CRD Designs	Comment
One-way CRD ***Treatment:*** Treatment ***Block:*** Plot	*Plot* is indexed 1 to **total number** of plots in the experiment (*Treatment* could be unequally replicated. If equally replicated from 1 to $r \times t$.) *Plot* can be omitted.
One-way CRD with Subsampling ***Treatment:*** Treatment ***Block:*** Plot/Subsample	*Plot* is indexed from 1 to $r \times t$ assuming equal replication. *Subsample* is indexed 1 to number of subsamples in each plot. *Subsample* can be omitted, *Plot* cannot.
Two-way CRD	
Treatment: Variety*Chemical ***Block:*** Plot	Must be equally replicated for ANOVA, otherwise use REML. *Plot* is indexed 1 to **total number** of plots in the experiment (= $reps \times v \times c$). *Plot* can be omitted. *This technique allows for any number of treatment factors.*
Split-Plot CRD ***Treatment:*** Variety*Chemical ***Block:*** W_Plot/S_Plot	If *Variety* is the whole-plot treatment (each replicated *r* times) then *W_Plot* is indexed 1 to $r \times v$. Each whole-plot is split into *c* split-units so *S_Plot* is indexed from 1 to *c* for each whole-plot. *S_Plot* can be omitted, *W_Plot* cannot. *This technique allows for any number of whole-plot factors and any number of split-plot factors.*
Split-Plot CRD via REML ***Fixed:*** Variety*Chemical ***Random:*** Plots/S_Plot	As above
Split-Split Plot CRD ***Treatment:*** Irrigation*Stand*Fertilizer ***Block:*** Plot/S_Plot/S_S_Plot ***Block:*** Block/Irrigation/Stand/Fertilizer	In this example, *Irrigation* is replicated *r* times each so *Plot* is indexed from 1 to $r \times i$. Each whole-plot is split into *s* split-units for *Stand* so *S_Plot* is indexed from 1 to *s* for each whole-plot. Each split-plot is split into *f* split-split-units for *Fertiliser*so S_*S_Plot* is indexed from 1 to *f* for each split-plot. *S_S_Plot* can be omitted, *S_Plot* cannot. *This technique allows for any number of whole-plot factors, split-plot factors and split-split-plot factors.* This structure is restricted to one factor per splitting.

RCB Designs	Comment
One-way RCB	
Treatment: Treatment ***Block:*** Block/Plot	*Block* is indexed from 1 to *b.* *Plot* is indexed 1 to *t* in each *block*. *Plot* can be omitted.
One-way RCB with Subsampling ***Treatment:*** Treatment ***Block:*** Block/Plot/Subsample	*Block* is indexed from 1 to *b.* *Plot* is indexed 1 to *t* in each block. *Subsample* is indexed 1 to *s* in each plot. *Subsample* can be omitted, *Plot* cannot.
Two-way RCB	
Treatment: Variety*Chemical ***Block:*** **Block**/Plot	*Block* is indexed from 1 to *b.* *Plot* is indexed 1 to $v \times c$ in each block. *This technique allows for any number of treatment factors.*
Split-Plot RCB ***Treatment:*** Variety*Chemical ***Block:*** Block/W_Plot/S_Plot	If *Variety* is the whole-plot treatment then *W_Plot* is indexed 1 to *v* in each block. Each whole-plot is split into *c* split-units so *S_Plot* is indexed from 1 to *c* for each whole-plot. *S_Plot* can be omitted, *W_Plot* cannot. *This technique allows for any number of whole-plot factors and any number of split-plot factors.*
Split-Plot RCB via REML ***Fixed:*** Cultivar*Chemical ***Random:*** Block/W_Plot/S_Plot	
Split-Split Plot RCB ***Treatment:*** Irrigation*Stand*Fertilizer ***Block:*** Block/W_Plot/S_Plot/S_S_Plot ***Block:*** Block/Irrigation/Stand/Fertilizer	In this example, *Irrigation* is replicated in *b* blocks each containing *i* whole-plots. Each whole-plot is split into *s* split-units for *Stand* so *S_Plot* is indexed from 1 to *s* for each whole-plot. Each split-plot is split into *f* split-split-units for *Fertiliser*so S_*S_Plot* is indexed from 1 to *f* for each split-plot. *S_S_Plot* can be omitted, *S_Plot* cannot. *This technique allows for any number of whole-plot factors, split-plot factors and split-split-plot factors.* This structure is restricted to one factor per splitting.
Strip-Plot (split-block) ***Treatment:*** Cultivar*Chemical ***Block:*** Block/(W_Plot1*W_Plot2) ***Block:*** Block/(Cultivar*Chemical)	Unlike a split-plot, both treatment factors are assigned to two different types of whole plots (*think rows and columns in each block*). The *Block* structure is equivalent to Block + Block.W_Plot1 + Block.W_Plot2 + Block. W_Plot1.W_Plot2 so only Block. W_Plot1.W_Plot2 can be omitted. *This technique allows for any number of whole-plot_1 factors and whole-plot_2 factors.* This structure is restricted to one factor of each whole-plot type.

Latin Square Designs	Comment
One-way Latin Square	
Treatment: Treatment ***Block:*** Row_Block*Column_Block	*Row_Block* and *Column_Block* are each indexed from 1 to *t*. The *Block* structure is equivalent to Row_Block + Column_Block + Row_Block.Column_Block so only Row_Block.Column_Block (which is a plot) can be omitted.
Two-way Latin Square	
Treatment: Variety*Chemical ***Block:*** Row_Block*Column_Block	Assumes both factors are randomised into plots of the Latin Square so you need a (v c) × (v c) square. *This technique allows for any number of treatment factors.*
Split-Plot Latin Square ***Treatment:*** Variety*Chemical ***Block:*** Row_Block*Column_Block	If *Variety* is the whole-plot treatment then a $v \times v$ square is required. Each of the v whole-plot is split into c split-units so *S_Plot* is indexed from 1 to c for each whole-plot. The lowest stratum has been omitted, as GenStat allows, since technically the 4 strata are defined as: Row_Block + Column_Block + Row_Block.Column_Block + Row_Block.Column_Block.S_Plot. *This technique allows for any number of whole-plot factors and any number of split-plot factors.*
Split-Plot Latin Square via REML ***Fixed:*** Cultivar*Chemical ***Random:*** Row_Block + Column_Block + Row_Block.Column_Block + Row_Block.Column_Block.S_Plot or simply ***Random:*** Row_Block*Column_Block and allows the residual term to be added automatically	
Split-Split Plot Latin Square ***Treatment:*** A*B*C ***Block:*** Row_Block + Column_Block + Row_Block.Column_Block + Row_Block.Column_Block.S_Plot + Row_Block.Column_Block.S_Plot.S_S_Plot	If A is the whole-plot treatment then an $a \times a$ square is required. Each of the a whole-plot is split into b split-units so *S_Plot* is indexed from 1 to b for each whole-plot. Each of these is split into c split-split-plots. There are 5 strata (rows, columns, whole plots, split-plots and split-split plots). The lowest stratum can be omitted. *This technique allows for any number of whole-plot factors and any number of split-plot factors.*