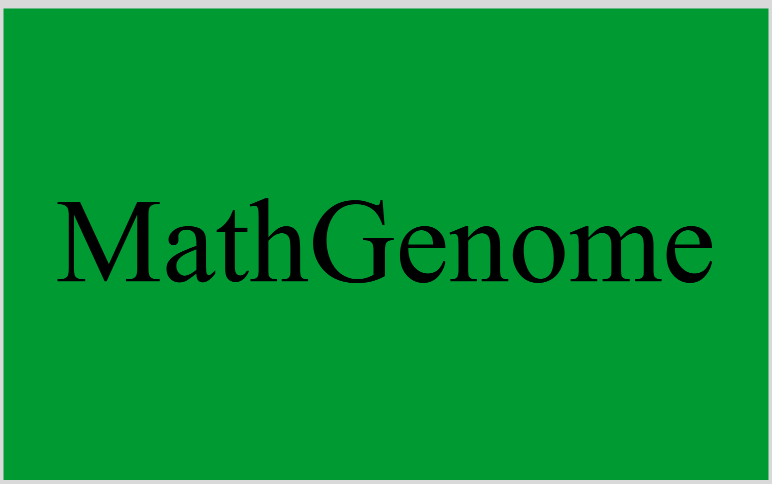
GUIDE TO USE *MathGenome*

M. Humberto Reyes-Valdés
Universidad Autónoma Agraria Antonio Narro

Open a Mathematica notebook

Load MathGenome

```
<< c:\dres\math\mathgenome.m
```



This Mathematica application is being developed by

Humberto Reyes−Valdés

Generate the list of MathGenome commands

```
?Mathgenome`*
```

MathGenome`

Abo	ChiTest	Eftab	HFun	HWMultAllele	IKFun	PathAnalysis	Ssd
ALC	Comp	FreqAl	Hw	ICFun	IPMFun	PMFun	TakeAllele
Avef	Crossing	Gametes	HwAbo	Iden	KFun	RGenotype	Varc
CFun	Cumul	GenDis	Hwmean	IHFun	Nsim	SelecInd	XAlFreq

Click any command to know its purpose and usage, e.g. Abo

```
Abo[# of A, # of B, # of AB, # of O] gives maximum
  likelihood  estimates of the allele frequencies
  for the ABO system f(A),  f(B), f(O) and the support
```

- **This is an example of allele frequency estimation for a set of population observations on the ABO blood group system**

```
Abo[10, 5, 1, 80]

{0.0589262, 0.0316961, 0.909378, -56.984}
```

More examples

- **Mapping functions**

MathGenome contains the mapping functions of Haldane, Kosambi, Carter & Falconer, and Pascoe & Morton. It includes their inverses, which for the second two cases are performed by a numerical method. For the Carter & Falconer function we have:

```
CFun[r] gives genetic distance in
  morgans for a given recombination  fraction r,
  based on Carter and Falconer mapping function
```

```
ICFun[d] gives a recombination fraction
  for a given genetic distance  in morgans d,
  based on Carter and Falconer mapping function
```

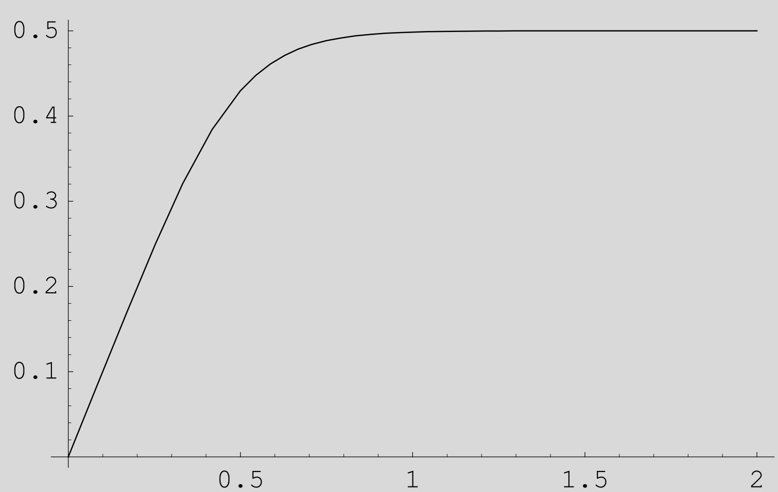
We can transform a recombination value of 0.15 into map distance in morgans, and then to transform this map distance back into recombination. The commands in *Mathematica* are executed with Shift-Enter.

```
CFun[.15]

0.150244
```

```
ICFun[0.150244]

0.15
```

Or we can construct a plot for recombination against map distance

```
Plot[ICFun[x], {x, 0, 2}, PlotRange → All]
```




```
- Graphics -
```

■ Normal simulation

The command NSim simulates sample data from a normal distribution

```
Nsim[mean, standard deviation, n] gives a list
  of n random numbers  from a Normal distribution
  with the especified mean and standard  deviation
```

