

mation. When we measure the new  $k_S$  value for the same nodes in the resulting networks (Fig. 6) we find that their relative ranking remains the same. We recover a practically linear dependence on the  $k_S$  values of the original and the incomplete networks, showing that this measure would work equally well for predicting the spreading efficiency of nodes in a network with missing information.

### III. PROBABILITY AND TIME OF INFECTION

We have demonstrated that the location of a node, as described through the  $k_S$  index, is important for the extent of spreading  $M_i$  when this node is the spreading origin. Here, we show that nodes with high  $k_S$  are more probable to be infected during an epidemic outbreak and are infected earlier than nodes with low  $k_S$ , when spreading starts at a random node. We introduce the quantity  $E_i$ , as the probability that a node  $i$  is going to be infected during an epidemic outbreak originating at a random location, and  $T_i$ , as the average time before node  $i$  is infected during the same process.

As shown in Figs. 7a-d all three quantities that characterize the role of a node in an epidemics process,  $M_i$ ,  $E_i$  and  $T_i$  are strongly correlated. The nodes that are infected by a given node  $i$  form a cluster of size  $\overline{M_i}$ , and they are statistically the nodes that can reach  $i$  when they act as origins themselves. Thus, the probability  $E_i$  to reach this node in general is directly proportional to the size  $M_i$ , as shown in the plots. The average time  $T_i$  to reach a node is inversely proportional to its spreading efficiency  $M_i$ , which emphasizes the fact that these nodes are easily reachable from different network locations. In conclusion, the nodes with the largest  $k_S$  values consistently a) are infecting larger parts of the network, b) are infected more frequently, and c) are infected earlier, than nodes with smaller  $k_S$  values.

### IV. THE IMPRECISION FUNCTIONS

We quantify the spreading efficiency of an individual origin  $i$  through the infected number of nodes  $M_i$ . In order to compare the different methods, we rank all network nodes according to their spreading efficiency, independently of their other properties, and we consider a fraction  $p$  of the most efficient spreaders ( $p \in [0, 1]$ ). We designate this set by  $\Upsilon_{eff}(p)$ . Similarly, we define  $\Upsilon_{k_S}(p)$  as the set of individuals with highest  $k$ -shell values. In order to