

Assana E., Awah-Ndukum J., Zoli A.P., Etchike C.A., Mebenga A.S., Chepnda V., Donadeu M., Dungu B., 2019. Assessing the pig population at risk of *Taenia solium* cysticercosis and subsequent financial losses in Western and Central Africa. Supplementary material. *Rev. Elev. Med. Vet. Pays Trop.*, 72 (2): 73-81, doi: 10.19182/remvt.31257

Supplementary material I: The codes for the R model

Countries	codes
Angola	ang
Burkina Faso	burk
Burundi	bur
Cameroon	cam
Chad	cha
Côte d'Ivoire	coi
Democratic republic of Congo	drc
Gambia	gam
Ghana	gha
Nigeria	nig
Senegal	sen
Togo	tog
Rwanda	rwa
Central African Republic	cen
Guinea Bissau	gub
Benin	ben
Liberia	lib
Gabon	gab
Guinea	gui
Congo	con
Cabo Verde	cab
Mali	mal
Sierra Leone	sie
Niger	nir
Sao Tomé and Príncipe	sao
South Sudan	sou
Equatorial Guinea	gue
Zambia	zam
Porcine cysticercosis	pc
Prevalence	prev
System	syst

Supplementary material II: Rmodel for the calculation of the number of pig at risk of *T. solium* infection, the number of infected pigs with *T. solium* cysticerci diagnosed by tongue and meat inspection and related economic losses

```
number.infected.pig <- function()
{
#####
number.iterations <- 100000
number.population.pig.scavenging.syst <- integer(number.iterations)
number.population.pig.semi.intensive.syst <- integer(number.iterations)
number.population.pig.modern.syst <- integer(number.iterations)
number.population.pig.risk <- integer(number.iterations)
number.population.pig.risk.ang<- integer(number.iterations)
number.population.pig.risk.burk <- integer(number.iterations)
number.population.pig.risk.bur <- integer(number.iterations)
number.population.pig.risk.cam <- integer(number.iterations)
number.population.pig.risk.cha <- integer(number.iterations)
number.population.pig.risk.coi <- integer(number.iterations)
number.population.pig.risk.drc <- integer(number.iterations)
number.population.pig.risk.gam <- integer(number.iterations)
number.population.pig.risk.gha <- integer(number.iterations)
number.population.pig.risk.nig <- integer(number.iterations)
number.population.pig.risk.sen <- integer(number.iterations)
number.population.pig.risk.tog <- integer(number.iterations)
number.population.pig.risk.rwa <- integer(number.iterations)
number.population.pig.risk.zam <- integer(number.iterations)
number.population.pig.risk.cen <- integer(number.iterations)
number.population.pig.risk.gub <- integer(number.iterations)
number.population.pig.risk.ben <- integer(number.iterations)
number.population.pig.risk.lib <- integer(number.iterations)
number.population.pig.risk.gab <- integer(number.iterations)
number.population.pig.risk.gui <- integer(number.iterations)
number.population.pig.risk.con <- integer(number.iterations)
number.population.pig.risk.cab <- integer(number.iterations)
number.population.pig.risk.mal <- integer(number.iterations)
number.population.pig.risk.sie <- integer(number.iterations)
number.population.pig.risk.nir <- integer(number.iterations)
number.population.pig.risk.sao <- integer(number.iterations)
number.population.pig.risk.sou <- integer(number.iterations)
number.population.pig.risk.gue <- integer(number.iterations)
number.infected.pig.ang <- integer(number.iterations)
number.infected.pig.burk <- integer(number.iterations)
number.infected.pig.bur <- integer(number.iterations)
number.infected.pig.cam <- integer(number.iterations)
number.infected.pig.cha <- integer(number.iterations)
number.infected.pig.coi <- integer(number.iterations)
```

```
number.infected.pig.drc <- integer(number.iterations)
number.infected.pig.gam <- integer(number.iterations)
number.infected.pig.gha <- integer(number.iterations)
number.infected.pig.nig <- integer(number.iterations)
number.infected.pig.sen <- integer(number.iterations)
number.infected.pig.tog <- integer(number.iterations)
number.infected.pig.rwa <- integer(number.iterations)
number.infected.pig.zam <- integer(number.iterations)
number.infected.pig.ben <- integer(number.iterations)