For example, we can simulate a sample of 200 from a standard normal distribution, i.e. with $\mu = 0$ and $\sigma = 1$

```
mysample = Nsim[0, 1, 200]

{-0.561891, 0.258305, 0.179564, -0.438205, -0.912881, -0.468627,
 -0.280339, 0.249431, 0.366764, 0.619422, 1.98379, 0.00212377,
 -1.10435, -0.588136, -0.179773, 2.22699, 0.0409233, -0.112186,
 -1.59086, 1.14094, -0.826195, 0.769667, 0.292622, 0.168142,
 -0.0214514, -0.091506, -1.6293, 0.0894836, -0.886382,
 -0.786392, 0.124985, -1.60116, 0.366544, -1.11537, -1.74754,
 -0.254965, 0.983607, -0.569193, -0.144348, 0.266146,
 -0.127154, -0.41339, -0.691838, 0.235439, 0.0822275,
 -0.494939, 1.06723, 1.0855, -0.228469, -0.506039, 0.44897,
 -0.0780587, 0.45277, -0.107007, -0.787005, -2.13444,
 1.43236, 0.2681, -0.335425, 0.678534, -1.43055, 0.349978,
 -1.45068, 0.191936, -0.0684144, 0.997098, -0.569324,
 -1.20399, -0.247695, -0.136629, 1.18771, 1.18224, -1.41044,
 -0.124207, 0.276234, 1.15919, 0.464814, 0.321296, -0.00290587,
 -0.529212, -1.29655, -0.567444, -0.39608, -0.548274,
 0.921998, 1.13399, 0.524335, 2.15566, 0.320497, 0.739519,
 -0.00353518, 0.495049, 0.2933, -0.0460152, -0.550596,
 -0.924254, -0.0519496, -2.09898, 0.662241, -0.322255,
 0.607771, -0.585044, 1.27602, -0.162633, 0.412164, 0.0683398,
 0.445419, -0.696536, -1.79346, 1.19839, -0.0972929, -1.08481,
 0.848691, 0.617653, 0.855598, -0.630013, 1.35713, -0.237966,
 0.0566369, -0.899957, 0.510921, -0.464171, -2.08617, 0.853679,
 -0.862431, 1.01763, 0.263956, -0.842318, 0.108626, 0.0466206,
 0.697298, -0.854815, 0.398324, 0.630055, -0.464294, 0.335415,
 -0.388245, -0.628315, 0.72075, 0.672186, 0.475877, 1.18903,
 2.42129, -0.405104, 0.124697, -2.46435, 0.765693, -0.957545,
 0.416229, 1.00443, 0.0289562, -0.395466, 1.90598, 0.179565,
 2.74414, -0.534851, 0.24759, 0.627013, 1.77965, -1.2596,
 -0.307537, -0.467281, -0.863006, 0.196116, -0.579369,
 1.92035, -0.392742, -1.23063, -0.502708, -1.02704, -0.478281,
 0.95271, 1.32598, -0.973757, -0.920142, 0.717374, 0.107631,
 0.749497, 0.257482, 0.0143882, -0.114028, -0.673028,
 -0.527083, -1.51451, -0.159976, 1.3773, -0.150772, 1.04948,
 0.266667, 0.85669, -1.14037, 1.44272, 0.281248, -0.0921035,
 -1.76936, 0.241436, 0.0716571, 1.20264, -2.45512, 0.526521}
```

Since MathGenome automatically loads statistical packages, we can use several commands for statistical calculations, e.g. mean and variance:

```
Mean[mysample]

-0.00102021
```

```
Variance[mysample]

0.841034
```

■ Mendelian crossing

The command Crossing gives the expected outcome of a mendelian crossing with any number of autosomic loci and alleles, for diploid organisms.

```
Crossing[genotype1, genotype2] works out
  the cross of genotype 1 and genotype 2  coded
  as :{{Ai, Aj},{Bi, Bj}, ...}. It gives the array
  of the progeny genotypes, their proportions and
  probabilities. Alleles must be coded as string variables
```

This is the way to cross AaBbCC X aaBBCc:

```
Crossing[{{"A", "a"}, {"B", "b"}, {"C", "C"}},
 {{"a", "a"}, {"B", "B"}, {"C", "c"}}]

{{{{A, a}, {B, B}, {C, C}}, {{A, a}, {B, B}, {C, c}},
  {{A, a}, {B, b}, {C, C}}, {{A, a}, {B, b}, {C, c}},
  {{a, a}, {B, B}, {C, C}}, {{a, a}, {B, B}, {C, c}},
  {{a, a}, {B, b}, {C, C}}, {{a, a}, {B, b}, {C, c}}},
 {1, 1, 1, 1, 1, 1, 1, 1}, {1/8, 1/8, 1/8, 1/8, 1/8, 1/8, 1/8, 1/8}}
```

The output will look better in a table format

```
TableForm[Crossing[{{"A", "a"}, {"B", "b"}, {"C", "C"}},
  {{"a", "a"}, {"B", "B"}, {"C", "c"}}]]
```

A a B B C C	A a B B C c	A a B b C C	A a B b C c	a a B B C C	a a B B C c	a a B b C C	a a B b C c
1	1	1	1	1	1	1	1
$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$	$\frac{1}{8}$

The output can be transposed

```
TableForm[
 Transpose[Crossing[{{"A", "a"}, {"B", "b"}, {"C", "C"}},
   {{"a", "a"}, {"B", "B"}, {"C", "c"}}]]]
```

A a B B C C		1	$\frac{1}{8}$
A a B B C c		1	$\frac{1}{8}$
A a B b C C		1	$\frac{1}{8}$
A a B b C c		1	$\frac{1}{8}$
a a B B C C		1	$\frac{1}{8}$
a a B B C c		1	$\frac{1}{8}$
a a B b C C		1	$\frac{1}{8}$
a a B b C c		1	$\frac{1}{8}$