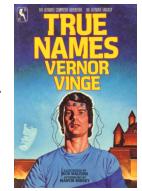
In the once upon a time days of the First Age of Magic, the prudent sorcerer regarded his own true name as his most valued possession but also the greatest threat to his continued good health, for--the stories go-once an enemy, even a weak unskilled enemy, learned the sorcerer's true name, then routine and widely known spells could destroy or enslave even the most powerful. As times passed, and we graduated to the Age of Reason and thence to the first and second industrial revolutions, such notions were discredited. Now it seems that the Wheel has turned full circle (even if there never really was a First Age) and we are back to worrying about true names again:

The first hint Mr. Slippery had that his own True Name might be known-and, for that matter, known to the Great Enemy--came with the appearance of two black Lincolns humming up the long dirt driveway ... Roger Pollack was in his garden weeding, had been there nearly the whole morning.... Four heavy-set men and a hard-looking female piled out, started purposefully across his well-tended cabbage patch....

This had been, of course, Roger Pollack's great fear. They had discovered Mr. Slippery's True Name and it was Roger Andrew Pollack TIN/SSAN 0959-34-2861.



Recap: soft joins/similarity joins

Input: Two Different Lists of Entity Names

Abraham Lincoln Birthplace NHS	Acadia NP		
Acadia NP	Allegheny Portage Railroad NHS		
Adams NHS	American Memorial Park		
Agate Fossil Beds NM	Amistad NRA		
Alagnak Wild River	Andersonville NHP		
Alaska Public Lands Inf. Center	Aniakchak NM		
Alibates Flint Quarries NM	Antietam NB		
Allegheny Portage Railroad NHS	Apostle Islands NL		
American Memorial Park	Appomattox Court House NHP		
Amistad NRA	Arches NP		
Andersonville NHS	Arkansas Post N. Mem.		
Andrew Johnson NHS	Assateague Island NS		
Aniakchak NM & NPRES	Aztec Ruins NM		
Antietam NB	Badlands NP		
Apostle Islands NL	Bandelier NM		
Appalachian National Scenic Trail	Bent's Old Fort NHS		
Appomattox Courthouse NHP	Bering Land Bridge N. Preserve		
Arches NP	Big Bend NP		
Arkansas Post NM	Big Cypress N. Preserve		

Recap: soft joins/similarity joins

Output: Pairs of Names Ranked by Similarity

. . .

identical

Chickamauga & Chattanooga NMP:d445 George Washington Carver NM:d499 Salinas Pueblo Missions NM:d597 Florissant Fossil Beds NM:d473 Hagerman Fossil Beds NM:d517 Gila Cliff Dwellings NM:d502 Booker T. Washington NM:d423

similar

Obed Wild & Scenic River:d570 Andersonville NHP:d401 Sitka NHP:d606 Bering Land Bridge N. Preserve:d413 Sequoia & Kings Canyon NP:d603 Glacier Bay NP & Preserve:d643 NP of American Samoa:d561 Kalaupapa NHS:d538 Chickamauga & Chattanooga NMP:d72 George Washington Carver NM:d153 Salinas Pueblo Missions NM:d329 Florissant Fossil Beds NM:d116 Hagerman Fossil Beds NM:d177 Gila Cliff Dwellings NM:d156 Booker T. Washington NM:d38

Obed Wild and Scenic River:d283 Andersonville NHS:d11 Sitka NHS:d342 Bering Land Bridge NPRES:d26 Sequoia and Kings Canyon NP:d339 Glacier Bay NP & NPRES:d157 National Park Of American Samoa:d267 Kalaupapa NHP:d210

 less similar
 Lake Mead NRA:d545
 Lake Mead NRA (Nevada):d224

 Upper Delaware Scenic & Rec. River:d617
 Upper Delaware Scenic & Recreational River:d368

Example: soft joins/similarity joins

Output: Pairs of Names Ranked by Similarity

. . .

A surprisingly good similarity score is TFIDF cosine distance.

- Mismatches on frequent terms ("&" vs "and", "N.", "Preserve", "NHP", ...) are discounted
- Matches on rare term ("Kalaupapa", "Samoa") are rewarded.

Obed Wild & Scenic River:d570 Andersonville NHP:d401 Sitka NHP:d606 Bering Land Bridge N. Preserve:d413 Sequoia & Kings Canyon NP:d603 Glacier Bay NP & Preserve:d643 NP of American Samoa:d561 Kalaupapa NHS:d538 Obed Wild and Scenic River:d283 Andersonville NHS:d11 Sitka NHS:d342 Bering Land Bridge NPRES:d26 Sequoia and Kings Canyon NP:d339 Glacier Bay NP & NPRES:d157 National Park Of American Samoa:d267 Kalaupapa NHP:d210

Lake Mead NRA:d545 Lake Mead NRA (Nevada):d224 Upper Delaware Scenic & Rec. River:d617 Upper Delaware Scenic & Recreational River:d368

Softjoin Example - 1

~ means "similar to"

FROM top500,hiTech SELECT * WHERE top500.name~hiTech.name

top 500:

hiTech:

Abott Laboratories

ACC CORP

ADC TELECOMMUNICATION INC.

Able Telcom Holding Corp. Table VI. Pairs of Names from the Hoovers and lontech Relations

TEXAS INSTRUMENTS INC Texas Instruments Incorporated The New York Times Company NEW YORK TIMES CO Campo Electronics, Appliances CAMPO ELECTRONICS $\sqrt{}$ APPLIANCES and Computers, Inc. CASCADE COMMUNICATION Cascade Communications Corp. $\sqrt{}$ The McGraw-Hill Companies, Inc. MCGRAW-HILL CO U S WEST Communications Group U S WEST INC Silicon Valley Group, Inc. SILICON VALLEY RESEARCH INC \times **REYNOLDS & REYNOLDS CO** The Reynolds and Reynolds Company Х INTIME SYSTEMS INTERNATIONAL I InTime Systems International, Inc.

