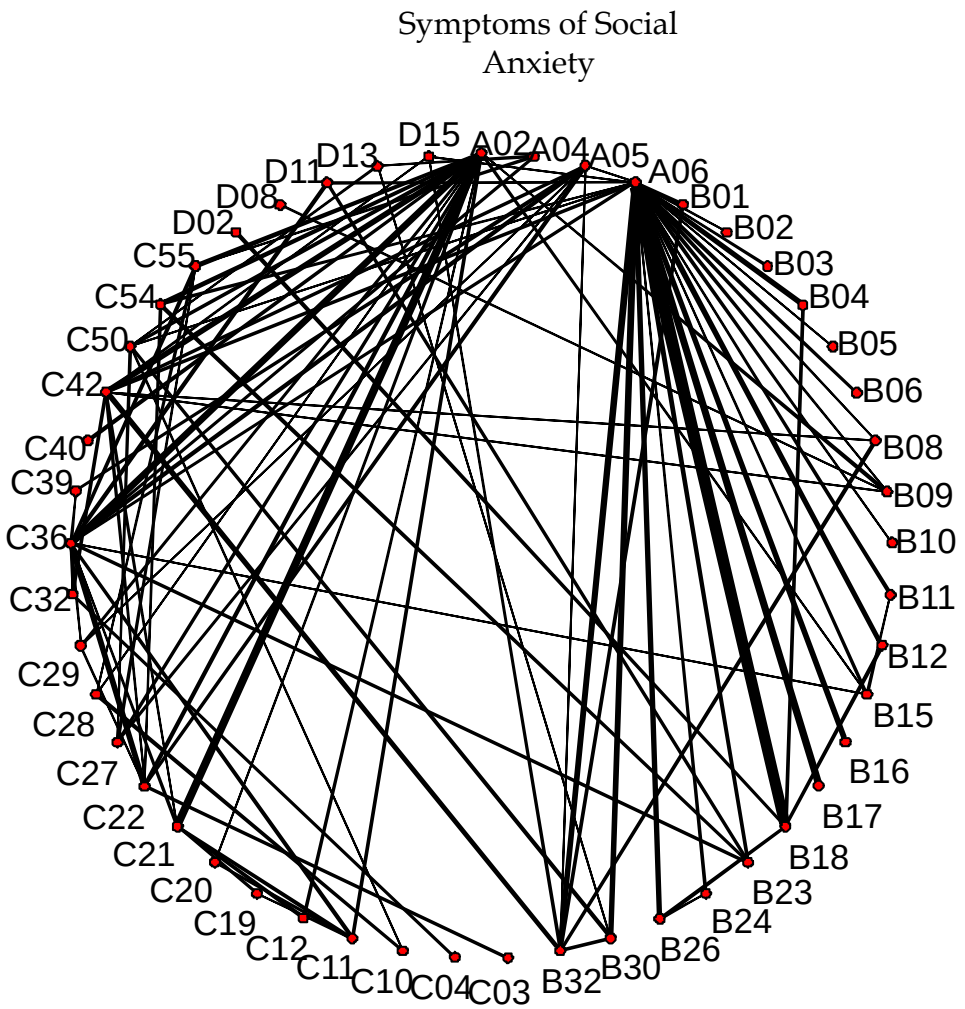
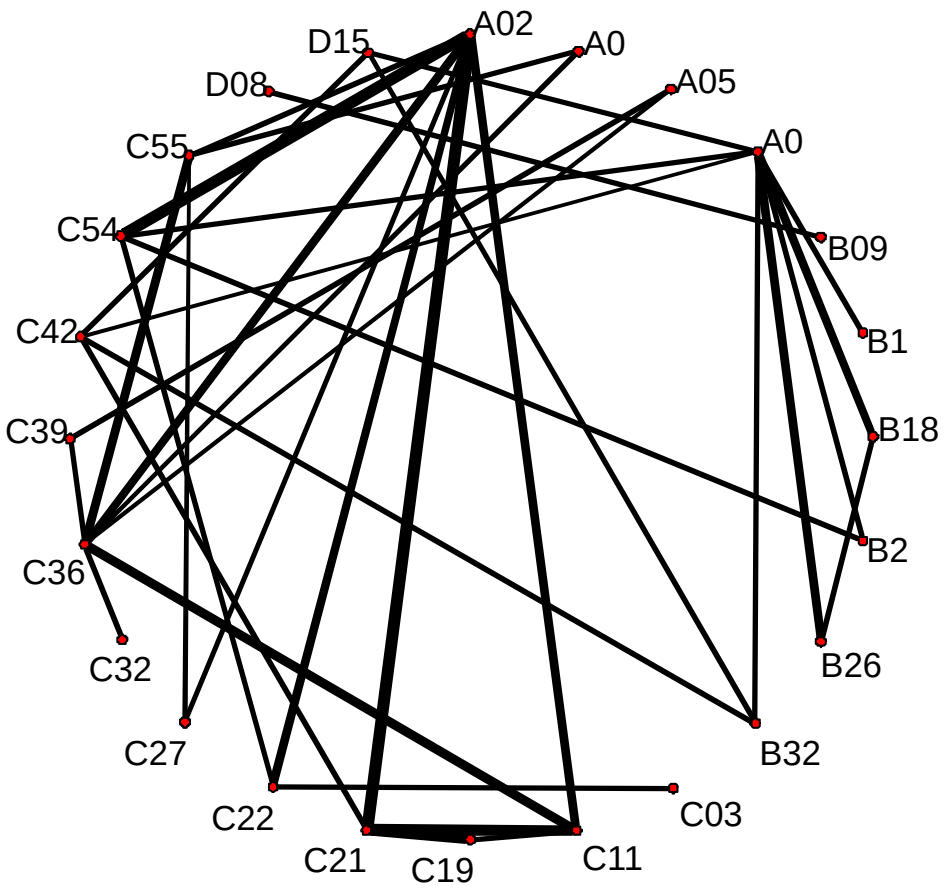
APPENDIX 11: NETWORK META-ANALYSIS RESULTS

