

Summary G2F Variance Components analyses

Variance components

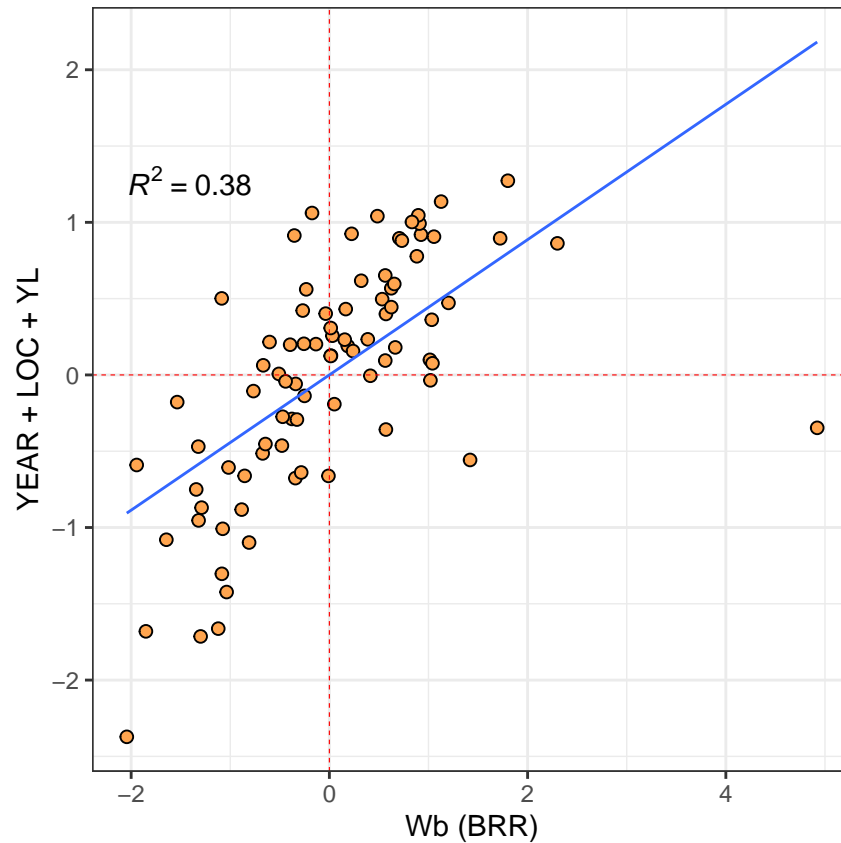
Model M2a was fitted including EC with Gaussian prior and model M2b EC are assumed a Bayes C prior

M	Model	Year	Loc	Year-Loc	(Year-Loc)	Wb	G	Error
M1	YEAR+LOC+YL+G	0.111	0.312	0.251	0.571		0.076	0.42
M2a	Wb+G					1.376	0.076	0.426
M2b	Wb+G					1.893	0.076	0.425
M3a	LOC+Wb+G		0.349			0.809	0.076	0.425
M3b	LOC+Wb+G		0.475			1.026	0.076	0.424