A useful scalable similarity metric: IDF weighting plus cosine distance!

One solution: Soft (Similarity) joins

- A similarity join of two sets A and B is
 - an ordered list of triples (s_{ij}, a_i, b_j) such that
 - a_i is from A
 - b_j is from B
 - s_{ij} is the *similarity* of a_i and b_j
 - the triples are in descending order
 - the list is either the top K triples by s_{ij} or ALL triples with s_{ij} >L ... or sometimes some approximation of these....

How well does TFIDF work?

- Input: query
- Output: ordered list of documents

1	\sim	a_1	b_1	
2	\checkmark	a_2	b_2	Precision at $K: G_K/K$
3	×	a_3	b_3	Recall at $K: G_K/G$
4	\checkmark	a_4	b_4	
5	\checkmark	a_5	b_5	
6	\checkmark	a_6	b_6	
7	×	a_7	b_7	
8	\checkmark	a_8	b_8	G: # good pairings
9	\checkmark	a_9	b_9	G_K : # good pairings in first K
10	×	a_{10}	b_{10}	
11	×	a_{11}	b_{11}	
12	\checkmark	a_{12}	b_{12}	

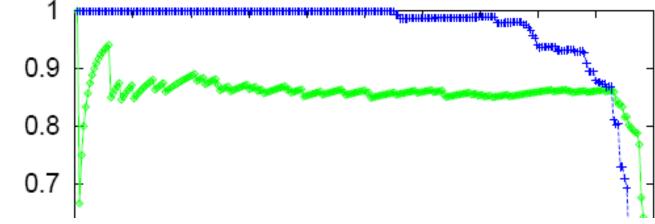


Table VI. Pairs of Names from the Hoovers and lontech Relations

Ч

\checkmark	Texas Instruments Incorporated	TEXAS INSTRUMENTS INC
\checkmark	The New York Times Company	NEW YORK TIMES CO
\checkmark	Campo Electronics, Appliances	CAMPO ELECTRONICS
	and Computers, Inc.	APPLIANCES
\checkmark	Cascade Communications Corp.	CASCADE COMMUNICATION
\checkmark	The McGraw-Hill Companies, Inc.	MCGRAW-HILL CO
	U S WEST Communications Group	U S WEST INC
×	Silicon Valley Group, Inc.	SILICON VALLEY RESEARCH INC
×	The Reynolds and Reynolds Company	REYNOLDS & REYNOLDS CO
\checkmark	InTime Systems International, Inc.	INTIME SYSTEMS INTERNATIONAL I

Domain	Relations Joined	Average Precision
Movies	MovieLink/Review	100.0%
Animals	IntFact1/SWFact	100.0%
	IntFact2/FWSFact	99.6%
	IntFact3/NMFSFact	97.1%
	Endanger/ParkAnim	95.2%
Birds	IntBirdPic1/DonBirdPic	100.0%
	IntBirdPic2/MBRBirdPic	99.1%
	IntBirdMap/BirdMap	91.4%
	BirdCall/BirdList	95.8%
Businesses	Fodor/Zagrat	99.5%
	HooverWeb/Iontech	84.9%
National Parks	IntPark/Park	95.7%
Computer Games	Demo/AgeList	86.1%

Table V. Average Precision for Similarity Joins

There are refinements to TFIDF distance – eg ones that extend with soft matching at the token level (e.g., softTFIDF)

distance is '[JaroWinklerTFIDF:threshold=0.9]' Pairs: 6806 Correct: 250 Matching time: 0.278 + 1 1.00 | Agate Fossil Beds NM | Agate Fossil Beds NM 2 1.00 Big Bend NP | Big Bend NP . . . 1.00 | + 194 Gateway NRA | Gateway NRA + 195 0.99 | Gulf Islands NS | Gulf Island NS Rainbow Bridge NM | Rainbow Bridges NM + 196 0.99 | + 1970.98 | Whiskeytown Shasta Trinity NRA | Whiskey-Shasta-Trinity NRA + 1980.97 | Capitol Reef NP | Capital Reef NP + 1990.95 | Timpanogos Cave NM | Timpanogas Caves NM + 200 0.94 | War in the Pacific NHP | War in Pacific NHP 0.94 | Chesapeake & Ohio Canal NHP | Chesapeake and Ohio Canal NHP + 201 + 203 0.92 1 Saguaro NP | Saguaro NM . . 0.88 | Aniakchak NM & NPRES | + 210 Aniakchak NM + 211 0.86 | National Park Of American Samoa | NP of American Samoa . . + 224 0.76 | Pu'uhonua a Honaunau NHP | Pu'uohonua O Honaunau NHP 0.75 | Bering Land Bridge NPRES | Bering Land Bridge N. Preserve + 225 + 226 0.75 | Yukon Charley Rivers NPRES | Yukon-Charley Rivers N. Preserve . . . 0.69 | Wolf Trap Farm Park for the Performing Arts + 241 Wolf Trap Farm Park + 242 0.69 | Fredericksburg and Spotsylvania County Battlefields Memorial NMP | Fredericksburg & Spotsylvania NMP + 243 0.69 | Great Smoky Mtn. NP | Great Smoky Mountains NP + 2450.67 | Mount Rushmore NM | Mount Rushmore N. Mem. + 2460.67 | Chattahoochee NSR | Chattahoochee River NRA . . .

