**Section 4 VC structures**

**4.1 Compound Symmetry**

Assumes that the variance-covariance structure has a single variance (represented by ) for all 3 of the time points and a single covariance (represented by ) for each of the pairs of trials.  This structure is illustrated by the half matrix below.

  
   
  

**4.2 Unstructured**

Assumes that each variance and covariance is unique.   Each trial has its own variance (e.g.  is the variance of trial 1) and each pair of trials has its own covariance (e.g.  is the covariance of trial 1 and trial2).  This structure is illustrated by the half matrix below.

  
   
  

|  |  |
| --- | --- |
| Unstructured (UN)  The variances are constrained to be nonnegative, and the covariances are unconstrained. | http://support.sas.com/documentation/cdl/en/statug/63033/HTML/default/images/statug_mixed0277.png |
| Compound Symmetry (CS)  This structure requires constant variance and constant covariance. | http://support.sas.com/documentation/cdl/en/statug/63033/HTML/default/images/statug_mixed0276.png |

**Diagonal**

> pd1 <- pdMat(diag(1:4), pdClass = "pdDiag")

> pd1

Positive definite matrix structure of class **pdDiag** representing

[,1] [,2] [,3] [,4]

[1,] 1 0 0 0

[2,] 0 2 0 0

[3,] 0 0 3 0

[4,] 0 0 0 4

**Compound Symmetry**

> pd1 <- pdCompSymm(diag(3) + 1, nam = c("A","B","C"))

> pd1

Positive definite matrix structure of class pdCompSymm representing

**A B C**

**A 2 1 1**

**B 1 2 1**

**C 1 1 2**

**Symmetric**

The symmetric variance-covariance matrix is the “unstructured” form in SAS terminology.

**Blocked**

> pd1 <- pdBlocked(list(diag(1:2), diag(c(0.1, 0.2, 0.3))),+ nam = list(c("A","B"), c("a1", "a2", "a3")))

> pd1

Positive definite matrix structure of class **pdBlocked** representing

**A B a1 a2 a3**

**A 1 0 0.0 0.0 0.0**

**B 0 2 0.0 0.0 0.0**

**a1 0 0 0.1 0.0 0.0**

**a2 0 0 0.0 0.2 0.0**

**a3 0 0 0.0 0.0 0.3**