

Using Epidemics and Diffusion for Decentralized Monitoring and Control of Fully Distributed Systems

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Outline

System Model

- Epidemics
- Diffusion
- Applications





System Model



Components

Random Communication Topology

> Neighbors ("knows about" relation)

 Maintained by specific protocols





BISON

Nodes



Push-Pull Protocol Skeleton

// active thread
do forever
wait(T time units)
peer = selectRandomNeighbor()
send state to peer
receive peer.state from peer
state = updateState(state,peer.state)

```
// passive thread
do forever
  (peer,peer.state) = waitMessage()
  send state to peer
  state = updateState(state,peer.state)
```





Some comments

- A cellular automaton-like model
 - cycles (each T time units interval)
 - state updates based on neighborhood state
- But: topology is
 - random (not regular, low diameter)
 - can be dynamically changing over time
 - maintained by protocols that can deal with
 - node failure
 - new nodes joining the network





Epidemics





Basic operation







Basic operation









BISON

Some Examples

Epidemics for database updates

- state: infected or not. Infected state means knowing a new piece of information
- updateState(s1, s2): if any of s1 or s2 is infected, new state is infected
- Epidemics for finding a maximal value
 - state: the maximal value seen so far
 - updateState(s1,s2):= max(s1,s2)





Convergence speed

In the push pull model the follwing is a good approximation of the superexponential convergence speed

$$p_{i+1} = p_i p_i \left(1 - \frac{1}{N} \right)^{N(1-p_i)} < p_i^2 < p_0^{2^{i+1}} = \left(1 - \frac{1}{N} \right)^{2^{i+1}}$$







Diffusion















BISON





Some Examples



- Diffusion has lots of other applications including
 - network size estimation
 - calculating variance (or any moments)





Some Comments

- Different from load balancing due to lack of constraints
- Diffusion is normally studied on regular topologies (grid)
- We are interested in realistic topologies: random, small-world, scale-free, etc.
- Diffusion is often the basis of biological selforganization like aggregation (2nd sense) and regeneration



Some Observations

- The procedure is convergent if the graph is connected
- Each node converges to the average of the original values





Summary of Our Theoretical Results

- On the fully connected topology convergence speed is exponential.
- On a random topology it is practically exponential.
- Node failure can destroy convergence above a theoretically described threshold.
- Dropping messages is not critical.





Case studies: realistic case

The rate of convergence is given by the formula

$$E(\boldsymbol{\sigma}_{i+1}^2) \approx \frac{E(\boldsymbol{\sigma}_i^2)}{2\sqrt{e}}$$

Where σ_i^2 is the empirical variance of the set of the approximations at the nodes in cycle i.







Conclusions

- Scalability: results independent of N
- Efficiency: convergence is very fast
- Robustness: the algorithm is highly robust to both node and message failure (not discussed in the present talk)





Applications



Epidemics: some examples

Critical Event Monitoring

- All nodes monitor their environment (temperature, amount of communication, available storage, etc)
- Critical events are treated as
 - database updates (when all are interesting)
 - maximization problem (when the most critical is important)

Control

- All nodes forward commands
- Commands are treated as database updates



Diffusion: some examples

- Calculating variance
 - calculate the average of the squares of the values and use it along with the average to approximate variance
- Calculating sum of values
 - calculate the average and multiply it by the size of the network
- Calculating network size
 - we will focus on this example in the following



Diffusion: a case study

- Network size estimation
 - one node is assigned value 1, all the others are assigned 0
 - the average is calculated which is a=1/N.
 - the estimation of the size is 1/a
- Practical Extensions
 - restarting in regular intervals (epochs): to make the protocol adaptive



initial value assignment

Initial Value Assignment

- We need to make sure exactly one node starts with 1, the rest with 0. Solution: parallel execution of approximations
 - With a probability P each node can start an approximation process. P is a previous approximation of 1/N
 - The initiator node starts with 1 and assigns a unique ID to the approximation process. The other (passive) nodes will assume 0 initial value for all IDs not initiated by themselves.



