

Peer-to-Peer Networks 08 Kelips and Epidemic Algorithms

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Kelips CoNe Freiburg

- Indranil Gupta, Ken Birman, Prakash Linga, Al Demers, Robbert van Renesse
 - Cornell University, Ithaca, New York
- Kelip-kelip
 - malay name for synchronizing fireflies
- P2P Network
 - uses DHT
 - constant lookup time
 - O(n^{1/2}) storage size
 - fast and robust update



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- Peers are organized in k affinity groups
 - peer position chosen by DHT mechanism
 - k is chosen as $n^{1/2}$ for n peers
- Data is mapped to an affinity group using DHT
 - all members of an affinity group store all data
- Routing Table
 - each peer knows all members of the affinity group
 - each peer knows at least one member of each affinity group
- Updates
 - are performed by epidemic algorithms



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- Affinity Group View
 - Links to all O(n/k) group members
 - This set can be reduced to a partial set as long as the update mechanism works
- Contacts
 - For each of the other affinity group a small (constant-sized) set of nodes
 - O(k) links
- Filetuples
 - A (partial) set of tuples, each detailing a file name and host IP address of the node storing the file
 - O(F/k) entries, if F is the overall number of files
- Memory Usage: O(n/k + k + F/k)

- for
$$\mathbf{k} = \mathbf{O}(\sqrt{n+F})$$

Affinity Groups

 $O(\sqrt{n+F})$



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N



M JM 100 10 10,000 100

- Lookup-Algorithm
 - compute index value
 - find affinity group using hash function
 - contact peer from affinity group
 - receive index entry for file (if it exists)
 - contact peer with the document
- Kelips needs four hops to retrieve a file





- Start an Epidemic Algorithm to Spread the news in the affinity group
- Such an algorithm uses O(n/k) messages and needs O(log n) time
- We introduce Epidemic Algorithms later on





- Kelips has lookup time O(1), but needs O(n^{1/2}) sized Routing Table
 - not counting the $O(F/n^{1/2})$ file tuples
- Chord, Pastry & Tapestry use lookup time O(log n) but only O(log n) memory units
- Kelips is a reasonable choice for medium sized networks
 - up to some million peers and some hundred thousands index entries





What is an Epidemic Algorithm



A Epidemic Spread of Viruses

Observation

- most viruses do not prosper in real life
- other viruses are very successful and spread fast
- How fast do viruses spread?
- How many individuals of the population are infected?
- Problem
 - social behavior and infection risk determine the spread
 - the reaction of a society to a virus changes the epidemy
 - viruses and individuals may change during the infection





- SI-Model (rumor spreading)
 - susceptible \rightarrow infected
- SIS-Model (birthrate/deathrate)
 - susceptible \rightarrow infected \rightarrow susceptible
- SIR-Model
 - susceptible \rightarrow infected \rightarrow recovered
- 7 Continuous models
 - deterministic
 - or stochastic
- Lead to differential equations
 - Discrete Models
 - graph based models
 - 1 random call based
 - Lead to the analysis of Markov Processes











- SI-Model (rumor spreading)
 - susceptible \rightarrow infected
 - At the beginning one individual is infected
 - Every contact infects another indiviual
 - In every time unit there are in the expectation ß contacts
- SIS-Model (birthrate/deathrate)
 - susceptible \rightarrow infected \rightarrow susceptible
 - similar as in the SI-Model, yet a share of δ of all infected individuals is healed and can receive the virus again
 - with probability $\boldsymbol{\delta}$ an individual is susceptible again
- SIR-Model
 - susceptible \rightarrow infected \rightarrow recovered
 - like SI-Model, but healed individuals remain immune against the virus and do not transmit the virus again





- Variables
 - n: total number of individuals
 - remains constant
 - S(t): number of (healthy) susceptible individuals at time t
 - I(t): number of infected individuals
- Relative shares
 - s(t) := S(t)/n
 - i(t) := I(t)/n
- At every time unit each individual contacts ß partners
- Assumptions:
 - Among ß contact partnres ß s(t) are susceptible
 - All I(t) infected individuals infect ß s(t) I(t) other individuals in each round
- Leads to the following recursive equations:
 - $I(t+1) = I(t) + I_s s(t) I(t)$
 - $-i(t+1) = i(t) + f_s i(t) s(t)$
 - S(t+1) = S(t) fs s(t) I(t)
 - $s(t+1) = s(t) \beta i(t) s(t)$





- The number of infected grows exponentially until half of all members are infected
- Then the number of susceptible decrease exponentially





- Assumptions:
 - Among ß contact partners ß s(t) are susceptible
 - All I(t) infected individuals infect ß s(t) I(t) other individuals in each round
 - A share of δ of all infected individuals is susceptible again
- Leads to the following recursive equations:

$$- I(t+1) = I(t) + \beta i(t) S(t) - \delta I(t) - i(t+1) = i(t) + \beta i(t) s(t) - \delta i(t) - S(t+1) = S(t) - \beta i(t) S(t) + \delta I(t) - s(t+1) = s(t) - \beta i(t) s(t) + \delta i(t)$$





