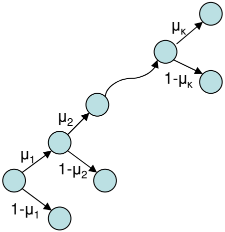
PageRank (PR)

- **Q:** What makes a web page important? **A:** many important pages contain links to it; however a page containing many links has reduced impact on the importance of the pages it contains links to. This is the basic idea in *PageRank* for ranking graph nodes.
- PageRank as a *random surfer process*: Start surfing from a random node and keep following links with probability μ restarting with probability $1 - \mu$; the node for restarting will be selected based on a personalization vector v. The ranking value x_i of a node i is the probability of visiting this node during surfing.
- PR can also be cast in power series representation as $x = (1 - \mu) \sum_{j=0}^{k} \mu^j S^j v$; S encodes column-stochastic adjacencies.

Functional rankings

- A general method to assign ranking values to graph nodes as $x = \sum_{j=0}^{k} \zeta_j S^j v$. PR is a functional ranking, $\zeta_j = (1 - \mu)\mu^j$.
- Terms attenuated by outdegrees in S *and* damping coefficients ζ_j.

Q: Is there a way to encode functional rankings as surfing processes?
A: Multidamping



Computing μ_j in multidamping

Simulate a functional ranking by random surfers following emanating links with probability μ_j at step *j* given by :

$$\mu_j = 1 - \frac{1}{1+\frac{\rho_{k-j+1}}{1-\mu_{j-1}}}, j = 1, ..., k,$$

where $\mu_0 = 0$ and $\rho_{k-j+1} = \frac{\zeta_{k-j+1}}{\zeta_{k-j}}$

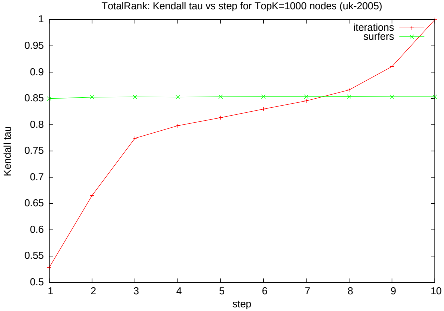
Examples

LinearRank (LR) $x^{\mathrm{LR}} = \sum_{j=0}^{k} \frac{2(k+1-j)}{(k+1)(k+2)} S^j v \,:\, \mu_j = \frac{j}{j+2}, j = 1, ..., k.$

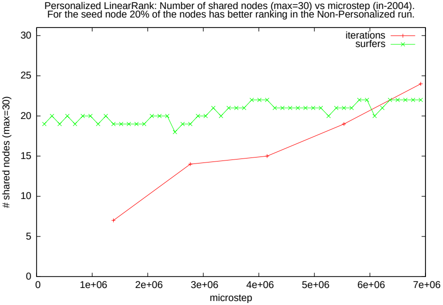
TotalRank (TR) $x^{\mathrm{TR}} = \sum_{j=0}^{\infty} \frac{1}{(j+1)(j+2)} S^j v \,:\, \mu_j = \frac{k-j+1}{k-j+2}, j = 1, ..., k.$

Advantages of multidamping

- Reduced computational cost in *approximating* functional rankings using the Monte Carlo approach. A random surfer terminates with probability $1 - \mu_j$ at step *j*.
- Inherently parallel and synchronization free computation.



TotalRank: Kendall tau vs step for TopK=1000 nodes (uk-2005)

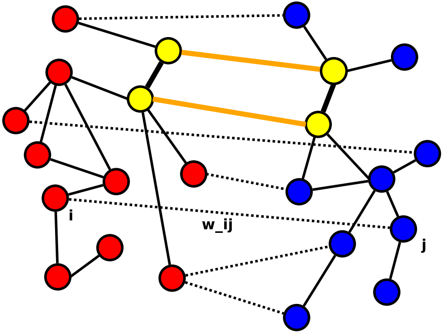


Personalized LinearRank: Number of shared nodes (max=30) vs microstep (in-2004).
For the seed node 20% of the nodes has better ranking in the Non-Personalized run.