distan	ce is '[J	VaroWinklerTFIDF:threshold=0.9]'	
Pairs:	6806 Cor	rect: 250	
Matchi	ng time:	0.278	
+ 1	1.00	Agate Fossil Beds NM	Agate Fossil Beds NM
+ 2	1.00	Big Bend NP	Big Bend NP
+ 194	1.00	Gateway NRA	Gateway NRA
+ 195	0.99	Gulf Islands NS	Gulf Island NS
+ 196	0.99	Rainbow Bridge NM	Rainbow Bridges NM
+ 197	0.98	Whiskeytown Shasta Trinity NRA	Whiskey-Shasta-Trinity NRA
+ 198	0.97	Capitol Reef NP	-
+ 199	0.95	Timpanogos Cave NM	Timpanogas Caves NM
+ 200	0.94	War in the Pacific NHP	War in Pacific NHP
+ 201	0.94	Chesapeake & Ohio Canal NHP C	Chesapeake and Ohio Canal NHP
+ 203	0.92	Saguaro NP	Saguaro NM
+ 210	0.88	Aniakchak NM & NPRES	Aniakchak NM
+ 211	0.86	National Park Of American Samoa	NP of American Samoa
+ 224	0.76	Pu'uhonua a Honaunau NHP	Pu'uohonua O Honaunau NHP
+ 225	0.75	Bering Land Bridge NPRES E	Bering Land Bridge N. Preserve
+ 226	0.75	Yukon Charley Rivers NPRES Y	/ukon-Charley Rivers N. Preserve
+ 241	0.69	Wolf Trap Farm Park for the Perfor	rming Arts
		1	Wolf Trap Farm Park
+ 242	0.69	Fredericksburg and Spotsylvania Co	ounty Battlefields Memorial NMP
		E	Fredericksburg & Spotsvlvania NMP
+ 243	0.69	Great Smoky Mtn. NP	Great Smoky Mountains NP
+ 245	0.67	Mount Rushmore NM	Mount Rushmore N. Mem.
+ 246	0.67	Chattahoochee NSR	Chattahoochee River NRA
-			

||

SOFT JOINS WITH TFIDF: HOW?

Rocchio's algorithm

formulae DF(w) = # different docs w occurs in TF(w,d) = # different times w occurs in doc d ...as long as u(w,d)=0 for $IDF(w) = \frac{|D|}{DF(w)}$ words not in d! $u(w,d) = \log(TF(w,d) + 1) \cdot \log(IDF(w))$ Store only non-zeros in $\mathbf{u}(d) = \left\langle u(w_1, d), \dots, u(w_{|V|}, d) \right\rangle$ $\mathbf{u}(d)$, so size is O(|d|) $\mathbf{u}(y) = \alpha \frac{1}{|C_y|} \sum_{d \in C_y} \frac{\mathbf{u}(d)}{\|\mathbf{u}(d)\|_2} - \beta \frac{1}{|D - C_y|} \sum_{d' \in D - C_y} \frac{\mathbf{u}(d')}{\|\mathbf{u}(d')\|_2}$ But size of $\mathbf{u}(y)$ is $O(|n_v|)$ $f(d) = \operatorname{arg\,max}_{y} \frac{\mathbf{u}(d)}{\|\mathbf{u}(d)\|_{2}} \cdot \frac{\mathbf{u}(y)}{\|\mathbf{u}(y)\|_{2}}$ $\left\|\mathbf{u}\right\|_2 = \sqrt{\sum_i u_i^2}$

Many variants

of these

TFIDF similarity

DF(w) = # different docs w occurs in TF(w,d) = # different times w occurs in doc d $IDF(w) = \frac{|D|}{DF(w)}$ $u(w,d) = \log(TF(w,d) + 1) \cdot \log(IDF(w))$ $\mathbf{u}(d) = \left\langle u(w_1, d), \dots, u(w_{|V|}, d) \right\rangle$ $\mathbf{v}(d) = \frac{\mathbf{u}(d)}{\|\mathbf{u}(d)\|_{2}}$ $sim(\mathbf{v}(d_1), \mathbf{v}(d_2)) = \mathbf{v}(d_1) \cdot \mathbf{v}(d_2) = \sum \frac{u(w, d_1)}{\|\mathbf{u}(d_1)\|_2} \frac{u(w, d_2)}{\|\mathbf{u}(d_2)\|_2}$

TFIDF soft joins

- A similarity join of two sets of TFIDF-weighted vectors A and B is
 - an ordered list of triples (s_{ij}, a_i, b_j) such that
 - a_i is from A
 - b_j is from B
 - s_{ii} is the dot product of a_i and b_i
 - the triples are in descending order
 - the list is either the top K triples by s_{ij} or ALL triples with s_{ij} >L ... or sometimes some approximation of these....

PARALLEL SOFT JOINS

Efficient Parallel Set-Similarity Joins Using MapReduce

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SIGMOD 2010

TFIDF similarity: variant for joins

DF(A, w) = # different docs w occurs in from A DF(B, w) = # different docs w occurs in from B TF(w,d) = # different times w occurs in doc d $IDF(w,d) = \frac{|C_d|}{DF(C_u,w)}$, where $C_d \in \{A,B\}$ $u(w,d) = \log(TF(w,d)+1) \cdot \log(IDF(w,d))$ $\mathbf{u}(d) = \left\langle u(w_1, d), \dots, u(w_{|V|}, d) \right\rangle$ $\mathbf{v}(d) = \frac{\mathbf{u}(d)}{\|\mathbf{u}(d)\|_{2}}$ $sim(\mathbf{v}(d_1), \mathbf{v}(d_2)) = \mathbf{v}(d_1) \cdot \mathbf{v}(d_2) = \sum_{w \in \mathcal{W}} \frac{u(w, d_1)}{\|\mathbf{u}(d_1)\|_2} \frac{u(w, d_2)}{\|\mathbf{u}(d_2)\|_2}$

