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 very 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 v1.0, dated 2019/02/01.

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
`\ktHat`	$\hat{\varphi}_{jk}^{T,\mathrm{std}}$	Standard kinship estimator
`\ftHat`	$\hat{f}_{j}^{T,\mathrm{std}}$	Standard inbreeding estimator (I)
`\ftHatII`	$\hat{f}_{j}^{T,\mathrm{stdII}}$	Alternate inbreeding estimator (II)
`\ftHatIII`	$\hat{f}_{j}^{T,\mathrm{stdIII}}$	Alternate inbreeding estimator (III)
`\ktHatPreadj`	$\hat{\varphi}_{jk}^{T,\mathrm{preadj}}$	Preadjusted kinship estimator
`\ktHatPreadjMin`	$\hat{\varphi}_{\mathrm{min}}^{T,\mathrm{preadj}}$	Asymptotic minimum value of $\hat{\varphi}_{jk}^{T,\mathrm{preadj}}$
`\ktHatNew`	$\hat{\varphi}_{jk}^{T,\mathrm{new}}$	New kinship estimator
`\ftHatNew`	$\hat{f}_{j}^{T,\mathrm{new}}$	New inbreeding estimator
`\klHatBeagle`	$\hat{\varphi}_{jk}^{L_{jk},\mathrm{beagle}}$	Beagle-based kinship estimator
`\flHatBeagle`	$\hat{f}_{j}^{L_{j},\mathrm{beagle}}$	Beagle-based inbreeding estimator
`\AMin`	A_{Emin}	Asymptotic minimum value of A_{jk}
`\AMinHat`	$\hat{A}_{\mathrm{Emin}}$	Estimator of A_{Emin}

Table 3: Commands for miscelaneous kinship and inbreeding estimators.

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

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

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

Table 5: Commands for historical quantities in statistical genetics.

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

Table 6: Commands for math operators.

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

Table 7: Commands for math convergence arrows.