number.heavy.infect <- integer(number.iterations)
cost.trader <- numeric(number.iterations)
cost.butcher <- numeric(number.iterations)
income.pig<- numeric(number.iterations)
income.per.farmer<- numeric(number.iterations)
cost.pc.reduce <- numeric(number.iterations)
cost.pc.reduce.farmer <- numeric(number.iterations)
cost.pc.reduce.farmer.country <- numeric(number.iterations)
cost.pc <- numeric(number.iterations)
cost.per.pc <- numeric(number.iterations)
number.infected.pig <- numeric(number.iterations)
total.cost.treat.pig <- numeric(number.iterations)
cost.pc.ang <- numeric(number.iterations)
cost.pc.ben <- numeric(number.iterations)
cost.pc.burk <- numeric(number.iterations)
cost.pc.bur <- numeric(number.iterations)
cost.pc.cam <- numeric(number.iterations)
cost.pc.cha <- numeric(number.iterations)
cost.pc.coi <- numeric(number.iterations)
cost.pc.drc <- numeric(number.iterations)
cost.pc.gam <- numeric(number.iterations)
cost.pc.gha <- numeric(number.iterations)
cost.pc.nig <- numeric(number.iterations)
cost.pc.sen <- numeric(number.iterations)
cost.pc.tog <- numeric(number.iterations)
cost.pc.rwa <- numeric(number.iterations)
cost.pc.zam <- numeric(number.iterations)
prob.heavy.infect.alpha <- 13
prob.heavy.infect.beta <- 114
population.pig <- 22562685
population.pig.ang <- 2874400
population.pig.burk <- 2345800
population.pig.bur <- 479197
population.pig.cam <- 1800000
population.pig.cha <- 33000
population.pig.coi <- 370000
population.pig.drc <- 991727
population.pig.gam <- 8192
population.pig.gha <- 682000
population.pig.nig <- 7066905
population.pig.sen <- 397400
```

population.pig.tog <- 467570
population.pig.rwa <- 1015000
population.pig.zam <- 1100000
population.pig.cen <- 1000000
population.pig.gub <- 463000
population.pig.ben <- 431000
population.pig.lib <- 290000
population.pig.gab <- 220000
population.pig.gui <- 106000
population.pig.con <- 95000
population.pig.cab <- 85000
population.pig.mal <- 77288
population.pig.sie <- 65000
population.pig.nir <- 42500
population.pig.sao <- 35000
population.pig.sou <- 14406
population.pig.gue <- 6800
number.pigs.per.farmer.li <- 2
number.pigs.per.farmer.ls <- 6
price.pig.li <- 70
price.pig.ls <- 122
price.pig.trader.level.li <- 90
price.pig.trader.level.ls <- 180
price.loss.pig.farmer <- 28.8
price.loss.pig.trader <- 40.5
cost.treat.pig.li <- 0.4
cost.treat.pig.ls <- 1.53
population.pig.scavenging.syst.li <- 0.2
population.pig.scavenging.syst.ls <- 0.4
population.pig.semi.intensive.syst.li <- 0.5
population.pig.semi.intensive.syst.ls <- 0.7
population.pig.modern.syst.li <- 0.1
population.pig.modern.syst.ls <- 0.2
population.pig.risk.li <- 0.6
population.pig.risk.ls <- 0.9
population.pig.risk.ang.li <- 0.6
population.pig.risk.ang.ls <- 0.9
population.pig.risk.burk.li <- 0.7
population.pig.risk.burk.ls <- 0.9
population.pig.risk.bur.li <- 0.6
population.pig.risk.bur.ls <- 0.9
population.pig.risk.cam.li <- 0.8
population.pig.risk.cam.ls <- 0.9
population.pig.risk.cha.li <- 0.8
population.pig.risk.cha.ls <- 0.9
population.pig.risk.coi.li <- 0.6
population.pig.risk.coi.ls <- 0.9
population.pig.risk.drc.li <- 0.8
population.pig.risk.drc.ls <- 0.9
population.pig.risk.gam.li <- 0.6

population.pig.risk.gam.ls <- 0.9
population.pig.risk.gha.li <- 0.6
population.pig.risk.gha.ls <- 0.9
population.pig.risk.nig.li <- 0.6
population.pig.risk.nig.ls <- 0.8
population.pig.risk.sen.li <- 0.6
population.pig.risk.sen.ls <- 0.9
population.pig.risk.tog.li <- 0.6
population.pig.risk.tog.ls <- 0.9
population.pig.risk.rwa.li <- 0.6
population.pig.risk.rwa.ls <- 0.9
population.pig.risk.zam.li <- 0.7
population.pig.risk.zam.ls <- 0.9
population.pig.risk.cen.li <- 0.6
population.pig.risk.cen.ls <- 0.9
population.pig.risk.gub.li <- 0.6
population.pig.risk.gub.ls <- 0.9
population.pig.risk.ben.li <- 0.6
population.pig.risk.ben.ls <- 0.9
population.pig.risk.lib.li <- 0.6
population.pig.risk.lib.ls <- 0.9
population.pig.risk.gab.li <- 0.6
