```
X[1..N] = Reference RNA 3D module (array of residues)
Y[1..M] =   Query   RNA 3D module (array of residues)

X5 = 5-atom representations of residues from X
Y5 = 5-atom representations of residues from Y

X3 = 3-atom representations of residues from X
Y3 = 3-atom representations of residues from Y

MATCHRANGE = 3.0 Å

Xcm = centers of mass of residues from X5
Ycm = centers of mass of residues from Y5

for i in 1..N:
  for j in 1..M:

    Rotation1, Translation1 = KABSCH([(X5[i],Y5[j])])
    Ycm' =  Ycm * Rotation1 + Translation1

    #MCS: mutually closest subset of matched residues
    MCS = [(r,s) | d(Xcm[r],Ycm'[s])
                   == min(d(Xcm[r],Ycm'[k]) for k in 1..M)
                   == min(d(Xcm[k],Ycm'[s]) for k in 1..N)
                   < MATCHRANGE]

    Rotation2, Translation2 = KABSCH([(X3[r],Y3[s])
                                      for r,s in MCS])

    X3mcs  = [X3[r] for r,s in MCS]
    Y3mcs  = [Y3[s] for r,s in MCS]
    Y3mcs' = Y3mcs * Rotation2 + Translation2
    Y'     =   Y   * Rotation2 + Translation2

    yield SIZE(MCS), RMSD(X3mcs,Y3mcs'), Y'
```