Symptoms of Social Anxiety Diagram

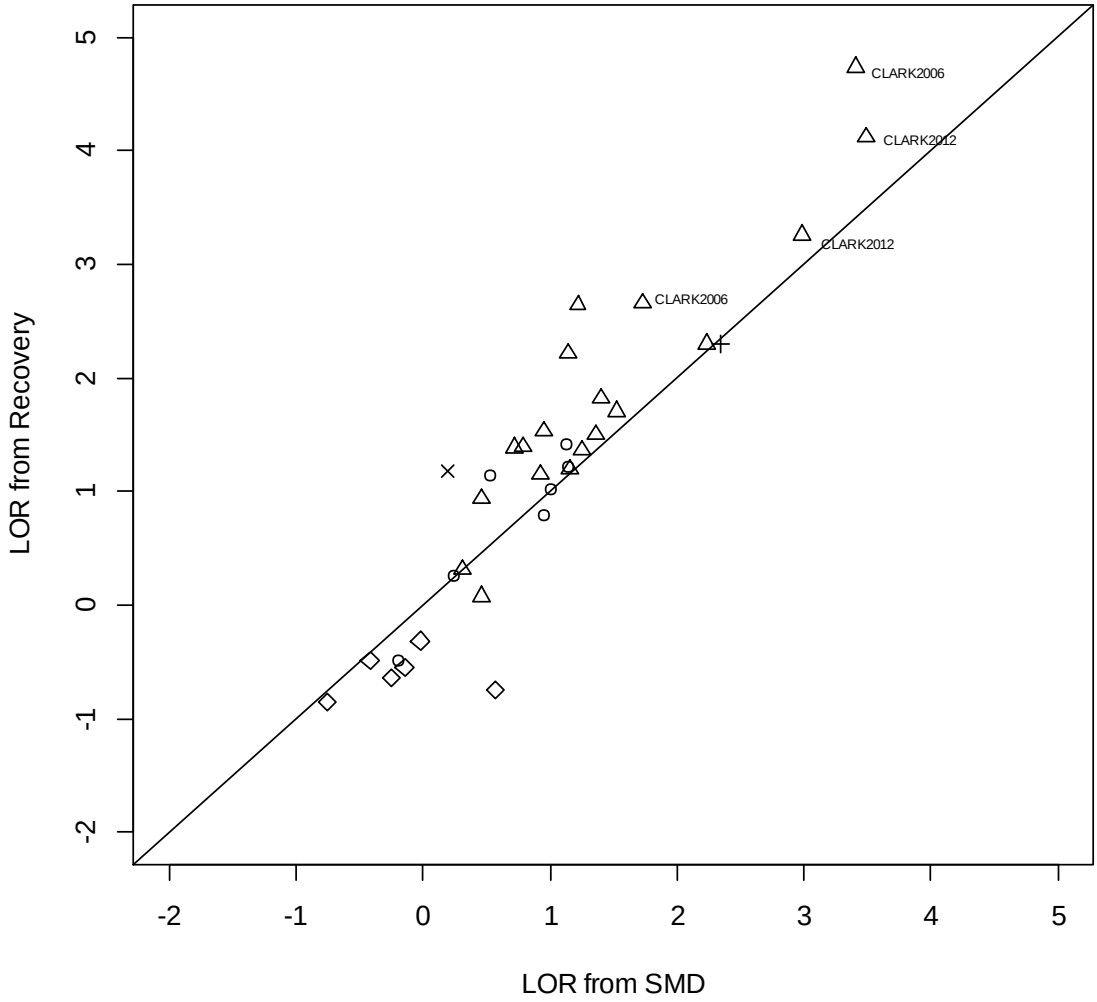


Recovery Diagram

Recovery



Symptom versus Recovery Relationship



Winbugs Code

Treatment codes: re-ordered

1	A02)	Wait list
2	A04)	Treatment as usual
3	A05)	Psychological Placebo
4	A06)	Pill Placebo
5	B01)	BB, Atenolol
6	B05)	St John's Wort
7	B06)	TC, Mirtazapine
8	B10)	NRI, Atomoxetine
9	B11)	NK1A
10	C03)	Social skills training
11	C04)	Exercise
12	C10)	Supportive Therapy
13	C22)	Exposure (in vivo)
14	C27)	Psychodynamic Psychotherapy
15	C28)	Interpersonal Psychotherapy
16	C32)	Mindfulness
17	D02)	Paroxetine + Clonazapam
18	D08)	Psychodynamic + Clonazepam
19	D11)	CBT, group + Fluoxetine
20	D13)	CBT, individual + Moclobemide
21	D15)	CBT (Heimberg), group + Phenelzine