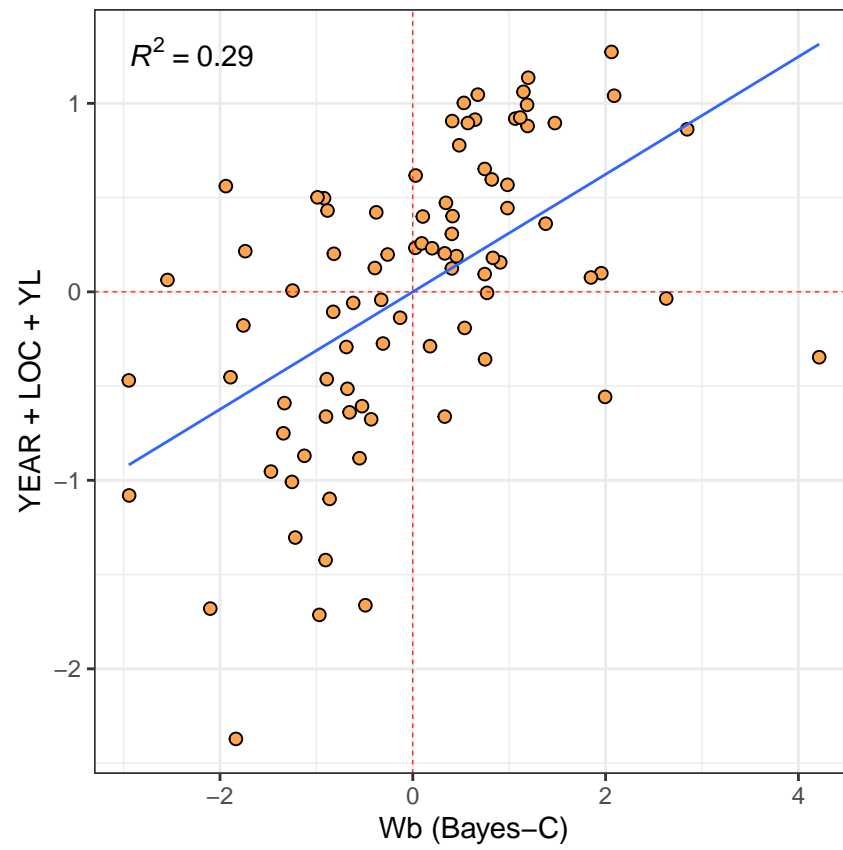
a: Effects are assumed Gaussian prior, b: Effects with Bayes C

Mean effects of *year – location* vs **Wb**

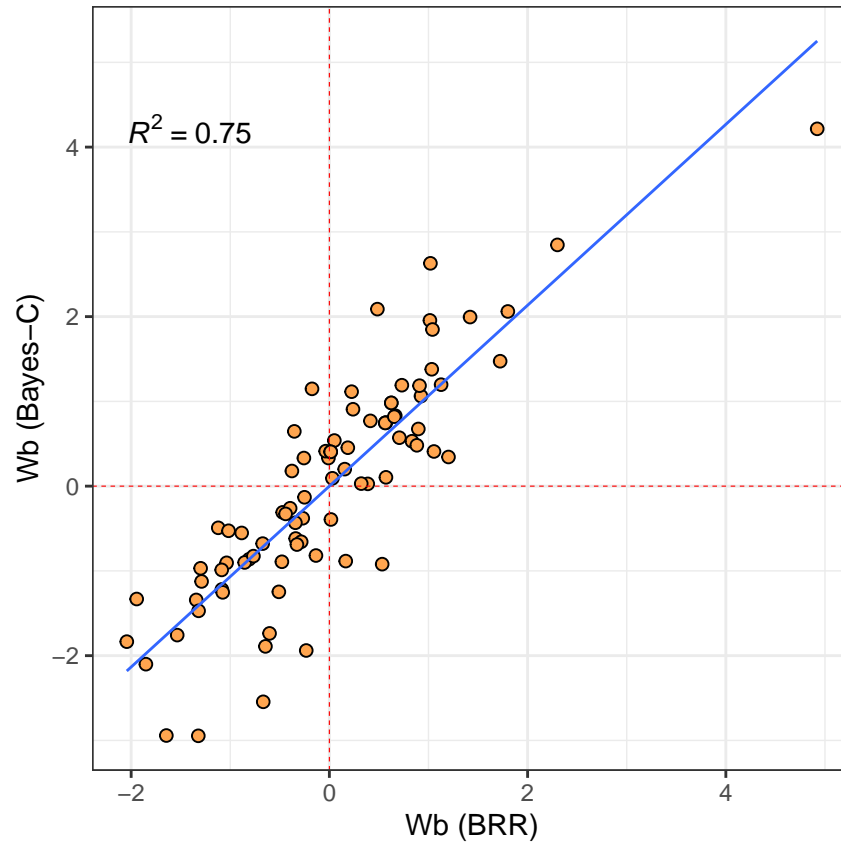
```
print(pp1)
```



```
print(pp2)
```



