The distribution $P(T)$ of the number of triangles passing by a node. The solid lines correspond to the best fit to a power law. In the case of the *S. cerevisiae* protein interaction network, the data is better fitted to two power laws, one for small and one for large $T$. Since the subgraph abundance is mainly determined by the large $k$ and $T$ properties we have estimated the exponent $\delta$ from the power law fit to the large $T$ region.

The probability that two neighbors are not connected is $1 - C(k)$. Therefore, the probability to obtain $t$ connected pairs and $n_p - t$ disconnected pairs is given by the binomial distribution

$$b_{nt}(k) = \binom{n_p}{t} C(k)^t [1 - C(k)]^{n_p - t}.$$  \hfill (12)

The average number of subgraphs formed by $n - 1$ neighbors and $t$ interactions among them and centered at a node with degree $k$ is given by

$$N_{nt}(k) = \binom{k}{n-1} b_{nt}(k).$$  \hfill (13)

We readily obtain that if $k$ is large, then $N_{nt}(k)$ scales as

$$N_{nt}(k) \sim k^{\beta_{nt}},$$  \hfill (14)

where

$$\beta_{nt} = n - 1 - \alpha t = n - 1 - \alpha (m - n + 1).$$  \hfill (15)

Using Eqs. (4) and (14) we find that the probability for a randomly selected node to participate in $T_{nt}$ subgraphs $(n, t)$ scales as

$$P(T_{nt}) \sim T_{nt}^{-\delta_{nt}},$$  \hfill (16)

where