Sim Joins on Product Descriptions

- Similarity can be **high** for descriptions of **distinct** items:
 - AERO TGX-Series Work Table -42" x 96" Model 1TGX 4296 All tables shipped KD AEROSPEC- 1TGX Tables are Aerospec Designed. In addition to above specifications; - All four sides have a V countertop edge ...
 - AERO TGX-Series Work Table -42" x 48" Model 1TGX-4248 All tables shipped KD AEROSPEC- 1TGX Tables are Aerospec Designed. In addition to above specifications; - All four sides have a V countertop ..
- Similarity can be **low** for descriptions of **identical** items:
 - Canon Angle Finder C 2882A002 Film Camera Angle Finders Right Angle Finder C (Includes ED-C & ED-D Adapters for All SLR Cameras) Film Camera Angle Finders & Magnifiers The Angle Finder C lets you adjust
 - CANON 2882A002 ANGLE FINDER & FOR EOS REBEL® SERIES
 PROVIDES A FULL SCREEN IMAGE SHOWS EXPOSURE DATA BUILT-IN
 DIOPTRIC ADJUSTMENT COMPATIBLE WITH THE CANON® REBEL, EOS
 & REBEL EOS SERIES.

Parallel Inverted Index Softjoin - 1



Statistics for computing TFIDF with IDFs local to each relation²⁰

Parallel Inverted Index Softjoin - 2

```
simpairs = Filter(softjoin, by=lambda(doc1,doc,sim):sim>0.75)
```

What's the algorithm?

- Step 1: create document vectors as (C_d, d, term, weight) tuples
- Step 2: *join* the tuples from A and B: one sort and reduce
 - Gives you tuples (*a*, *b*, *term*, *w*(*a*,*term*)**w*(*b*,*term*))
- Step 3: *group* the common terms by (a,b) and reduce to aggregate the components of the sum

An alternative TFIDF pipeline

def loadDictView(view):
 result = {}
 for (key,val) in GPig.rowsOf(view):
 result[key] = val
 return result

class TFIDF(Planner):

```
D = GPig.getArgvParams()
data = ReadLines(D.get('corpus','idcorpus.txt')) \
     Map(by=lambda line:line.strip().split("\t")) \
     Map(by=lambda (docid,doc): (docid,doc.lower().split())) \
     FlatMap(by=lambda (docid,words): map(lambda w:(docid,w),words))
#compute document frequency and inverse doc freq
docFreq = Distinct(data) \
    | Group(by=lambda (docid,term):term, retaining=lambda(docid,term):docid, reducingTo=ReduceToCount())
ndoc = Map(data, by=lambda (docid,term):docid) \
    Distinct() \
    Group(by=lambda row:'ndoc', reducingTo=ReduceToCount())
inverseDocFreq = Augment(docFreq, sideview=ndoc, loadedBy=lambda v:GPig.onlyRowOf(v)) \setminus
    | Map(by=lambda((term,df),(dummy,ndoc)):(term,math.log(ndoc/df)))
#compute unweighted document vectors
udocvec = Augment(data, sideview=inverseDocFreq, loadedBy=loadDictView) \
    Map(by=lambda ((docid,term),idfDict):(docid,term,idfDict[term]))
#normalize
norm = Group( udocvec, by=lambda(docid,term,weight):docid,
                       retaining=lambda(docid,term,weight):weight*weight,
                       reducingTo=ReduceToSum() )
docvec = Augment(udocvec, sideview=norm, loadedBy=loadDictView) \
                                                                                                    22
```

| Map(by=lambda ((docid,term,weight),normDict): (docid,term,weight/math.sqrt(normDict[docid])))

Inverted Index Softjoin – PIG 1/3

-- invoke as: pig --param input=id-park --param rel=icepark ... phirl.pig

```
%default output sim
%default rel a
%default def_par 10
SET default parallel $def par;
-- load and tokenize the data as data:{rel,id,str,term}
raw = LOAD 'phirl/$input' AS (rel,docid,keyid,str);
data = FOREACH raw GENERATE rel,docid,FLATTEN(TOKENIZE(LOWER(str))) AS term;
-- compute relation-dependent document frequencies as docfreq:{rel,term,df:int}
docfreg =
  FOREACH (GROUP data by (rel,term))
  GENERATE group.rel AS rel, group.term as term, COUNT(data) as df;
-- find the total number of documents in each relation as ndoc:{rel,c:long}
ndoc1 = DISTINCT(FOREACH data GENERATE rel,docid);
ndoc = FOREACH (GROUP ndoc1 by rel) GENERATE group AS rel, COUNT(ndoc1) AS c;
```

Inverted Index Softjoin – 2/3

```
-- find the un-normalized document vectors as udocvec:{rel.docid,term,weight}
udocvec1 = JOIN data BY (rel,term), docfreq BY (rel,term);
udocvec2 = JOIN udocvec1 BY data::rel, ndoc BY rel;
udocvec =
   FOREACH udocvec2
   GENERATE data::rel, data::docid, data::term,
     LOG(2.0)*LOG(ndoc::c/(double)docfreg::df) AS weight;
-- find the square of the normalizer for each document: norm:{rel,docid,z2:double}
norm1 = FOREACH udocvec GENERATE rel,docid,term,weight*weight as w2;
norm =
   FOREACH (GROUP norm1 BY (rel,docid))
   GENERATE group.rel AS rel, group.docid AS docid, SUM(norm1.w2) AS z2;
-- compute the TFIDF weighted document vectors as: docvec:{rel,docid,term,weight:double}
docvec =
   FOREACH (JOIN udocvec BY (rel,docid), norm BY (rel,docid))
   GENERATE data::rel AS rel, data::docid AS docid, data::term AS term,
      weight/SQRT(z2) as weight;
```