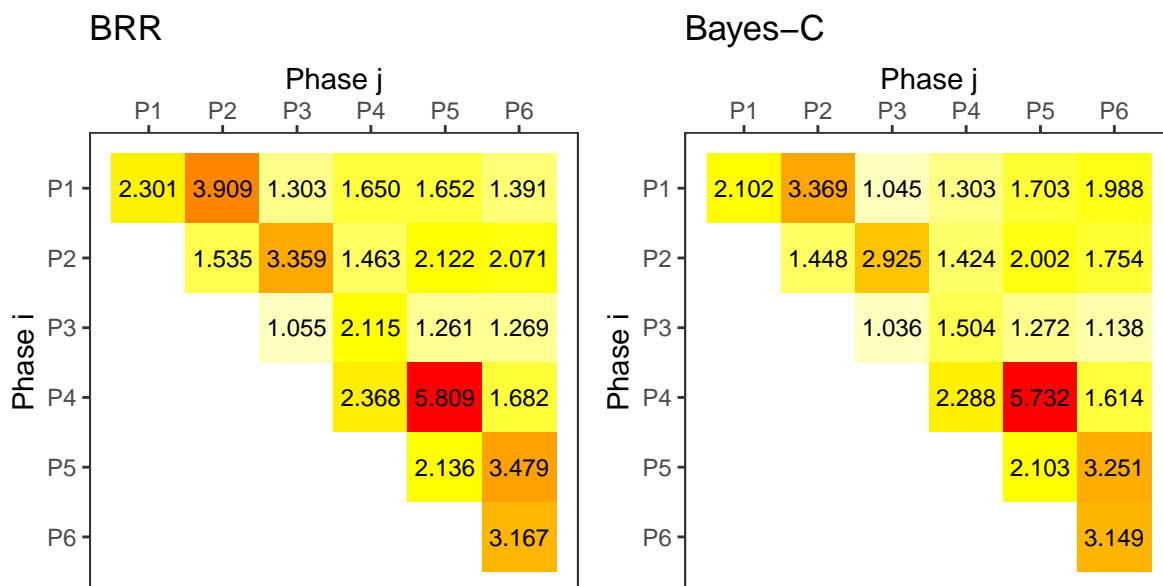
```
print(pp3)
```



Sequential variance

Variance explained by Wb using EC from Phase i to Phase j

```
ggarrange(pp1, pp2)
```