population.pig.risk.gab.ls <- 0.9
population.pig.risk.gui.li <- 0.6
population.pig.risk.gui.ls <- 0.9
population.pig.risk.con.li <- 0.6
population.pig.risk.con.ls <- 0.9
population.pig.risk.cab.li <- 0.6
population.pig.risk.cab.ls <- 0.9
population.pig.risk.mal.li <- 0.6
population.pig.risk.mal.ls <- 0.9
population.pig.risk.sie.li <- 0.6
population.pig.risk.sie.ls <- 0.9
population.pig.risk.nir.li <- 0.6
population.pig.risk.nir.ls <- 0.9
population.pig.risk.sao.li <- 0.6
population.pig.risk.sao.ls <- 0.9
population.pig.risk.sou.li <- 0.6
population.pig.risk.sou.ls <- 0.9
population.pig.risk.gue.li <- 0.6
population.pig.risk.gue.ls <- 0.9
prev.pc.ang.li <- 0.01
prev.pc.ang.ls <- 0.07
prev.pc.ben.li <- 0.03
prev.pc.ben.ls <- 0.09
prev.pc.burk.li <- 0.06
prev.pc.burk.ls <- 0.32
prev.pc.bur.li <- 0.02
prev.pc.bur.ls <- 0.39
prev.pc.cam.li <- 0.11

```

prev.pc.cam.ls <- 0.22
prev.pc.cha.li <- 0.16
prev.pc.cha.ls <- 0.26
prev.pc.coi.li <- 0.001
prev.pc.coi.ls <- 0.025
prev.pc.drc.li <- 0.05
prev.pc.drc.ls <- 0.12
prev.pc.gam.li <- 0.001
prev.pc.gam.ls <- 0.020
prev.pc.gha.li <- 0.06
prev.pc.gha.ls <- 0.12
prev.pc.nig.li <- 0.06
prev.pc.nig.ls <- 0.21
prev.pc.sen.li <- 0.010
prev.pc.sen.ls <- 0.041
prev.pc.tog.li <- 0.06
prev.pc.tog.ls <- 0.17
prev.pc.rwa.li <-0.02
prev.pc.rwa.ls <- 0.2
prev.pc.zam.li <- 0.09
prev.pc.zam.ls <- 0.12
#####
####
for(i in 1:number.iterations)
{
prev.pc.ang <- runif(1, prev.pc.ang.li, prev.pc.ang.ls)
number.infected.pig.ang[i] <- rbinom(1,population.pig.ang,prev.pc.ang)
cost.pc.ang[i] <- number.infected.pig.ang[i]*price.loss.pig.farmer
prev.pc.ben <- runif(1, prev.pc.ben.li, prev.pc.ben.ls)
number.infected.pig.ben[i] <- rbinom(1,population.pig.ben,prev.pc.ben)
cost.pc.ben[i] <- number.infected.pig.ben[i]*price.loss.pig.farmer
prev.pc.burk <- runif(1, prev.pc.burk.li, prev.pc.burk.ls)
number.infected.pig.burk[i] <- rbinom(1,population.pig.burk,prev.pc.burk)
cost.pc.burk[i] <- number.infected.pig.burk[i]*price.loss.pig.farmer
prev.pc.bur <- runif(1, prev.pc.bur.li, prev.pc.bur.ls)
number.infected.pig.bur[i] <- rbinom(1,population.pig.bur,prev.pc.bur)
cost.pc.bur[i] <- number.infected.pig.bur[i]*price.loss.pig.farmer
prev.pc.cam <- runif(1, prev.pc.cam.li, prev.pc.cam.ls)
number.infected.pig.cam[i] <- rbinom(1,population.pig.cam,prev.pc.cam)
cost.pc.cam[i] <- number.infected.pig.cam[i]*price.loss.pig.farmer
prev.pc.cha <- runif(1, prev.pc.cha.li, prev.pc.cha.ls)
number.infected.pig.cha[i] <- rbinom(1,population.pig.cha,prev.pc.cha)
cost.pc.cha[i] <- number.infected.pig.cha[i]*price.loss.pig.farmer
prev.pc.coi <- runif(1, prev.pc.coi.li, prev.pc.coi.ls)
number.infected.pig.coi[i] <- rbinom(1,population.pig.coi,prev.pc.coi)
cost.pc.coi[i] <- number.infected.pig.coi[i]*price.loss.pig.farmer
prev.pc.drc <- runif(1, prev.pc.drc.li, prev.pc.drc.ls)
number.infected.pig.drc[i] <- rbinom(1,population.pig.drc,prev.pc.drc)
cost.pc.drc[i] <- number.infected.pig.drc[i]*price.loss.pig.farmer
prev.pc.gam <- runif(1, prev.pc.gam.li, prev.pc.gam.ls)

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```

number.infected.pig.gam[i] <- rbinom(1,population.pig.gam,prev.pc.gam)
cost.pc.gam[i] <- number.infected.pig.gam[i]*price.loss.pig.farmer
prev.pc.gha <- runif(1, prev.pc.gha.li, prev.pc.gha.ls)
number.infected.pig.gha[i] <- rbinom(1,population.pig.gha,prev.pc.gha)
cost.pc.gha[i] <- number.infected.pig.gha[i]*price.loss.pig.farmer
prev.pc.nig <- runif(1, prev.pc.nig.li, prev.pc.nig.ls)
number.infected.pig.nig[i] <- rbinom(1,population.pig.nig,prev.pc.nig)
cost.pc.nig[i] <- number.infected.pig.nig[i]*price.loss.pig.farmer
prev.pc.sen <- runif(1, prev.pc.sen.li, prev.pc.sen.ls)
number.infected.pig.sen[i] <- rbinom(1,population.pig.sen,prev.pc.sen)
cost.pc.sen[i] <- number.infected.pig.sen[i]*price.loss.pig.farmer
prev.pc.tog <- runif(1, prev.pc.tog.li, prev.pc.tog.ls)
number.infected.pig.tog[i] <- rbinom(1,population.pig.tog,prev.pc.tog)
