

Drug-ADR Associations Network

In our method, a bipartite network was employed to represent drug-ADR associations, in which vertex are drugs/ADRs and edges are their associations. In such a network, drugs were connected with ADRs only, vice versa. So it could be divided into two disjoint subsets: drugs and ADRs. Here, a bipartite network G could therefore be defined as $G = (\perp, T, E)$, in which $\perp$ represents nodes of drugs, while T represents nodes of ADRs, and $E \subseteq \perp \times T$ represents the links between drugs and ADRs associations. Then, two kinds of homogeneous nodes' projection could be defined: $\perp$ -projection (drug projection) and T -projection (ADR projection). In the $\perp$ -projection, nodes were drugs and edges are connected for those sharing one or more common ADRs in the bipartite network. It is the same in the case of the T -projection. Depending on those two projections, external links prediction method was then proposed.

External Link Prediction Method

In our method, two kinds of *external links* could be defined depending on those two projections. Take the *external link* definition on basis of drug-projection ($\perp$ -projection), for instance. Edge (μ, ν) , μ and ν represent a drug and an ADR respectively, is a newly added link in the bipartite network of drug-ADR associations. The link (μ, ν) was external only if the number of the intersection of ν 's neighbours in G and μ 's neighbours in the $\perp$ -projection is equal to or larger than n , $n \in \{1, 2, 3, \dots\}$. An *external link* could also be similarly defined based on ADRs projection (T -projection).

Then, each new link (μ, ν) was scored as the following scoring function:

$$P(\mu, \nu) = \max(P_{drug}(\mu, \nu), P_{ADR}(\mu, \nu)) \dots\dots\dots (1)$$

Where $P(\mu, \nu)$ is the scoring function which take the maximum score of $P_{drug}(\mu, \nu)$ and $P_{ADR}(\mu, \nu)$.

$P_{drug}(\mu, \nu)$ is a scoring function of link (μ, ν) while we define the *external links* based on the drug-projection ($\perp$ -projection). If the link (μ, ν) is an *external link*,

$$P_{drug}(\mu, \nu) = \max(\{w(\mu, a_i), a_i \in N(\nu) \cap N_{\perp}(\mu)\}) \dots\dots\dots (2)$$

Otherwise, $P_{drug}(\mu, \nu) = 0$.

$P_{ADR}(\mu, \nu)$ is a scoring function of link (μ, ν) while we define the *external links* based on the ADRs projection (T -projection). If the link (μ, ν) is an *external link*,

$$P_{ADR}(\mu, \nu) = \max(\{w(b_j, \nu), b_j \in N(\mu) \cap N_T(\nu)\}) \dots\dots\dots (3)$$

Otherwise, $P_{ADR}(\mu, \nu) = 0$.

Where a_i is the intersection node of ν 's neighbours in G and μ 's neighbours in the $\perp$ -projection, $i = 1, \dots, |N(\nu) \cap N_{\perp}(\mu)|$; and b_j is the intersection node of μ 's neighbours in G and ν 's neighbours in the T -projection, $j = 1, \dots, |N(\mu) \cap N_T(\nu)|$.

The weight of links (μ, a_i) and (b_j, ν) were calculated by a Jaccard coefficient[33]:

$$w(x, y) = \frac{|N(x) \cap N(y)|}{|N(x) \cup N(y)|} \dots\dots\dots (4)$$

$N(x)$ and $N(y)$ is the neighbour of node x and y .

Finally, given a weight threshold τ , the link (μ, ν) could be predicted only if $P(\mu, \nu)$ equal to or larger than τ .