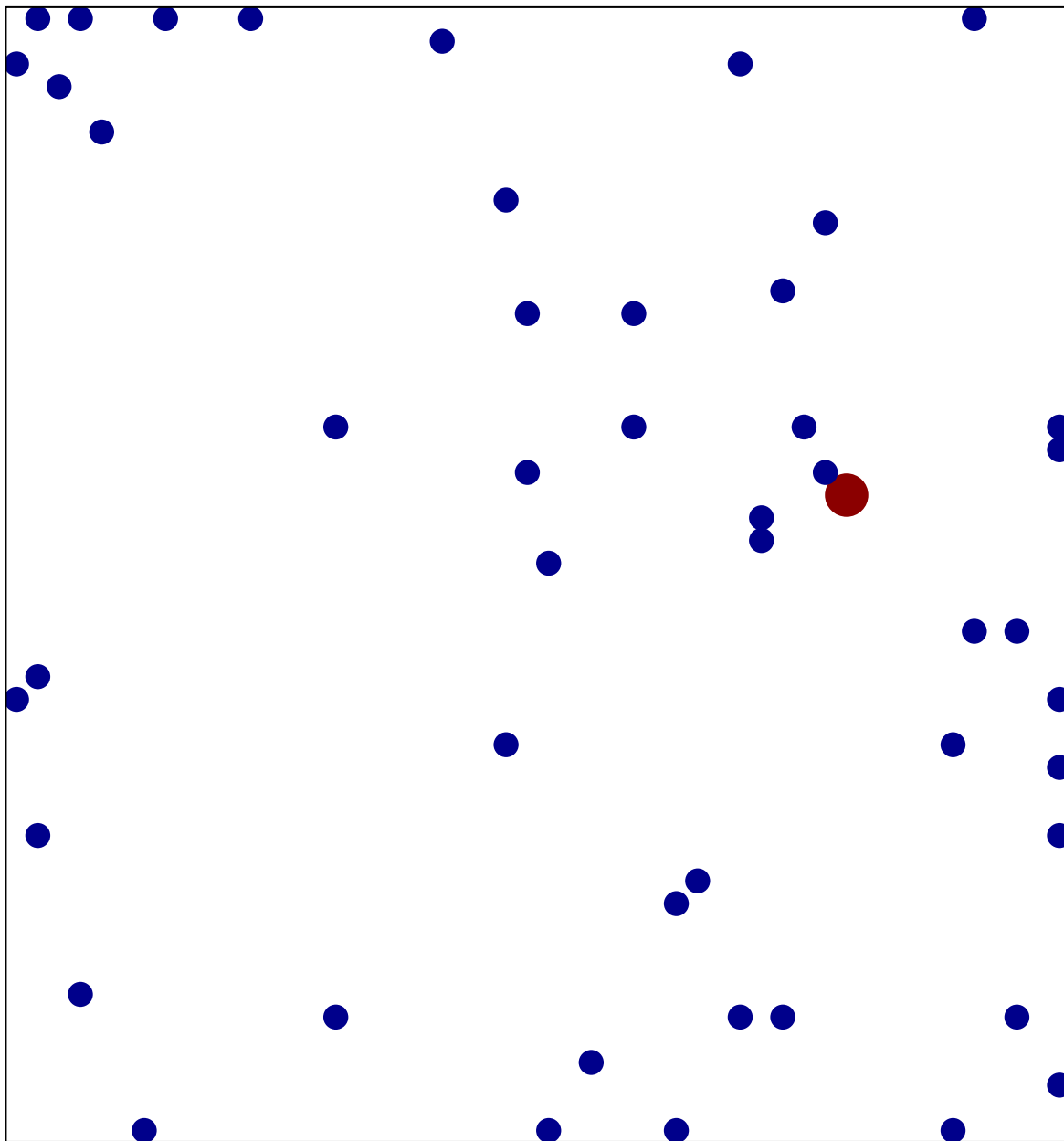
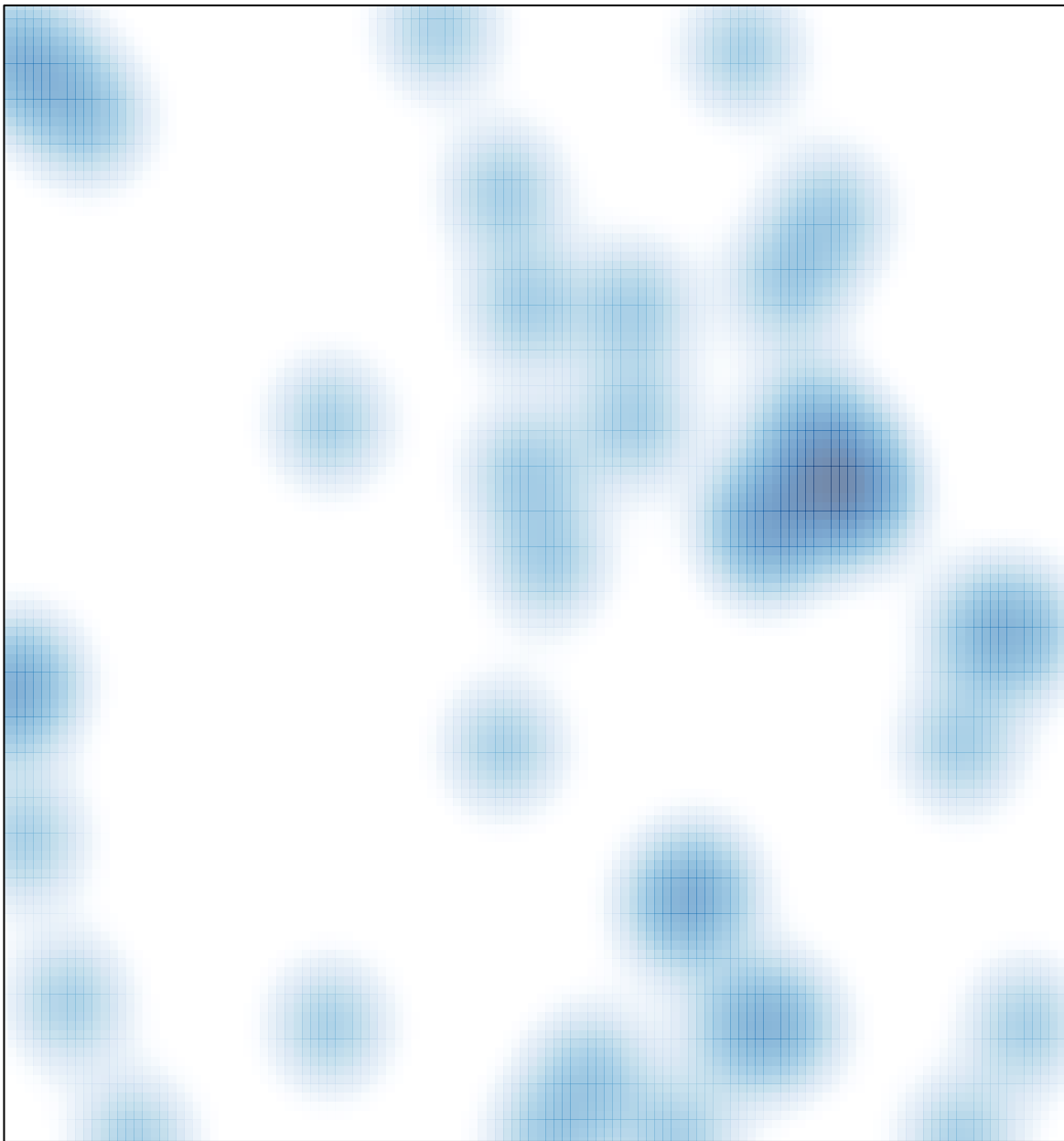


# CORRE\_MULTIPLE\_MYELOMA\_DN



# features = 50  
chi-square p = 0.81

# CORRE\_MULTIPLE\_MYELOMA\_DN



# features = 50 , max = 2