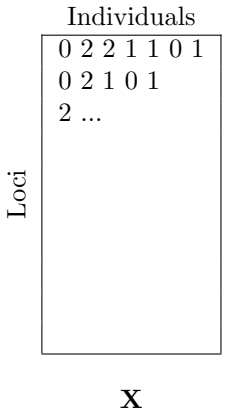

Figure 1: The cartoon genotype matrix generated by `\sampleGenMat`

- 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 and inbreeding coefficients (φ_{jk}^T and f_j^T) become dark green. Highlighted since these are the 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, $f_{L_{jk}}^T$, $\hat{\varphi}_{jk}^{T,\text{std}}$, $\hat{f}_j^{T,\text{std}}$, $\hat{f}_j^{T,\text{stdII}}$, $\hat{f}_j^{T,\text{stdIII}}$, $\hat{\varphi}_{jk}^{T,\text{preadj}}$, $\hat{\varphi}_{\min}^{T,\text{preadj}}$, $\hat{\varphi}_{jk}^{T,\text{new}}$, $\hat{f}_j^{T,\text{new}}$, 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.

```
\RequirePackage{amsmath}
\RequirePackage{xspace}
\RequirePackage{xcolor}
\RequirePackage{colortbl}
\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). Note that by default these colors are all black.

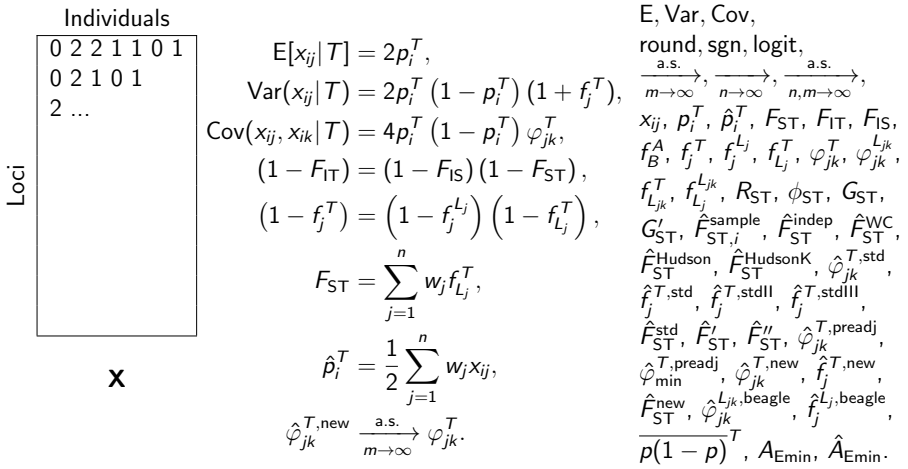

Figure 2: The vanilla version of the symbols (no colors and no omission of ancestral population T in superscripts

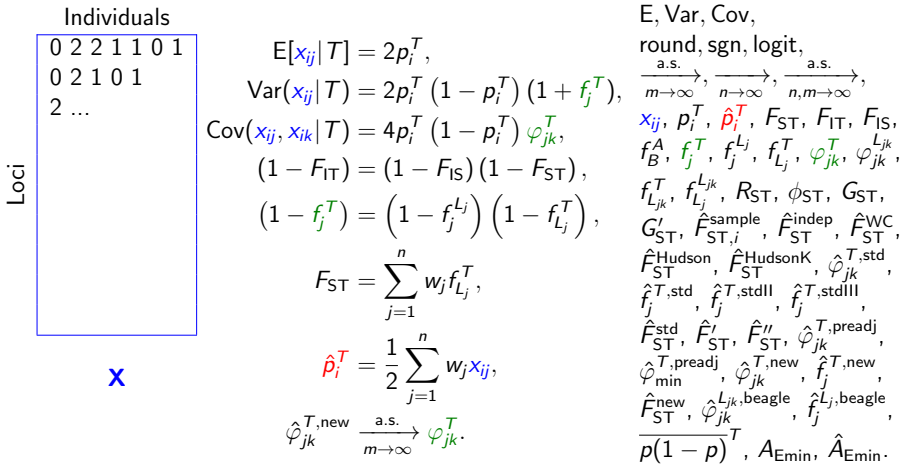

Figure 3: The `color` version of the symbols (with no omission of ancestral population T in superscripts

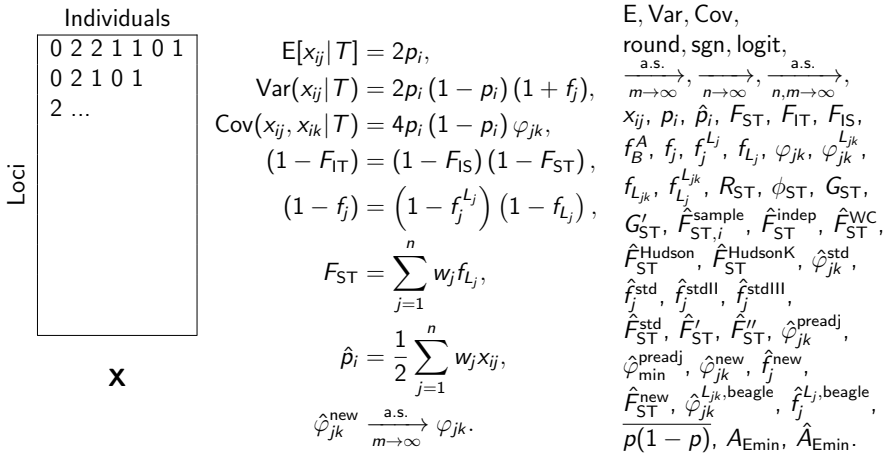

Figure 4: The `noT` version of the symbols (no color, with omission of ancestral population T in superscripts as appropriate

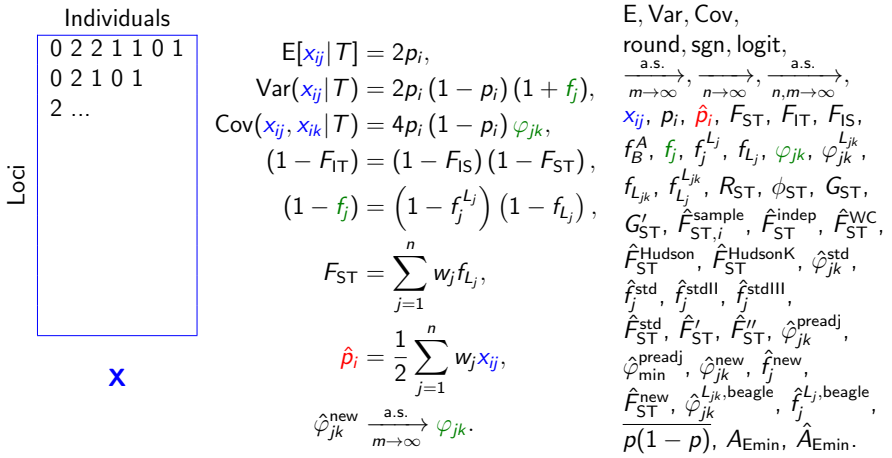

Figure 5: The `color,noT` version of the symbols (with color and omission of ancestral population T in superscripts as appropriate

`genColor` This "genotype color" is black by default, turns blue if the `color` package option is set.

