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#### This file contains first a collation of the parameters for ML analyses in
     Table 1
#### Then the parameters for the real life sampling designs
# For REML analyses, use HLmethod='REML'
# For PQL/L analyses, use HLmethod='PQL/L'
####
## binomial/CAn40r10s40v01b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=40,rho=10,size=40,sigma2_u=0.1,beta=0,alpha
    =0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CBn40r10s40v2p5b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=40,rho=10,size=40,sigma2_u=2.5,alpha=0,beta
    =0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CCn40r10n4s40v01b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=40,rho=10,nu=4,size=40,sigma2_u=0.1,alpha
    =0,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CDn40r10n4s40v2p5b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=40,rho=10,nu=4,size=40,sigma2_u=2.5,alpha
    =0,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CEn40r10sp6s40v01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=40,rho=10,size=40,sigma2_u=0.1,
    alpha=0,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CFn40r10sp6s40v2p5b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=40,rho=10,size=40,sigma2_u=2.5,
    alpha=-1,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CGn40r10n4sp6s40v01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=40,rho=10,nu=4,size=40,sigma2_u
    =0.1,alpha=-1,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binomial/CHn40r10n4sp6s40v2p5b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=40,rho=10,nu=4,size=40,sigma2_u
    =2.5,alpha=-1,eta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))

## binary/Kn100r10s1v01b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=100,rho=10,size=1,sigma2_u=0.1,beta=0,
    HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(lambda=5))
## binary/Nn100r10s1v2p5b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=100,rho=10,nu=0.5,size=1,sigma2_u=2.5,beta
    =0,HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(lambda=5))
## binary/Mn100r10n4s1v01b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=100,rho=10,nu=4,size=1,sigma2_u=0.1,beta=0,
    HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(lambda=5))
## binary/Ln100r10n4s1v2p5b0H11iYes/arglist.R
arglist <- list(objective="p_v",nb=100,rho=10,nu=4,size=1,sigma2_u=2.5,beta=0,
    HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(lambda=5))
## binary/APn100r10sp6s1v01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=100,rho=10,size=1,sigma2_u=0.1,
    beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(lambda=5)
    )
## binary/AQn100r10sp6s1v2p5b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=100,rho=10,nu=0.5,size=1,sigma2
    _u=2.5,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05))
## binary/ARn100r10n4sp6s1v01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective="p_v",nb=100,rho=10,nu=4,size=1,sigma2_u
    =0.1,beta=0,HLmethod='ML',init.corrHLfit=list(lambda=0.05),upper=list(
    lambda=5))
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## binary/ASn100r10n4sp6s1v2p5b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,nb=100,rho=10,nu=4,size=1,sigma2_u
    =2.5,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05),upper=list(
    lambda=5))

## poisson/BQn40r10b16vlowb0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”poisson”,nb=40,rho=10,base=15,alpha=0,
    sigma2_u=0.06,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05))
## poisson/BRn40r10b11vhighb0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”poisson”,nb=40,rho=10,base=10,alpha=0,
    sigma2_u=0.763,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05))
## poisson/BSn40r10n4b16vlowb0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”poisson”,nb=40,nu=4,rho=10,alpha=0,
    base=15,sigma2_u=0.06,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda
    =0.05))
## poisson/BTn40r10n4b11vhighb0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”poisson”,nu=4,nb=40,rho=10,alpha=0,
    base=10,sigma2_u=0.763,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda
    =0.05))
## poisson/BUn40r10sp6b16vlowb0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”poisson”,nb=40,rho=10,
    alpha=0,base=15,sigma2_u=0.06,beta=0,HLmethod=’ML’,init.corrHLfit=list(
    lambda=0.05))
## poisson/BVn40r10sp6b11vhighb0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”poisson”,nb=40,rho=10,
    alpha=0,base=10,sigma2_u=0.763,beta=0,HLmethod=’ML’,init.corrHLfit=list(
    lambda=0.05))
## poisson/BWn40r10n4sp6b16vlowb0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”poisson”,nb=40,nu=4,rho
    =10,alpha=0,base=15,sigma2_u=0.06,beta=0,HLmethod=’ML’,init.corrHLfit=list
    (lambda=0.05))
## poisson/BXn40r10n4sp6b11vhighb0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”poisson”,nu=4,nb=40,rho
    =10,alpha=0,base=10,sigma2_u=0.763,beta=0,HLmethod=’ML’,init.corrHLfit=
    list(lambda=0.05))

## LMM/Vn40r10s40v01p01b0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”gaussian”,nb=40,rho=10,size=40,sigma2_
    u=0.1,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,phi=0.05))
## LMM/Wn40r10s40v2p5P01b0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”gaussian”,nb=40,rho=10,size=40,sigma2_
    u=2.5,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,phi=0.05))
## LMM/Xn40r10n4s40v01P01b0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”gaussian”,nb=40,rho=10,nu=4,size=40,
    sigma2_u=0.1,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,phi
    =0.05))
## LMM/Yn40r10n4s40v2p5P01b0H11iYes/arglist.R
arglist <- list(objective=”p_v”,family=”gaussian”,nb=40,rho=10,nu=4,size=40,
    sigma2_u=2.5,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,phi
    =0.05))
## LMM/ALn40r10sp6s40v01P01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”gaussian”,nb=40,rho=10,
    size=40,sigma2_u=0.1,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,
    phi=0.05))
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## LMM/AMn40r10sp6s40v2p5P01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”gaussian”,nb=40,rho=10,
    size=40,sigma2_u=2.5,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,
    phi=0.05))
## LMM/AVn40r10n4s40v01P01b0H11iYes/arglist.R
# Example with bootstrap replicates:
# arglist <- list(boot.repl=100,spread=6/10,objective=”p_v”,family=”gaussian”,
    nb=40,rho=10,nu=4,size=40,sigma2_u=0.1,beta=0,HLmethod=’ML’,init.corrHLfit
    =list(lambda=0.05,phi=0.05))
## LMM/AOn40r10n4s40v2p5P01b0H11iYes/arglist.R
arglist <- list(spread=6/10,objective=”p_v”,family=”gaussian”,nb=40,rho=10,nu
    =4,size=40,sigma2_u=2.5,beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda
    =0.05,phi=0.05))

#### Sampling design from Loa loa prevalence study
arglist <- list(objective=”p_v”,rbdesign=”Loaloa”,rho=1/0.7,sigma2_u=1,beta=0,
    HLmethod=’ML’,init.corrHLfit=list(lambda=0.5))

#### Same for analysis by glmmPQL
arglist <- list(corSt=”corMatern”,objective=”p_v”,rbdesign=”Loaloa”,rho=1/0.7,
    sigma2_u=1,beta=0,init.corrHLfit=list(lambda=0.5),upper=list(loglambda=5),
    minimalOutput=T)

#### Sampling desing from migration gene study, example with bootstrap
    replicates:
arglist <- list(boot.repl=100,family=”gaussian”,objective=”p_v”,rbdesign=”
    blackcap”,rho=0.055,nu=0.63,sigma2_u=0.55,phi=0.0003,
beta=0,HLmethod=’ML’,init.corrHLfit=list(lambda=0.05,phi=0.05),upper=list(
    loglambda=5))
```