22 B02) AC, Gabapentin

23 B03) AC, Levetiracetam

24 B04) AC, Pregabalin (400mg)

25 B08) BD, Alprazolam

26 B09) BD, Clonazapam

27 B12) SS, Escitalopram

28 B15) SS, Citalopram

29 B16) SS, Fluvoxamine

30 B17) SS, Sertraline

31 B18) SS, Paroxetine

32 B23) SS, Fluoxetine

33 B24) SS, Venlafaxine (<75mg/day)

34 B26) SN, Venlafaxine (>75mg/day)

35 B30) MA, Moclobemide

36 B32) MA, Phenelzine

37 C11) Self-help (book) no support

38 C12) Self-help (internet) no support

39 C19) Self-help (book) with discussion group

40 C20) Self-help (book) with support

41 C21) Self-help (internet) with support

42 C36) CBT, group

43 C39) CBT, group (enhanced exposure)

44 C42) CBT (Heimberg), group

45 C40) CBT (Heimberg), individual

46 C50) CBT, individual

47 C54) CT (Clark & Wells), individual

48 C55) CT (Clark & Wells), individual shortened

```
# Normal likelihood, identity link for trial-level data given as SMD
# Class model: Random effects model for multi-arm trials
# Includes calibration regression for Recovery
model{                    # *** PROGRAM STARTS
# 2 ARM STUDIES SMD
for(i in 1:ns2) {         # LOOP THROUGH 2-ARM STUDIES
   prec[i,2] <- 1/Var[i,2]     # set precisions
   y[i,2] ~ dnorm(delta[i,2],prec[i,2]) # normal likelihood for 2-arm trials
#Deviance contribution for trial i
   resdev[i] <- (y[i,2]-delta[i,2])*(y[i,2]-delta[i,2])*prec[i,2]
  }
# 3 ARM STUDIES SMD
for(i in 1:ns3) {         # LOOP THROUGH THREE-ARM STUDIES
   for (k in 1:(na[i+ns2]-1)) { # set variance-covariance matrix
      for (j in 1:(na[i+ns2]-1)) {
         Sigma[i,j,k] <- V[i+ns2]*(1-equals(j,k)) + Var[i+ns2,k+1]*equals(j,k)
        }
```

```
    }
# Precision matrix
   Omega[i,1:(na[i+ns2]-1),1:(na[i+ns2]-1)] <- inverse(Sigma[i,,])
# multivariate normal likelihood for 3-arm trials
   y[i+ns2,2:na[i+ns2]] ~ dmnorm(delta[i+ns2,2:na[i+ns2]],Omega[i,1:2,1:2])
# Deviance contribution for trial i
   for (k in 1:(na[i+ns2]-1)){  # multiply vector & matrix
      ydiff[i,k]<- y[i+ns2,(k+1)] - delta[i+ns2,(k+1)]
      z[i,k]<- inprod2(Omega[i,k,1:2], ydiff[i,1:2])
                    }
   resdev[i+ns2]<- inprod2(ydiff[i,1:(na[i+ns2]-1)], z[i,1:(na[i+ns2]-1)])
  }
# 4 ARM STUDIES SMD
for(i in 1:ns4) {             # LOOP THROUGH FOUR-ARM STUDIES
  for (k in 1:(na[i+ns2+ns3]-1)) {  # set variance-covariance matrix
   for (j in 1:(na[i+ns2+ns3]-1)) {
    Sigma4[i,j,k] <- V[i+ns2+ns3]*(1-equals(j,k)) +
Var[i+ns2+ns3,k+1]*equals(j,k)
    }
  }
# Precision matrix
   Omega4[i,1:(na[i+ns2+ns3]-1),1:(na[i+ns2+ns3]-1)] <- inverse(Sigma4[i,,])
# multivariate normal likelihood for 4-arm trials
```