Approximate ranking: Run n surfers to completion for graph size n. How well does the computed ranking capture the "reference" ordering for top$-k$ nodes (Kendall τ, y-axis) in comparison to the one calculated by standard iteration (for a number of steps, x-axis) of equivalent computational cost/number of operations? *[Left]*

Approximate personalized ranking: Run $< n$ surfers to completion (each called a microstep, x-axis), but only from a selected node (personalized). How well can we capture the "reference" top$-k$ nodes, i.e. how many of them are shared (y-axis), compared to the iterative approach of equivalent computational load? *[Right]*

[uk-2005: $39,459,925$ nodes, $936,364,282$ edges. in-2004: $1,382,908$ nodes, $16,917,053$ edges]



- **Node similarity:** Two nodes are similar if they are linked by other similar node pairs. By pairing similar nodes, the two graphs become *aligned*.
- In *IsoRank*, a state-of-the-art graph alignment method, first a matrix X of similarity scores between the two sets of nodes is computed and then maximum-weight bipartite matching approaches extract the most similar pairs.

- Let $\tilde{A}$, $\tilde{B}$ the adjacencies A^T, B^T of the two graphs normalized by columns (network data), H_{ij} independently known similarity scores (preferences matrix) between nodes $i \in V_B$ and $j \in V_A$ and μ the percentage of contribution of network data in the algorithm.
- To compute X, IsoRank iterates:

$$X \leftarrow \mu \tilde{B} X \tilde{A}^T + (1-\mu) H$$

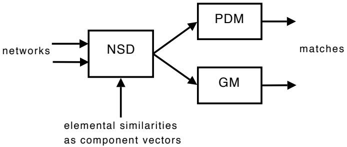
Network Similarity Decomposition (NSD)

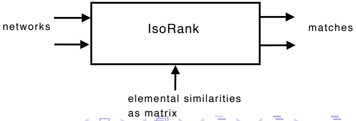
- We reformulate IsoRank iteration and gain speedup and parallelism.
- In n steps of we reach $X^{(n)} = (1-\mu)\sum_{k=0}^{n-1} \mu^k \tilde{B}^k H (\tilde{A}^T)^k + \mu^n \tilde{B}^n H (\tilde{A}^T)^n$
- Assume for a moment that $H = uv^T$ (1 component). Two phases for X:

  1. $u^{(k)} = \tilde{B}^k u$ and $v^{(k)} = \tilde{A}^k v$ *(preprocess/compute iterates)*
  2. $X^{(n)} = (1-\mu)\sum_{k=0}^{n-1} \mu^k u^{(k)} {v^{(k)}}^T + \mu^n u^{(n)} {v^{(n)}}^T$ *(construct X)*

  This idea extends to s components, $H \sim \sum_{i=1}^{s} w_i z_i^T$.
- NSD computes matrix-vector iterates and builds X as a sum of outer products of vectors; these are much cheaper than triple matrix products.

We can then apply Primal Dual Matching (PDM) or Greedy Matching (1/2 approximation, GM) to extract the actual node pairs.





Species	Nodes	Edges
celeg (worm)	2805	4572
dmela (fly)	7518	25830
ecoli (bacterium)	1821	6849
hpylo (bacterium)	706	1414
hsapi (human)	9633	36386
mmusc (mouse)	290	254
scere (yeast)	5499	31898

Species pair	NSD (secs)	PDM (secs)	GM (secs)	IsoRank (secs)
celeg-dmela	**3.15**	152.12	7.29	783.48
celeg-hsapi	**3.28**	163.05	9.54	1209.28
celeg-scere	**1.97**	127.70	4.16	949.58
dmela-ecoli	**1.86**	86.80	4.78	807.93
dmela-hsapi	**8.61**	590.16	28.10	7840.00
dmela-scere	**4.79**	182.91	12.97	4905.00
ecoli-hsapi	**2.41**	79.23	4.76	2029.56
ecoli-scere	**1.49**	69.88	2.60	1264.24
hsapi-scere	**6.09**	181.17	15.56	6714.00

- We computed the similarity matrices X for various possible pairs of species using Protein-Protein Interaction (PPI) networks. $\mu = 0.80$, uniform initial conditions (outer product of suitably normalized 1's for each pair), 20 iterations, one component.
- Then we extracted node matches using PDM and GM.
- *3 orders of magnitude speedup* of NSD-based approaches compared to IsoRank ones.

Parallelization: NSD has also been ported to parallel/distributed platforms:

- We have aligned up to million-node graph instances using up to $3,072$ cores in a supercomputer installation.
- We have managed to process graph pairs of over a billion nodes and twenty billion edges each, over MapReduce-based platforms.