SIS-Model

Interpretation of Solution

$$i(t) = \frac{1-\rho}{1+\left(\frac{1-\rho}{i(0)}-1\right)e^{-(\beta-\delta)t}} \qquad \rho = \frac{\delta}{\beta}$$
If $\beta < \delta$

- then i(t) is strictly decreasing
- If ß > δ
 - then i(t) converges against $1 \rho = 1 \delta/\beta$
- Same behavior in discrete model₂₀
 has been observed
 - [Kephart,White'94]



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- Variables
 - n: total number of individuals
 - remains constant
 - S(t): number of (healthy) susceptible individuals at time t
 - I(t): number of infected individuals
 - R(t): number or recovered individ.
- Relative shares
 - -s(t) := S(t)/n
 - -i(t) := I(t)/n
 - -r(t) := R(t)/n
- At every time unit each individual contacts ß partners





- Assumptions:
 - Among ß contact partners ß s(t) are susceptible
 - All I(t) infected individuals infect ß s(t) I(t) other individuals in each round
 - A share of δ of all infected individuals is immune (recovered) and never infected again
- Leads to the following recursive equations:

$$-I(t+1) = I(t) + \beta i(t) S(t) - \delta I(t)$$

$$-i(t+1) = i(t) + \beta i(t) i(t) - \delta i(t)$$

$$-S(t+1) = S(t) - \beta i(t) S(t)$$

$$- s(t+1) = s(t) - \beta i(t) s(t)$$

$$-R(t+1) = R(t) + \delta I(t)$$

 $-r(t+1) = r(t) + \delta i(t)$





 The equations and its differential equations counterpart

$$-i(t+1) = i(t) + \beta i(t) i(t) - \delta i(t)$$

- $s(t+1) = s(t) \beta i(t) s(t)$
- $r(t+1) = r(t) + \delta i(t)$
- No closed solution known
 hence numeric solution
- Example
 - s(0) = 1
 - $-i(0) = 1.27 \ 10^{-6}$
 - r(0) = 0
 - ß = 0.5
 - -δ = 0.3333

$$\begin{aligned} \frac{ds(t)}{dt} &= -\beta \cdot i(t)s(t) \\ \frac{di(t)}{dt} &= \beta \cdot i(t)s(t) - \delta i(t) \\ \frac{dr(t)}{dt} &= -\delta i(t) \end{aligned}$$





- Epicast
 - new information is a rumor
 - as long the rumor is new it is distributed
 - Is the rumor old, it is known to all servers
- Epidemic Algorithm [Demers et al 87]
 - distributes information like a virus
 - robust alternative to BFS or flooding
- Communication method
 - Push & Pull, d.h. infection after log₃ n + O(log log n) rounds with high probability
- Problem:
 - growing number of infections increases comunication effort
 - trade-off between robustness and communication overhead





- Given a contact graph G=(V,E)
 - n: number of nodes
 - I(t) := number of infected nodes in round t
 - i(t) = I(T)/n
 - S(t) := number of susceptible nodes in round t
 - I(t)+S(t)=n
 - s(t) = S(T)/n
- Infection:
 - If u is infected in round t and $(u,v) \in E$, then v is infected in round t+1
- Graph determines epidemics
- Complete graph:
 - 1 time unit until complete infection
- Line graph
 - n-1 time units until complete infection





- In each round a new contact graph G_t=(V,E_t):
 - Each node in Gt has out-degree 1
 - chooses random node v out of V
- Infection models:
 - <u>Pus</u>h-Model
 - if u is infected and $(u,v) \in E_t$, then v is infected in the next round
 - Pull-Modell:
 - if v is infected and $(u,v) \in E_t$, then u is infected in the next round





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A Push Model CoNe Freiburg Start phase & Exponential Growth

- If $i(t) \le s(t)/2$:
 - E[i(t+1)] ≥ 2 i(t) 2i(t)2 ≈ 2 i(t)
- Start phase: $I(t) \le 2 c (\ln n)^2$
 - Variance of i(t+1) relatively large
 - Exponential growth starts after some O(1) with high probability
- Exponential growth:
 - $I(t) \in [2 c (ln n)^2, n/(log n)]$
 - Nearly doubling of infecting nodes with high probability, i.e. 1-O(n-c)
- Proof by Chernoff-Bounds
 - For independent random variables X_i \in {0,1} with $X_m = \sum_{i=1}^m X_i$
 - and any $0 \le \delta \le 1$
 - Let $\delta = 1/(\ln n)$ $\mathbf{P}[X_m \le (1-\delta)\mathbf{E}[X_m]] \le e^{-\delta^2 \mathbf{E}[X_m]/2}$
 - **E**[X_m] ≥ 2 c (ln n)³
 - Then $\delta^2 \mathbf{E}[X_m] / 2 \ge c \ln n$

- This implies
$$\mathbf{P}[X_m \le (1-\delta)\mathbf{E}[X_m]] \le e^{-\delta^2 \mathbf{E}[X_m]/2} \le n^{-c}$$













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