Inverted Index Softjoin – 3/3

docvec:{rel,docid,term,weight:double}

```
-- naive algorithm: use all terms for finding potentil matches
docsA = FILTER docvec BY rel=='$rel';
docsB = FILTER docvec BY rel!='$rel';
softjoin1 = JOIN docsA BY term, docsB BY term;
softjoin2 =
   FOREACH softjoin1
   GENERATE docsA::docid AS idA, docsB::docid AS idB, docsA::weight*docsB::weight AS p;
softjoin =
   FOREACH (GROUP softjoin2 BY (idA,idB))
   GENERATE group.idA, group.idB, SUM(softjoin2.p) AS sim;
# naive algorithm: use all pairs for finding matches
rel1Docs = Filter(docvec, by=lambda(rel,doc,term,weight):rel=='icepark')
rel2Docs = Filter(docvec, by=lambda(rel,doc,term,weight):rel=='npspark')
softjoin = Join( Jin(rel1Docs,by=lambda(rel,doc,term,weight):term),
               Jin(rel2Docs,by=lambda(rel,doc,term,weight):term)) \
     ReplaceEach(by=lambda((rel1,doc1,term,weight1),(rel2,doc2,term2,weight2)): (doc1,doc2,weight1*weight2)) \
    Group(by=lambda(doc1,doc2,p):(doc1,doc2), \
           retaining=lambda(doc1,doc2,p):p, \
           reducingTo=ReduceToSum()) \
    ReplaceEach(by=lambda((doc1,doc2),sim):(doc1,doc2,sim))
```

Inverted Index Softjoin – 3/3

docvec:{rel,docid,term,weight:double}

```
-- naive algorithm: use all terms for finding potentil matches
docsA = FILTER docvec BY rel=='$rel';
docsB = FILTER docvec BY rel!='$rel';
softjoin1 = JOIN docsA BY term, docsB BY term;
softjoin2 =
  FOREACH softjoin1
  GENERATE docsA::docid AS idA, docsB::docid AS idB, docsA::weight*docsB::weight AS p;
softjoin =
  FOREACH (GROUP softjoin2 BY (idA,idB))
  GENERATE group.idA, group.idB, SUM(softjoin2.p) AS sim;
-- diagnostic output: look: {sim, [01], idA, idB, str1, str2}
look1 = JOIN topSimPairs BY idA, raw BY docid;
look2 = JOIN look1 BY idB, raw BY docid;
look =
   FOREACH look2
   GENERATE sim, (look1::raw::keyid==raw::keyid ? 1 : 0),
      idA, idB, look1::raw::str AS str1, raw::str AS str2;
```

```
STORE look INTO 'phirl/$output';
```

Results.....

0.99436717611623	1	d00059	d00436	Carl Sandburg Home NHS Carl Sandburg Home NHS
0.9937688379278058	1	d00354	d00611	Theodore Roosevelt NP Theodore Roosevelt NP
0.9920648281782544	1	d00286	d00573	Oregon Caves NM Oregon Caves NM
0.9914077975044103	1	d00274	d00566	New River Gorge NR New River Gorge NR
0.9881961852455996	1	d00009	d00399	American Memorial Park American Memorial Park
0.9878514547862078	1	d00154	d00500	George Washington Memorial Parkway George Washington Me
0.9422676645498852	1	d00376	d00623	War in the Pacific NHP War in Pacific NHP
0.92307133361005	1	d00323	d00594	Saguaro NP Saguaro NM
0.8914304226443976	1	d00292	d00577	Pea Ridge NHS Pea Ridge NMP
0.890829830425262	1	d00200	d00532	Jean Lafitte NHP & NPRES Jean Lafitte NHP & Preserve
0.8873463623037525	0	d00283	d00570	Obed Wild and Scenic River Obed Wild & Scenic River
0.8838421147370781	1	d00342	d00606	Sitka NHS Sitka NHP
0.8838421147370781	1	d00011	d00401	Andersonville NHS Andersonville NHP
0.8700042867436217	1	d00026	d00413	Bering Land Bridge NPRES Bering Land Bridge N. Preser
0.8684330615122184	1	d00157	d00643	Glacier Bay NP & NPRES Glacier Bay NP & Preserve
0.8680495192463105	1	d00339	d00603	Sequoia and Kings Canyon NP Sequoia & Kings Canyon NP
0.8660286476353838	1	d00267	d00561	National Park Of American Samoa NP of American Samoa
0.8593112749780314	1	d00210	d00538	Kalaupapa NHP Kalaupapa NHS
0.8500226387429363	1	d00208	d00536	Johnstown Flood NM Johnstown Flood N. Mem.
0.8424859579540737	1	d00222	d00646	Lake Clark NP & NPRES Lake Clark NP & Preserve
0.8398407018438242	1	d00187	d00523	Homestead National Monument of America Homestead NM of Amer
0.8395526626941698	1	d00230	d00548	Lincoln Boyhood NM Lincoln Boyhood N. Mem.
0.8390553468895996	1	d00349	d00610	Sunset Crater NM Sunset Crater Volcano NM
0.8344604123961857	1	d00259	d00559	Mount Rushmore NM Mount Rushmore N. Mem.
0.8313853772986841	0	d00353	d00611	Theodore Roosevelt Island Theodore Roosevelt NP
0.8301435671019225	1	d00071	d00444	Chesapeake & Ohio Canal NHP Chesapeake and Ohio Canal NH
0.82492593280652	1	d00019	d00407	Arkansas Post NM Arkansas Post N. Mem.
0.8202902347497227	1	d00212	d00644	Katmai NP & NPRES Katmai NP & Preserve
0.8202902347497227	1	d00098	d00464	Denali NP & NPRES Denali NP & Preserve
0.7965479702996782	1	d00013	d00402	Aniakchak NM & NPRES Aniakchak NM
0.7835432589199314	1	d00031	d00417	Big Thicket NPRES Big Thicket N. Preserve
0.7835432589199314	1	d00028	d00415	Big Cypress NPRES Big Cypress N. Preserve 27

```
raw = LOAD 'phirl/$input' AS (rel,docid,keyid,str);
data = FOREACH raw GENERATE rel,docid,FLATTEN(TOKENIZE(LOWER(str))) AS term;
-- compute relation-dependent document frequencies as docfreq:{rel,term,df:int}
docfreg =
  FOREACH (GROUP data by (rel,term))
  GENERATE group.rel AS rel, group.term as term, COUNT(data) as df;
-- find the total number of documents in each relation as ndoc:{rel,c:long}
ndoc1 = DISTINCT(FOREACH data GENERATE rel,docid);
ndoc = FOREACH (GROUP ndoc1 by rel) GENERATE group AS rel, COUNT(ndoc1) AS c;
-- find the un-normalized document vectors as udocvec:{rel.docid,term,weight}
udocvec1 = JOIN data BY (rel,term), docfreq BY (rel,term);
udocvec2 = JOIN udocvec1 BY data::rel, ndoc BY rel;
udocvec =
   FOREACH udocvec2
   GENERATE data::rel, data::docid, data::term,
     LOG(2.0)*LOG(ndoc::c/(double)docfreg::df) AS weight;
-- find the square of the normalizer for each document: norm:{rel,docid,z2:double}
norm1 = FOREACH udocvec GENERATE rel,docid,term,weight*weight as w2;
norm =
   FOREACH (GROUP norm1 BY (rel,docid))
   GENERATE group.rel AS rel, group.docid AS docid, SUM(norm1.w2) AS z2;
-- compute the TFIDF weighted document vectors as: docvec:{rel,docid,term,weight:double}
docvec =
FOREACH (JOIN udocvec BY (rel,docid), norm BY (rel,docid))
   GENERATE data::rel AS rel, data::docid AS docid, data::term AS term,
      weight/SQRT(z2) as weight;
fs -rmr phirl/docvec
STORE docvec INTO 'phirl/docvec';
-- naive algorithm: use all terms for finding potentil matches
docsA = FILTER docvec BY rel=='$rel';
docsB = FILTER docvec BY rel!='$rel';
softjoin1 = JOIN docsA BY term, docsB BY term;
softjoin2 =
   FOREACH softjoin1
   GENERATE docsA::docid AS idA, docsB::docid AS idB, docsA::weight*docsB::weight AS p;
softjoin =
   FOREACH (GROUP softjoin2 BY (idA,idB))
   GENERATE group.idA, group.idB, SUM(softjoin2.p) AS sim;
```