cost.pc.tog[i] <- number.infected.pig.tog[i]*price.loss.pig.farmer
prev.pc.rwa <- runif(1, prev.pc.rwa.li, prev.pc.rwa.ls)
number.infected.pig.rwa[i] <- rbinom(1,population.pig.rwa,prev.pc.rwa)
cost.pc.rwa[i] <- number.infected.pig.rwa[i]*price.loss.pig.farmer
prev.pc.zam <- runif(1, prev.pc.zam.li, prev.pc.zam.ls)
number.infected.pig.zam[i] <- rbinom(1,population.pig.zam,prev.pc.zam)
cost.pc.zam[i] <- number.infected.pig.zam[i]*price.loss.pig.farmer
population.pig.scavenging.syst <- runif(1, population.pig.scavenging.syst.li,
population.pig.scavenging.syst.ls)
number.population.pig.scavenging.syst[i] <-
rbinom(1,population.pig,population.pig.scavenging.syst)
population.pig.semi.intensive.syst <- runif(1, population.pig.semi.intensive.syst.li,
population.pig.semi.intensive.syst.ls)
number.population.pig.semi.intensive.syst[i] <-
rbinom(1,population.pig,population.pig.semi.intensive.syst)
population.pig.modern.syst <- runif(1, population.pig.modern.syst.li,
population.pig.modern.syst.ls)
number.population.pig.modern.syst[i] <-
rbinom(1,population.pig,population.pig.modern.syst)
population.pig.risk <- runif(1, population.pig.risk.li, population.pig.risk.ls)
number.population.pig.risk[i] <- rbinom(1,population.pig,population.pig.risk)
population.pig.risk.ang <- runif(1, population.pig.risk.ang.li, population.pig.risk.ang.ls)
number.population.pig.risk.ang <- rbinom(1,population.pig.ang,population.pig.risk.ang)
population.pig.risk.burk <- runif(1, population.pig.risk.burk.li, population.pig.risk.burk.ls)
number.population.pig.risk.burk <- rbinom(1,population.pig.burk,population.pig.risk.burk)
population.pig.risk.bur <- runif(1, population.pig.risk.bur.li, population.pig.risk.bur.ls)
number.population.pig.risk.bur <- rbinom(1,population.pig.bur,population.pig.risk.bur)
population.pig.risk.cam <- runif(1, population.pig.risk.cam.li, population.pig.risk.cam.ls)
number.population.pig.risk.cam <- rbinom(1,population.pig.cam,population.pig.risk.cam)
population.pig.risk.cha <- runif(1, population.pig.risk.cha.li, population.pig.risk.cha.ls)
number.population.pig.risk.cha <- rbinom(1,population.pig.cha,population.pig.risk.cha)
population.pig.risk.coi <- runif(1, population.pig.risk.coi.li, population.pig.risk.coi.ls)
number.population.pig.risk.coi <- rbinom(1,population.pig.coi,population.pig.risk.coi)
population.pig.risk.drc <- runif(1, population.pig.risk.drc.li, population.pig.risk.drc.ls)
number.population.pig.risk.drc <- rbinom(1,population.pig.drc,population.pig.risk.drc)
population.pig.risk.gam <- runif(1, population.pig.risk.gam.li, population.pig.risk.gam.ls)
number.population.pig.risk.gam <- rbinom(1,population.pig.gam,population.pig.risk.gam)

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```

population.pig.risk.gha <- runif(1, population.pig.risk.gha.li, population.pig.risk.gha.ls)
number.population.pig.risk.gha <- rbinom(1,population.pig.gha,population.pig.risk.gha)
population.pig.risk.nig <- runif(1, population.pig.risk.nig.li, population.pig.risk.nig.ls)
number.population.pig.risk.nig <- rbinom(1,population.pig.nig,population.pig.risk.nig)
population.pig.risk.sen <- runif(1, population.pig.risk.sen.li, population.pig.risk.sen.ls)
number.population.pig.risk.sen <- rbinom(1,population.pig.sen,population.pig.risk.sen)
population.pig.risk.tog <- runif(1, population.pig.risk.tog.li, population.pig.risk.tog.ls)
number.population.pig.risk.tog <- rbinom(1,population.pig.tog,population.pig.risk.tog)
population.pig.risk.rwa <- runif(1, population.pig.risk.rwa.li, population.pig.risk.rwa.ls)
number.population.pig.risk.rwa <- rbinom(1,population.pig.rwa,population.pig.risk.rwa)
population.pig.risk.zam <- runif(1, population.pig.risk.zam.li, population.pig.risk.zam.ls)
number.population.pig.risk.zam <- rbinom(1,population.pig.zam,population.pig.risk.zam)
population.pig.risk.cen<- runif(1, population.pig.risk.cen.li, population.pig.risk.cen.ls)
