\Ajk}[1][k]{%
197   \ensuremath{%
198     A_{j#1}%
199   }%
200   \xspace%
201 }%
```

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

```
202 \newcommand{\AMinHat}{%
203   \ensuremath{%
204     \hat{A}_{\text{min}}%
205   }%
206   \xspace%
207 }%
```

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

```
208 \newcommand{\AAvgHat}{%
209   \ensuremath{%
210     \hat{A}_{\text{avg}}%
211   }%
212   \xspace%
213 }%
```

`\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.

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

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.

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

`\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).

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

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`

```
232 % after package colortbl is loaded
233 \makeatletter
234 \@ifclassloaded{beamer}{%
235   \patchcmd\@cline
236       {\arrayrulewidth\hfill}% search
237       {\arrayrulewidth\hfill\kern\z@}% replace
238       {}% success
239       {\errmessage{Patching \string\@cline\space failed}}% failure
240 }{%
```

```
241   % nothing to do here?
242 }
243 \makeatother
```

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

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

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

v1.0
    General: Initial version   1

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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.