Making the algorithm smarter....

Inverted Index Softjoin - 2

```
-- naive algorithm: use all terms for finding potentil matches
docsA = FILTER docvec BY rel=='$rel';
docsB = FILTER docvec BY rel!='$rel';
softjoin1 = JOIN docsA BY term, docsB BY term;
softjoin2 =
FOREACH softjoin1
GENERATE docsA::docid AS idA, docsB::docid AS idB, docsA::weight*docsB::weight AS p;
softjoin =
FOREACH (GROUP softjoin2 BY (idA,idB))
GENERATE group.idA, group.idB, SUM(softjoin2.p) AS sim;
```

we should make a smart choice about which terms to use

Adding heuristics to the soft join - 1

-- compute maximum weight for rel2docs as: maxweight2:{term,weight}

```
maxweightB =
    FOREACH (GROUP docsB BY (rel,term))
    GENERATE group.term AS term, MAX(docsB.weight) AS weight;
-- augment the docvecs for rel1 with maxweight2 and docfreq information to get
-- augdocsA: {rel,docid,term, w,df,maxw,score}
docfreqB = FILTER docfreq BY rel!='$rel';
augdocsA1 = JOIN docsA BY term, docfreqB BY term, maxweightB BY term;
augdocsA =
    FOREACH augdocsA1
    GENERATE docsA::rel, docsA::docid, docsA::term, docsA::weight AS w,
        docfreqB::df AS df, maxweightB::weight AS maxw,
        docsA::weight*maxweightB::weight AS score;
```

$$\mathbf{v}_{a}\mathbf{v}_{b} = \sum_{w} \mathbf{v}_{a}[w] * \mathbf{v}_{b}[w] \le \sum_{w} \mathbf{v}_{a}[w] * \text{maxweight2}[w]$$

score for w in doc a

Adding heuristics to the soft join - 1

```
auqdocsA =
   FOREACH augdocsA1
   GENERATE docsA::rel, docsA::docid, docsA::term, docsA::weight AS w,
     docfreqB::df AS df, maxweightB::weight AS maxw,
     docsA::weight*maxweightB::weight AS score;
-- filter out useful terms to join on, using the info in augdocsA.
-- the heuristics used here are:
--- (1) only use top K by maxscore w/in each document;
--- (2) filter by df<=maxDF
--- (3) filter by score>=minscore
usefulTerms1 =
   FOREACH (GROUP augdocsA BY (rel,docid))
   GENERATE group, TOP($top_k,6,augdocsA) AS top;
usefulTerms2 =
   FOREACH usefulTerms1 {
      filteredTop = FILTER top BY (df<=$max_df) AND score>$min_sim;
      topTerms = FOREACH filteredTop GENERATE term;
      GENERATE flatten(topTerms);
   }:
usefulTerms = DISTINCT usefulTerms2;
```