number.population.pig.risk.cen<- rbinom(1,population.pig.cen,population.pig.risk.cen)
population.pig.risk.gub<- runif(1, population.pig.risk.gub.li, population.pig.risk.gub.ls)
number.population.pig.risk.gub<- rbinom(1,population.pig.gub,population.pig.risk.gub)
population.pig.risk.ben<- runif(1, population.pig.risk.ben.li, population.pig.risk.ben.ls)
number.population.pig.risk.ben<- rbinom(1,population.pig.ben,population.pig.risk.ben)
population.pig.risk.lib<- runif(1, population.pig.risk.lib.li, population.pig.risk.lib.ls)
number.population.pig.risk.lib<- rbinom(1,population.pig.lib,population.pig.risk.lib)
population.pig.risk.gab<- runif(1, population.pig.risk.gab.li, population.pig.risk.gab.ls)
number.population.pig.risk.gab<- rbinom(1,population.pig.gab,population.pig.risk.gab)
population.pig.risk.gui<- runif(1, population.pig.risk.gui.li, population.pig.risk.gui.ls)
number.population.pig.risk.gui<- rbinom(1,population.pig.gui,population.pig.risk.gui)
population.pig.risk.con<- runif(1, population.pig.risk.con.li, population.pig.risk.con.ls)
number.population.pig.risk.con<- rbinom(1,population.pig.con,population.pig.risk.con)
population.pig.risk.cab<- runif(1, population.pig.risk.cab.li, population.pig.risk.cab.ls)
number.population.pig.risk.cab<- rbinom(1,population.pig.cab,population.pig.risk.cab)
population.pig.risk.mal<- runif(1, population.pig.risk.mal.li, population.pig.risk.mal.ls)
number.population.pig.risk.mal<- rbinom(1,population.pig.mal,population.pig.risk.mal)
population.pig.risk.sie<- runif(1, population.pig.risk.sie.li, population.pig.risk.sie.ls)
number.population.pig.risk.sie<- rbinom(1,population.pig.sie,population.pig.risk.sie)
population.pig.risk.nir<- runif(1, population.pig.risk.nir.li, population.pig.risk.nir.ls)
number.population.pig.risk.nir<- rbinom(1,population.pig.nir,population.pig.risk.nir)
population.pig.risk.sao<- runif(1, population.pig.risk.sao.li, population.pig.risk.sao.ls)
number.population.pig.risk.sao<- rbinom(1,population.pig.sao,population.pig.risk.sao)
population.pig.risk.sou<- runif(1, population.pig.risk.sou.li, population.pig.risk.sou.ls)
number.population.pig.risk.sou<- rbinom(1,population.pig.sou,population.pig.risk.sou)
population.pig.risk.gue<- runif(1, population.pig.risk.gue.li, population.pig.risk.gue.ls)
number.population.pig.risk.gue<- rbinom(1,population.pig.gue,population.pig.risk.gue)
cost.treat.pig <- runif(1, cost.treat.pig.li, cost.treat.pig.ls)
total.cost.treat.pig[i] <- number.population.pig.risk[i]*cost.treat.pig
number.infected.pig[i] <-
number.infected.pig.ang[i]+number.infected.pig.ben[i]+number.infected.pig.burk[i]+number.i
nfectd.pig.bur[i]+number.infected.pig.cam[i]+number.infected.pig.cha[i]+number.infected.pi
g.coi[i]+number.infected.pig.drc[i]+number.infected.pig.gam[i]+number.infected.pig.gha[i]+
number.infected.pig.nig[i]+number.infected.pig.sen[i]+number.infected.pig.tog[i]+number.inf
ected.pig.rwa[i]+number.infected.pig.zam[i]
prob.heavy.infect <- rbeta(1, prob.heavy.infect.alpha,prob.heavy.infect.beta)
number.heavy.infect[i] <- rbinom(1,number.infected.pig[i],prob.heavy.infect)

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```

price.pig.trader.level <- runif(1,price.pig.trader.level.li,price.pig.trader.level.ls)
cost.trader [i] <- number.infected.pig[i]*price.loss.pig.trader
cost.butcher[i] <- number.heavy.infect[i]*price.pig.trader.level
cost.pc.reduce[i] <-
cost.pc.ang[i]+cost.pc.ben[i]+cost.pc.burk[i]+cost.pc.bur[i]+cost.pc.cam[i]+cost.pc.cha[i]+co
st.pc.coi[i]+cost.pc.drc[i]+cost.pc.gam[i]+cost.pc.gha[i]+cost.pc.nig[i]+cost.pc.sen[i]+cost.pc.
tog[i]+cost.pc.rwa[i]+cost.pc.zam[i]+cost.trader [i]
cost.pc[i] <- total.cost.treat.pig[i]+cost.butcher[i]+cost.pc.reduce[i]
cost.pc.reduce.farmer[i] <-
cost.pc.ang[i]+cost.pc.ben[i]+cost.pc.burk[i]+cost.pc.bur[i]+cost.pc.cam[i]+cost.pc.cha[i]+co
st.pc.coi[i]+cost.pc.drc[i]+cost.pc.gam[i]+cost.pc.gha[i]+cost.pc.nig[i]+cost.pc.sen[i]+cost.pc.
tog[i]+cost.pc.rwa[i]+cost.pc.zam[i]
