Arena

orgdat = data.frame
specs = list
media = list
phenotypes = list
mediac = character
occmat = Matrix
tstep = numeric
stir = logical
n = integer
m = integer

addOrg()
addSubs()
changeSub()
changeOrg()
checkPhen()
simulate()
stirEnv()
dat2mat()
changeDiff()
getSublb()

Substance

smax = numeric
diffmat = Matrix
name = character
difunc = character
difspeed = numeric

diffuseR()
diffuseCpp()

Organism

lbnd = numeric
ubnd = numeric
type = character
medium = character
lpobj = sysBiolAlg
fbasol = list
lyse = logical
feat = list
deathrate = numeric
duplirate = numeric
growthlimit = numeric
growtype = character

constrain()
consume()
emptyHood()
getHood()
getPhenotype()
growExp()
growLin()
optimizeLP()
lysis()

Eval

medlist = list
simlist = list
subchange = numeric

addEval()
evalArena()
getArena()
extractMed()
plotCurves()
getPhenoMat()
minePheno()

Bac

speed = integer
budge = logical
chem = character

growth()
move()
chemotaxis()
budging()
simBac()

Human

objective = character

changeFobj()
cellgrowth()
simHum()