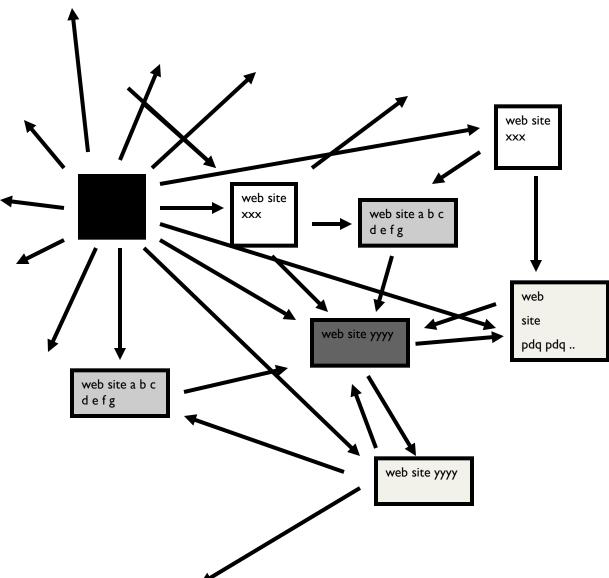
Adding heuristics to the soft join - 2

```
-- use the restricted sets of terms to get candidate pairs
pairs1 = JOIN usefulTerms BY term, docsA BY term, docsB BY term;
pairs2 = FOREACH pairs1 GENERATE docsA::docid AS idA, docsB::docid AS idB;
pairs = DISTINCT pairs2;
--- STORE pairs INTO 'phirl/pairs';
softjoin1 = JOIN pairs BY idA, docsA by docid;
softjoin2 = JOIN softjoin1 BY (idB,term), docsB by (docid,term);
softjoin3 =
FOREACH softjoin2
GENERATE idA, idB, docsA::term AS term, docsA::weight*docsB::weight AS p;
softjoin =
FOREACH (GROUP softjoin3 BY (idA,idB))
GENERATE group.idA, group.idB, SUM(softjoin3.p) AS sim;
```

```
docsA = FILTER docvec BY rel=='$rel';
docsB = FILTER docvec BY rel!='$rel';
-- compute maximum weight for rel2docs as: maxweight2:{term,weight}
maxweightB =
   FOREACH (GROUP docsB BY (rel,term))
   GENERATE group.term AS term, MAX(docsB.weight) AS weight;
-- augment the docvecs for rel1 with maxweight2 and docfreq information to get
-- augdocsA: {rel,docid,term, w,df,maxw,score}
docfreqB = FILTER docfreq BY rel!='$rel';
augdocsA1 = JOIN docsA BY term, docfreqB BY term, maxweightB BY term;
augdocsA =
   FOREACH augdocsA1
   GENERATE docsA::rel, docsA::docid, docsA::term, docsA::weight AS w,
     docfreqB::df AS df, maxweightB::weight AS maxw,
     docsA::weight*maxweightB::weight AS score;
usefulTerms1 =
   FOREACH (GROUP augdocsA BY (rel,docid))
   GENERATE group, TOP($top_k,6,augdocsA) AS top;
usefulTerms2 =
   FOREACH usefulTerms1 {
      filteredTop = FILTER top BY (df<=$max_df) AND score>$min_sim;
      topTerms = FOREACH filteredTop GENERATE term;
      GENERATE flatten(topTerms);
   };
usefulTerms = DISTINCT usefulTerms2;
pairs1 = JOIN usefulTerms BY term, docsA BY term, docsB BY term;
pairs2 = FOREACH pairs1 GENERATE docsA::docid AS idA, docsB::docid AS idB;
pairs = DISTINCT pairs2;
-- STORE pairs INTO 'phirl/pairs';
softjoin1 = JOIN pairs BY idA, docsA by docid;
softjoin2 = JOIN softjoin1 BY (idB,term), docsB by (docid,term);
softjoin3 =
   FOREACH softjoin2
   GENERATE idA, idB, docsA::term AS term, docsA::weight*docsB::weight AS p;
softjoin =
   FOREACH (GROUP softjoin3 BY (idA,idB))
   GENERATE group.idA, group.idB, SUM(softjoin3.p) AS sim;
```

PageRank at Scale

Google's PageRank



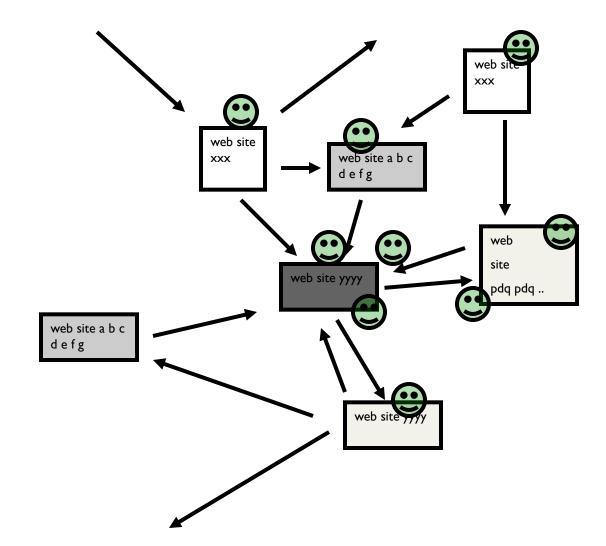
Inlinks are "good" (recommendations)

Inlinks from a "good" site are better than inlinks from a "bad" site

but inlinks from sites with many outlinks are not as "good"...

"Good" and "bad" are relative.

Google's PageRank

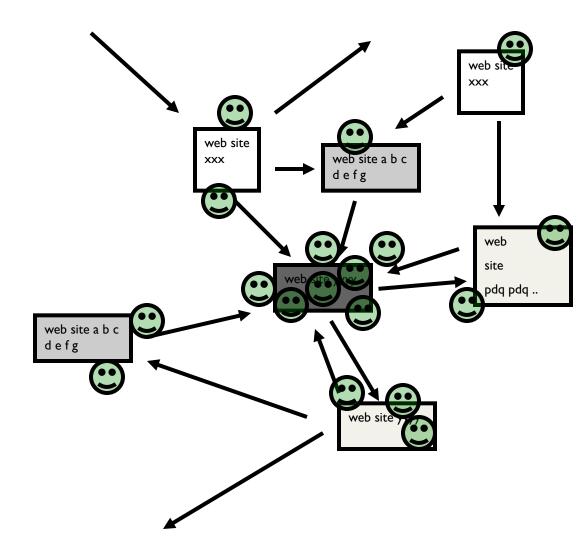


Imagine a "pagehopper" that always either

- follows a random link, or
- jumps to random page

Google's PageRank

(Brin & Page, http://www-db.stanford.edu/~backrub/google.html)