cost.pc.reduce.farmer.country[i] <- cost.pc.reduce.farmer[i]/15
cost.per.pc[i] <- cost.pc[i] / number.infected.pig[i]
price.pig <- runif(1,price.pig.li,price.pig.ls)
number.pigs.per.farmer <- runif(1,number.pigs.per.farmer.li,number.pigs.per.farmer.ls)
income.per.farmer[i] <- number.pigs.per.farmer*price.pig
income.pig[i] <- population.pig*price.pig
}
print("income pig:")
print(quantile(income.pig,probs=c(.025,.5,.975))); print(mean(income.pig))
print("number heavy infect:")
print(quantile(number.heavy.infect,probs=c(.025,.5,.975))); print(mean(number.heavy.infect))
print("cost trader:")
print(quantile(cost.trader,probs=c(.025,.5,.975))); print(mean(cost.trader))
print("income per farmer:")
print(quantile(income.per.farmer,probs=c(.025,.5,.975))); print(mean(income.per.farmer))
print("cost butcher:")
print(quantile(cost.butcher,probs=c(.025,.5,.975))); print(mean(cost.butcher))
print("number population pig scavenging syst:")
print(quantile(number.population.pig.scavenging.syst,probs=c(.025,.5,.975)));
print(mean(number.population.pig.scavenging.syst))
print("number population pig semi intensive syst:")
print(quantile(number.population.pig.semi.intensive.syst,probs=c(.025,.5,.975)));
print(mean(number.population.pig.semi.intensive.syst))
print("number population pig modern syst:")
print(quantile(number.population.pig.modern.syst,probs=c(.025,.5,.975)));
print(mean(number.population.pig.modern.syst))
print("number population pig risk:")
print(quantile(number.population.pig.risk,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk))
print("number population pig risk ang:")
print(quantile(number.population.pig.risk.ang,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.ang))
print("number population pig risk burk:")
print(quantile(number.population.pig.risk.burk,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.burk))
print("number population pig risk bur:")
print(quantile(number.population.pig.risk.bur,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.bur))

```

```
print("number population pig risk cam:")
print(quantile(number.population.pig.risk.cam,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.cam))
print("number population pig risk cha:")
print(quantile(number.population.pig.risk.cha,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.cha))
print("number population pig risk coi:")
print(quantile(number.population.pig.risk.coi,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.coi))
print("number population pig risk drc:")
print(quantile(number.population.pig.risk.drc,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.drc))
print("number population pig risk gam:")
print(quantile(number.population.pig.risk.gam,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gam))
print("number population pig risk gha:")
print(quantile(number.population.pig.risk.gha,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gha))
print("number population pig risk nig:")
print(quantile(number.population.pig.risk.nig,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.nig))
print("number population pig risk sen:")
print(quantile(number.population.pig.risk.sen,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.sen))
print("number population pig risk tog:")
print(quantile(number.population.pig.risk.tog,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.tog))
print("number population pig risk rwa:")
print(quantile(number.population.pig.risk.rwa,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.rwa))
print("number population pig risk zam:")
print(quantile(number.population.pig.risk.zam,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.zam))
print("number population pig risk cen:")
print(quantile(number.population.pig.risk.cen,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.cen))
print("number population pig risk gub:")
print(quantile(number.population.pig.risk.gub,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gub))
print("number population pig risk ben:")