```
   y[i+ns2+ns3,2:na[i+ns2+ns3]] ~
dmnorm(delta[i+ns2+ns3,2:na[i+ns2+ns3]],Omega4[i,1:3,1:3])

#Deviance contribution for trial i

   for (k in 1:(na[i+ns2+ns3]-1)){  # multiply vector & matrix

      ydiff4[i,k]<- y[i+ns2+ns3,(k+1)] - delta[i+ns2+ns3,(k+1)]

      z4[i,k]<- inprod2(Omega4[i,k,1:3], ydiff4[i,1:(na[i+ns2+ns3]-1)])

                    }

   resdev[i+ns2+ns3]<- inprod2(ydiff4[i,1:(na[i+ns2+ns3]-1)],
z4[i,1:(na[i+ns2+ns3]-1)])

  }

# 5 ARM STUDIES SMD

for(i in 1:ns5) {              # LOOP THROUGH FIVE-ARM STUDIES

# set variance-covariance matrix

  for (k in 1:(na[i+ns-ns5]-1)) {  # set variance-covariance matrix

   for (j in 1:(na[i+ns-ns5]-1)) {

     Sigma5[i,j,k] <- V[i+ns-ns5]*(1-equals(j,k)) + Var[i+ns-ns5,k+1]*equals(j,k)

     }

  }

# Precision matrix

   Omega5[i,1:(na[i+ns-ns5]-1),1:(na[i+ns-ns5]-1)] <- inverse(Sigma5[i,,])

# multivariate normal likelihood for 5-arm trials

   y[i+ns-ns5,2:na[i+ns-ns5]] ~ dmnorm(delta[i+ns-ns5,2:na[i+ns-
ns5]],Omega5[i,1:4,1:4])

# Deviance contribution for trial i

   for (k in 1:(na[i+ns-ns5]-1)){  # multiply vector & matrix
```

```
      ydiff5[i,k]<- y[i+ns-ns5,(k+1)] - delta[i+ns-ns5,(k+1)]

      z5[i,k]<- inprod2(Omega5[i,k,1:4], ydiff5[i,1:(na[i+ns-ns5]-1)])

                  }

   resdev[i+ns-ns5]<- inprod2(ydiff5[i,1:(na[i+ns-ns5]-1)], z5[i,1:(na[i+ns-ns5]-
1)])

  }

# ALL STUDIES WITH SMD, RE MODEL

for(i in 1:ns){              #   LOOP THROUGH ALL STUDIES

   w[i,1] <- 0    # adjustment for multi-arm trials is zero for control arm

   delta[i,1] <- 0            # treatment effect is zero for control arm

   for (k in 2:na[i]) {        # LOOP THROUGH ARMS

# trial-specific LOR distributions

      delta[i,k] ~ dnorm(md[i,k],taud[i,k])

# mean of random effects distributions, with multi-arm trial correction

      md[i,k] <-  d[t[i,k]] - d[t[i,1]] + sw[i,k]

# precision of random effects distributions (with multi-arm trial correction)

      taud[i,k] <- tau *2*(k-1)/k

# adjustment, multi-arm RCTs

      w[i,k] <- (delta[i,k] - d[t[i,k]] + d[t[i,1]])

# cumulative adjustment for multi-arm trials

      sw[i,k] <- sum(w[i,1:k-1])/(k-1)

     }

  }
```

```
totresdev <- sum(resdev[])      # Total Residual Deviance

#

d[1] <- 0      # treatment effect (SMD) is zero for reference treatment

for (k in 2:21){

   d[k] ~ dnorm(0, .0001)      # vague prior for treatment effects (SMD)

  }

# Class model

for (k in 22:nt){

   d[k] ~ dnorm(m[D[k]], prec2[D[k]]) # treatment effects from Class (SMD)

  }

for (k in 1:nc){

   m[k] ~ dnorm(0, .0001)      # prior for mean class effect