```
\colorlet{genColor}{black}
```

`kinColor` This "kinship color" is black by default, turns a dark green if the `color` package option is set.

```
\colorlet{kinColor}{black}
```

`pithColor` This "`\pith` color" is black by default, turns red if the `color` package option is set.

```
\colorlet{pithColor}{black}
```

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.

```
\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).

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

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

```
\DeclareOption{color}{
  \colorlet{genColor}{blue}
  \colorlet{kinColor}{green!50!black}
  \colorlet{pithColor}{red}
}
```

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.

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

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

```
\DeclareOption*{\PackageWarning{examplepackage}{Unknown `\CurrentOption'}}
\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.

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

`\Var` Variance of a random variable.

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

`\Cov` Covariance of a random variable.

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

`\round` The rounding function.

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

`\sgn` The sign function.

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

`\logit` The logit function.

```
\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).

```
\newcommand{\xij}[1][j]{%
  \ensuremath{%
    \textcolor{genColor}{%
      x_{i#1}%
    }%
  }%
  \xspace%
}%
```

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.

```
\newcommand{\pit}{%
  \ensuremath{%
    p_i\kinshipsymbols@T%
  }%
  \xspace%
}%
```

`\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).

```
\newcommand{\pith}{%
  \ensuremath{%
    \textcolor{pithColor}{%
      \hat{p}_i\kinshipsymbols@T%
    }%
  }%
  \xspace%
}%
```

2.6 Wright's $F_{\mathbf{ST}}$

`\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.

```
\newcommand{\Fst}{%
  \ensuremath{%
    F_{\text{ST}}%
  }%
  \xspace%
}%
```

`\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.

```
\newcommand{\Fit}{%
  \ensuremath{%
    F_{\text{IT}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\Fis}{%
  \ensuremath{%
    F_{\text{IS}}%
  }%
  \xspace%
}%
```

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.

```
\newcommand{\f}[2]{%
```

```
  \ensuremath{%
    f^{#1}_{#2}%
  }%
  \xspace%
}%
```

`\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. If the package option `color` is passed, then this symbol turns the color `kinColor` (default dark green).

```
\newcommand{\ft}[1][j]{%
  \ensuremath{%
    \textcolor{kinColor}{%
      f_{#1}\kinshipsymbols@T%
    }%
  }%
  \xspace%
}%
```

`\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).

```
\newcommand{\fl}[1][j]{%
  \ensuremath{%
    f_{#1}^{L_{#1}}%
  }%
  \xspace%
}%
```

`\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.

```
\newcommand{\fs}[1][j]{%
  \ensuremath{%
    f_{L_{#1}}\kinshipsymbols@T%
  }%
  \xspace%
}%
```

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).

```
\newcommand{\kt}[1][k]{%
  \ensuremath{%
    \textcolor{kinColor}{%
      \varphi_{j#1}\kinshipsymbols@T%
    }%
  }%
  \xspace%
}%
```

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

```
\newcommand{\kl}{%
  \ensuremath{%
    \varphi_{jk}^{L_{jk}}%
  }%
  \xspace%
}%
```

`\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.

```
\newcommand{\ks}{%
  \ensuremath{%
    f_{L_{jk}}\kinshipsymbols@T%
  }%
  \xspace%
}%
```

`\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 $f_{L_k}^{L_{jk}}$.

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

2.9 Review of previous work

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

```
\newcommand{\Rst}{%
  \ensuremath{%
    R_{\text{ST}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\PhiSt}{%
  \ensuremath{%
    \phi_{\text{ST}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\Gst}{%
  \ensuremath{%
    G_{\text{ST}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\GstPrime}{%
  \ensuremath{%
    G_{\text{ST}}'%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatSample}{%
  \ensuremath{%
    \hat{F}_{\text{ST},i}^{\text{sample}}%
  }%
  \xspace%
}%
```

2.10 Convergence arrows

`\toas` $\xrightarrow[m\to\infty]{\text{a.s.}}$: Almost sure convergence as m goes to ∞.