print(quantile(number.population.pig.risk.ben,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.ben))
print("number population pig risk lib:")
print(quantile(number.population.pig.risk.lib,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.lib))
print("number population pig risk gab:")
print(quantile(number.population.pig.risk.gab,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gab))
print("number population pig risk gui:")
```

```

print(quantile(number.population.pig.risk.gui,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gui))
print("number population pig risk con:")
print(quantile(number.population.pig.risk.con,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.con))
print("number population pig risk cab:")
print(quantile(number.population.pig.risk.cab,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.cab))
print("number population pig risk mal:")
print(quantile(number.population.pig.risk.mal,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.mal))
print("number population pig risk sie:")
print(quantile(number.population.pig.risk.sie,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.sie))
print("number population pig risk nir:")
print(quantile(number.population.pig.risk.nir,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.nir))
print("number population pig risk sao:")
print(quantile(number.population.pig.risk.sao,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.sao))
print("number population pig risk sou:")
print(quantile(number.population.pig.risk.sou,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.sou))
print("number population pig risk gue:")
print(quantile(number.population.pig.risk.gue,probs=c(.025,.5,.975)));
print(mean(number.population.pig.risk.gue))
print("cost treat pig:")
print(quantile(cost.treat.pig,probs=c(.025,.5,.975))); print(mean(cost.treat.pig))
print("total cost treat pig:")
print(quantile(total.cost.treat.pig,probs=c(.025,.5,.975))); print(mean(total.cost.treat.pig))
print("number infected pig:")
print(quantile(number.infected.pig,probs=c(.025,.5,.975))); print(mean(number.infected.pig))
print("cost pc reduce:")
print(quantile(cost.pc.reduce,probs=c(.025,.5,.975))); print(mean(cost.pc.reduce))
print("cost pc reduce farmer country:")
print(quantile(cost.pc.reduce.farmer.country,probs=c(.025,.5,.975)));
print(mean(cost.pc.reduce.farmer.country))
print("cost pc reduce farmer:")
print(quantile(cost.pc.reduce.farmer,probs=c(.025,.5,.975)));
print(mean(cost.pc.reduce.farmer))
print("cost pc:")
print(quantile(cost.pc,probs=c(.025,.5,.975))); print(mean(cost.pc))
print("cost per pc:")
print(quantile(cost.per.pc,probs=c(.025,.5,.975))); print(mean(cost.per.pc))
print("cost pc ang:")
print(quantile(cost.pc.ang,probs=c(.025,.5,.975))); print(mean(cost.pc.ang))
print("number infected pig ang:")
print(quantile(number.infected.pig.ang,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.ang))
print("cost pc ben:")

```

```
print(quantile(cost.pc.ben,probs=c(.025,.5,.975))); print(mean(cost.pc.ben))
print("number infected pig ben:")
print(quantile(number.infected.pig.ben,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.ben))
print("cost pc burk:")
print(quantile(cost.pc.burk,probs=c(.025,.5,.975))); print(mean(cost.pc.burk))
print("number infected pig burk:")
print(quantile(number.infected.pig.burk,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.burk))
print("cost pc bur:")
print(quantile(cost.pc.bur,probs=c(.025,.5,.975))); print(mean(cost.pc.bur))
print("number infected pig bur:")
print(quantile(number.infected.pig.bur,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.bur))
print("cost pc cam:")
print(quantile(cost.pc.cam,probs=c(.025,.5,.975))); print(mean(cost.pc.cam))
print("number infected pig cam:")
print(quantile(number.infected.pig.cam,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.cam))
print("cost pc cha:")
print(quantile(cost.pc.cha,probs=c(.025,.5,.975))); print(mean(cost.pc.cha))