Separation of variance by groups

```
B1 <- readBinMat(paste0("../Output/run_VC_full_model/M",names(models0)[1],"_ETA_W1_b.bin"))
B2 <- readBinMat(paste0("../Output/run_VC_full_model/M",names(models0)[2],"_ETA_W2_b.bin"))

hc <- hclust(dist(t(W)), method="ward.D")

get_VC_partition <- function(ng,hc,W=W,B=B)
{
  group <- cutree(hc, k=ng)
  Groups <- unique(group)

  # Get variances and covariances
  COV <- matrix(NA,nrow=length(Groups),ncol=length(Groups))
  dimnames(COV) <- list(Groups,Groups)

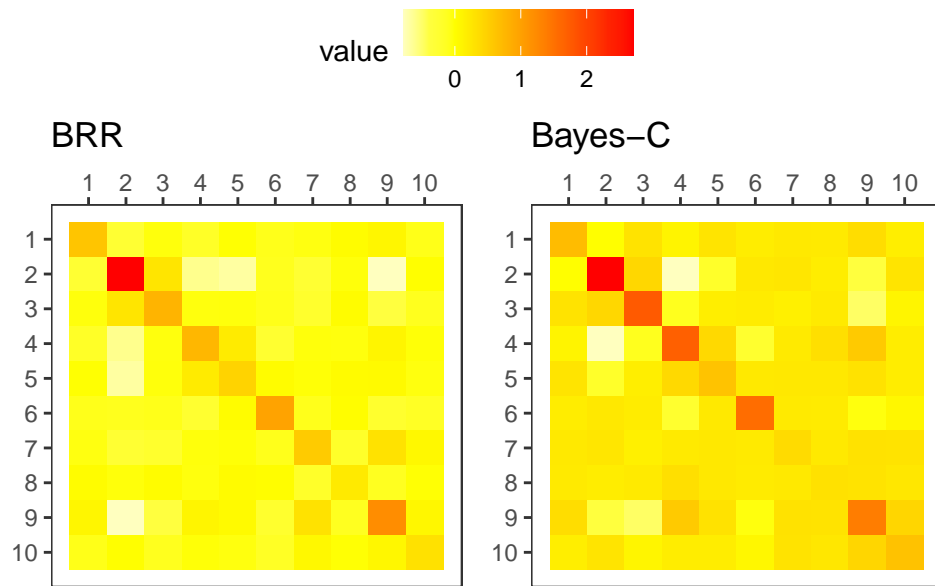
  for(i in 1:length(Groups)){
    index <- which(group %in% Groups[i])
    ffi <- W[,index] %*% t(as.matrix(B[,index]))

    for(j in i:length(Groups)){
      index <- which(group %in% Groups[j])
      ffj <- W[,index] %*% t(as.matrix(B[,index]))

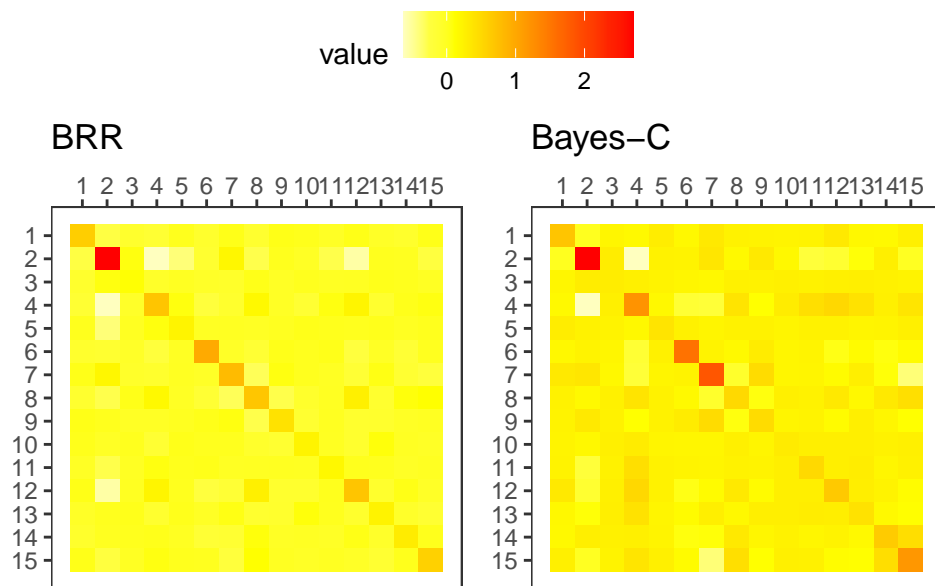
      tmp <- unlist(lapply(1:nrow(B),function(k)cov(ffi[,k],ffj[,k])))
      COV[i,j] <- COV[j,i] <- mean(tmp)
    }
  }
  COV
}
```

Hierarchical clustering applied to a distance among ECs.

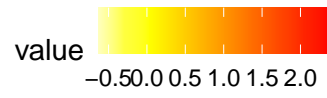
$k = 10$ groups



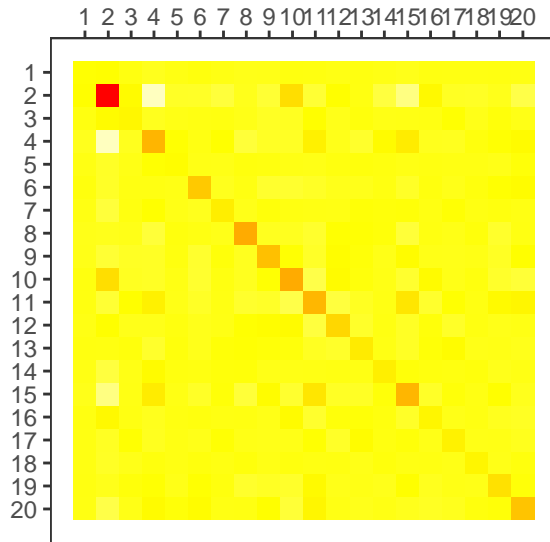
$k = 15$ groups



$k = 20$ groups



BRR



Bayes-C