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

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

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

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

```
\newcommand{\toasNM}{%
```

```
  \xrightarrow[n,m \rightarrow \infty]{\text{a.s.}}%
}%
```

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

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

```
\newcommand{\FstHatIs}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{indep}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatWc}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{WC}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatHudson}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{Hudson}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatHudsonK}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{HudsonK}}%
  }%
  \xspace%
}%
```

2.12 Estimators based on the standard kinship

`\ktHat` $\hat{\varphi}_{jk}^{T,\mathrm{std}}$: Standard kinship estimator for individuals j and 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.

```
\newcommand{\ktHat}{%
  \ensuremath{%
    \hat{\varphi}_{jk}\kinshipsymbols@Ts{std}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\ftHat}{%
  \ensuremath{%
    \hat{f}_j\kinshipsymbols@Ts{std}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\ftHatII}{%
  \ensuremath{%
    \hat{f}_j\kinshipsymbols@Ts{stdII}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\ftHatIII}{%
  \ensuremath{%
    \hat{f}_j\kinshipsymbols@Ts{stdIII}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHat}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{std}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatPrime}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}'%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatPrimeDbl}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}''%
  }%
  \xspace%
}%
```

2.13 New kinship and F_{ST} estimators

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

```
\newcommand{\ktHatPreadj}[1][k]{%
  \ensuremath{%
    \hat{\varphi}_{j#1}\kinshipsymbols@Ts{preadj}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\ktHatPreadjMin}{%
  \ensuremath{%
    \hat{\varphi}_{\text{min}}\kinshipsymbols@Ts{preadj}%
  }%
  \xspace%
}%
```

\ktHatNew $\hat{\varphi}_{jk}^{T,\mathrm{new}}$: New kinship estimator for the pair of individuals j and k (default). The optional argument allows setting another second individual (\ktHatNew[l] gives $\hat{\varphi}_{jl}^{T,\mathrm{new}}$ 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.

```
\newcommand{\ktHatNew}[1][k]{%
  \ensuremath{%
    \hat{\varphi}_{j#1}\kinshipsymbols@Ts{new}%
  }%
  \xspace%
}%
```

\ftHatNew $\hat{f}_{j}^{T,\mathrm{new}}$: New inbreeding estimator for individual j (default). The optional argument allows setting other individuals (\ftHatNew[k] gives $\hat{f}_{k}^{T,\mathrm{new}}$ 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.

```
\newcommand{\ftHatNew}[1][j]{%
  \ensuremath{%
    \hat{f}_{#1}\kinshipsymbols@Ts{new}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\FstHatNew}{%
  \ensuremath{%
    \hat{F}_{\text{ST}}^{\text{new}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\AMin}{%
  \ensuremath{%
    A_{\text{Emin}}%
  }%
  \xspace%
}%
```

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

```
\newcommand{\AMinHat}{%
  \ensuremath{%
    \hat{A}_{\text{Emin}}%
  }%
  \xspace%
}%
```

`\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.

```
\newcommand{\mav}{%
  \ensuremath{%
    \overline{p(1-p)}\kinshipsymbols@T%
  }%
  \xspace%
}%
```

2.14 Estimates from Beagle

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

```
\newcommand{\klHatBeagle}{%
  \ensuremath{%
    \hat{\varphi}_{jk}^{L_{jk},\text{beagle}}%
  }%
  \xspace%
}%
```

\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).

```
\newcommand{\flHatBeagle}[1][j]{%
  \ensuremath{%
    \hat{f}_{#1}^{L_{#1},\text{beagle}}%
  }%
  \xspace%
}%
```

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`

```
% after package colortbl is loaded
\makeatletter
\@ifclassloaded{beamer}{%
  \patchcmd\@cline
      {\arrayrulewidth\hfill}% search
      {\arrayrulewidth\hfill\kern\z@}% replace
      {}% success
      {\errmessage{Patching \string\@cline\space failed}}% failure
}{%
  % nothing to do here?
}
\makeatother
```

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

```
\newcommand{\sampleGenMat}{%
  \begin{tabular}{cc}%
    & Individuals \\%
    \arrayrulecolor{genColor}\cline{2-2}%
    \multirow{10}{*}{\rotatebox[origin=c]{90}{Loci}}%
    & \multicolumn{1}{|l|}{0 2 2 1 1 0 1} \\%
    & \multicolumn{1}{|l|}{0 2 1 0 1 } \\%
    & \multicolumn{1}{|l|}{2 ...} \\%
    & \multicolumn{1}{|l|}{ } \\%
    & \multicolumn{1}{|l|}{ } \\%
```

```
304     & \multicolumn{1}{|l|}{ } \\%
305     & \multicolumn{1}{|l|}{ } \\%
306     & \multicolumn{1}{|l|}{ } \\%
307     & \multicolumn{1}{|l|}{ } \\%
308     & \multicolumn{1}{|l|}{ } \\%
309     \arrayrulecolor{genColor}\cline{2-2}%
310     & \\%
311     & $\mathbf{\textcolor{genColor}{X}}$ \\%
312   \end{tabular}%
313 }%
```

Change History

v1.0

General: Initial version 1

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