print("number infected pig cha:")
print(quantile(number.infected.pig.cha,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.cha))
print("cost pc coi:")
print(quantile(cost.pc.coi,probs=c(.025,.5,.975))); print(mean(cost.pc.coi))
print("number infected pig coi:")
print(quantile(number.infected.pig.coi,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.coi))
print("cost pc drc:")
print(quantile(cost.pc.drc,probs=c(.025,.5,.975))); print(mean(cost.pc.drc))
print("number infected pig drc:")
print(quantile(number.infected.pig.drc,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.drc))
print("cost pc gam:")
print(quantile(cost.pc.gam,probs=c(.025,.5,.975))); print(mean(cost.pc.gam))
print("number infected pig gam:")
print(quantile(number.infected.pig.gam,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.gam))
print("cost pc gha:")
print(quantile(cost.pc.gha,probs=c(.025,.5,.975))); print(mean(cost.pc.gha))
print("number infected pig gha:")
print(quantile(number.infected.pig.gha,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.gha))
print("cost pc nig:")
print(quantile(cost.pc.nig,probs=c(.025,.5,.975))); print(mean(cost.pc.nig))
print("number infected pig nig:")
print(quantile(number.infected.pig.nig,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.nig))
print("cost pc sen:")
```

```
print(quantile(cost.pc.sen,probs=c(.025,.5,.975))); print(mean(cost.pc.sen))
print("number infected pig sen:")
print(quantile(number.infected.pig.sen,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.sen))
print("cost pc tog:")
print(quantile(cost.pc.tog,probs=c(.025,.5,.975))); print(mean(cost.pc.tog))
print("number infected pig tog:")
print(quantile(number.infected.pig.tog,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.tog))
print("cost pc rwa:")
print(quantile(cost.pc.rwa,probs=c(.025,.5,.975))); print(mean(cost.pc.rwa))
print("number infected pig rwa:")
print(quantile(number.infected.pig.rwa,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.rwa))
print("cost pc zam:")
print(quantile(cost.pc.zam,probs=c(.025,.5,.975))); print(mean(cost.pc.zam))
print("number infected pig zam:")
print(quantile(number.infected.pig.zam,probs=c(.025,.5,.975)));
print(mean(number.infected.pig.zam))
}
```

Supplementary material III: Rmodel for the calculation of the true number of infected pigs with *T. solium* cysticerci and true prevalence of porcine cysticercosis in Western and Central Africa

```
find.true.prevalence.solium <- function(Positive_pigs=2914526, Negative_pigs=19648159,
Sensitivity_min=.20, Sensitivity_max=.50, Specificity=1, iterations=10000, conf=.95)
{
  N <- Positive_pigs + Negative_pigs
  true_prevalence<-numeric(iterations)
  total_positive_pigs <-numeric(iterations)
  true_prevalence[1] <- .5
  for (i in 2:iterations)
  {
    Sensitivity<- runif(1, Sensitivity_min, Sensitivity_max)
    pp_value <- true_prevalence[i-1]* Sensitivity /(true_prevalence[i-1]*
Sensitivity +(1-true_prevalence[i-1])*(1- Specificity))
    true_positive_pigs <- rbinom(1, Positive_pigs, pp_value)
    pn_value <- true_prevalence[i-1]*(1- Sensitivity)/(true_prevalence[i-1]*(1-
Sensitivity)+(1-true_prevalence[i-1])*Specificity)
    false_negative_pigs <- rbinom(1, Negative_pigs, pn_value)
    total_positive_pigs[i] <- true_positive_pigs+ false_negative_pigs
    true_prevalence[i] <-total_positive_pigs[i]/N
  }
  print(paste("True positive simulated   :", mean(total_positive_pigs), sep=""), quote=F)
  print(paste(100*conf, "% confidence interval:", sep=""), quote=F)
  print(quantile(total_positive_pigs, probs=c((1-conf)/2,.5,(1+conf)/2)))

  print(paste("True prevalence solium simulated   :", mean(true_prevalence), sep=""),
quote=F)
  print(paste(100*conf, "% confidence interval:", sep=""), quote=F)
  print(quantile(true_prevalence, probs=c((1-conf)/2,.5,(1+conf)/2)))
  print(paste("Range: ",min(true_prevalence), " - ", max(true_prevalence), sep=""), quote=F)
}
```