   prec2[k] ~ dgamma(a,b)      # prior for class precision

   sd2[k] <- pow(prec2[k], -0.5)

}

#

sd ~ dunif(0,5)                # vague prior for between-trial SD

tau <- pow(sd,-2)   # between-trial precision = (1/between-trial variance)

#

# REGRESSION FOR RECOVERY

for (j in 1:nR){               # LOOP THROUGH STUDIES REPORTING
RECOVERY

   lambda[j,1] <- 0           # treatment effect is zero for control arm

   mu[j] ~ dnorm(0,.0001)      # vague priors for all trial baselines
```

```
   for (k in 1:naR[j]) {       # LOOP THROUGH ARMS
      r[j,k] ~ dbin(p[j,k],n[j,k]) # binomial likelihood for recovery data
      logit(p[j,k]) <- mu[j] + lambda[j,k]  # model for linear predictor
      rhat[j,k] <- p[j,k] * n[j,k] # expected value of the numerators
#Deviance contribution
      devR[j,k] <- 2 * (r[j,k] * (log(r[j,k])-log(rhat[j,k]))
         +  (n[j,k]-r[j,k]) * (log(n[j,k]-r[j,k]) - log(n[j,k]-rhat[j,k])))
   }

   for (k in 2:naR[j]) {       # LOOP THROUGH ARMS
# regression equation: LOR(Rec) = beta * LOR(SMD)
      lambda[j,k] <- beta * (-3.1416/sqrt(3)) * delta[C[j],k]
   }
#  summed residual deviance contribution for this trial
   resdevR[j] <- sum(devR[j,1:naR[j]])
}
totresdevR <- sum(resdevR[])     #Total Residual Deviance Recovery
beta ~ dnorm(0,.0001)
#
for (k in 1:nc)  {  mCal[k] <- (-3.1416/sqrt(3)) * beta * m[k]  }
for (k in 1:nt)  {
   g[k] <- (-3.1416/sqrt(3)) * d[k]  # Transform SMD to LOR (change sign)
   gCal[k] <- beta * g[k]   # Transform SMD to LOR (change sign): Calibrated
```

```
# rank all treatments on SMD
   rk[k]  <- rank(d[],k)       # Smallest is best (i.e. rank 1)
   best[k]  <- equals(rk[k],1)
   for (h in 1:nt) { prob[h,k] <- equals(rk[k],h) }
# rank all treatments on LOR (calibrated)
   rk.g[k]  <- nt+1-rank(gCal[],k)  # Largest is best (i.e. rank 1)
   best.g[k]  <- equals(rk.g[k],1)
   for (h in 1:nt) { prob.g[h,k] <- equals(rk.g[k],h) }
  }
for (c in 1:(nt-1)) {
  for (k in (c+1):nt) {
   diff[c,k] <- d[k] - d[c]     # pairwise SMDs
   lor[c,k] <- g[k] - g[c]      # pairwise LORs
   or[c,k] <- exp(g[k] - g[c])  # Paiwise ORs
   lorCal[c,k] <- gCal[k] - gCal[c]     # pairwise LORs (calibrated)
   orCal[c,k] <- exp(gCal[k] - gCal[c]) # Paiwise ORs (calibrated)
  }
 }
# Provide estimates of treatment effects T[k] on the natural scale
# Given a Mean Effect, meanA, for 'standard' treatment A,
# with precision (1/variance) precA
A ~ dnorm(meanA,precA)
for (k in 1:nt) { logit(T[k]) <- A + gCal[k]  }
```

```
for (k in 1:nc) { logit(TClass[k]) <- A + mCal[k]  }

}                          # *** PROGRAM ENDS
```