Imagine a "pagehopper" that always either

- follows a random link, or
- jumps to random page

PageRank ranks pages by the amount of time the pagehopper spends on a page:

• or, if there were many pagehoppers, PageRank is the expected "crowd size"

PageRank in Memory

- Let u = (1/N, ..., 1/N)
 dimension = #nodes N
- Let A = adjacency matrix: $[a_{ij}=1 \Leftrightarrow i \text{ links to } j]$
- Let $W = [w_{ij} = a_{ij} / outdegree(i)]$
 - $-w_{ij}$ is probability of jump from i to j
- Let $\mathbf{v}^0 = (1, 1, ..., 1)$
 - or anything else you want
- Repeat until converged:
 - $-\operatorname{Let} \mathbf{v}^{t+1} = c\mathbf{u} + (1-c)\mathbf{W}\mathbf{v}^{t}$
 - c is probability of jumping "anywhere randomly"

Streaming PageRank

- Assume we can store **v** but not **W** in memory
- Repeat until converged:

 $-\operatorname{Let} \mathbf{v}^{t+1} = c\mathbf{u} + (1-c)\mathbf{W}\mathbf{v}^{t}$

• Store **A** as a row matrix: each line is

- i $j_{i,1},...,j_{i,d}$ [the neighbors of i]

- Store **v'** and **v** in memory: **v'** starts out as c**u**
- For each line "i $j_{i,1},...,j_{i,d}$ " – For each j in $j_{i,1},...,j_{i,d}$ • v'[j] += (1-c)v[i]/d

Everything needed for update is right there in row....

Streaming PageRank: with some long rows

• Repeat until converged:

 $-\operatorname{Let} \mathbf{v}^{t+1} = c\mathbf{u} + (1-c)\mathbf{W}\mathbf{v}^{t}$

- Store **A** as a list of edges: each line is: "i d(i) j"
- Store **v'** and **v** in memory: **v'** starts out as c**u**
- For each line "i d j"

• v'[j] += (1-c)v[i]/d

We need to get the degree of *i* and store it locally

Streaming PageRank: preprocessing

- Original encoding is edges (i,j)
- Mapper replaces i,j with i,1
- Reducer is a SumReducer
- Result is pairs (i,d(i))
- Then: join this back with edges (i,j)
- For each i,j pair:
 - send j as a message to node i in the degree table
 - messages always sorted after non-messages
 - the reducer for the degree table sees i,d(i) first
 - then j1, j2,
 - can output the key, value pairs with key=i, value=d(i), j

Preprocessing Control Flow: 1

	J					1	
i1	j1,1		i1	1		i1	1
i1	j1,2		i1	1		i1	1
i1	j1,k1		i1	1		i1	1
i2	j2,1		i2	1		i2	1
							•••
i3	j3,1		i3	1		i3	1
				•••		•••	•••
	MAP			SORT			

Preprocessing Control Flow: 2

		1	J		
	J	i1	~j1,1		
	j1,1	i1	~j1,2		
-	j1,2		, ,		
		i2	···· ~:⊃ 1		
	j2,1		~j2,1		
•					
_			d(i)		
	d(i)	i1	d(i1)		
1	d(i1)	11			
2	d(i2)	i2	d(i2)		
	MA	MAP			

copy or convert to messages

d(i1) i1 ~j1,1 i1 ~j1,2 i1 •• ... d(i2) i2 ~j2,1 i2 i2 ~j2,2 • • • ...

I		
i1	d(i1)	j1,1
i1	d(i1)	j1,2
i1	d(i1)	j1,n1
i2	d(i2)	j2,1
i3	d(i3)	j3,1



join degree with edges

Streaming PageRank: with some long rows

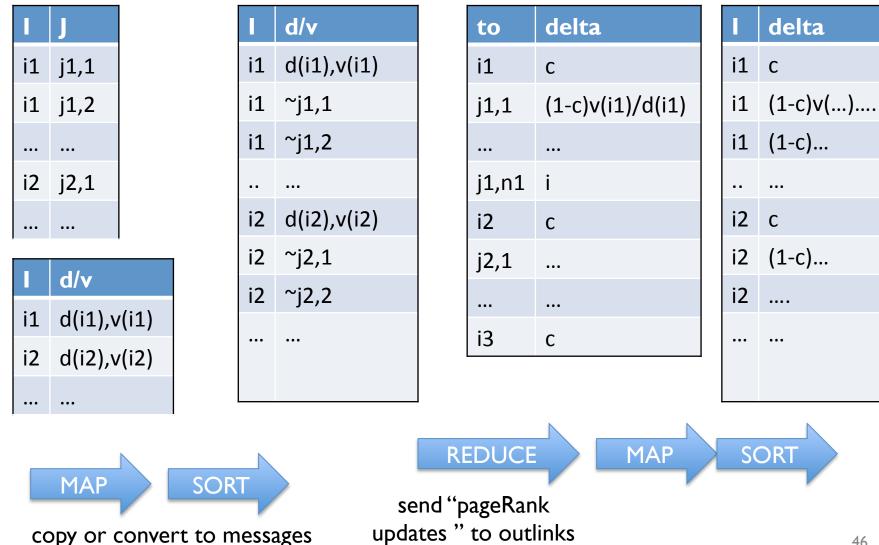
- Repeat until converged: - Let $\mathbf{v}^{t+1} = c\mathbf{u} + (1-c)\mathbf{W}\mathbf{v}^{t}$
- Pure streaming: use a table of nodes \rightarrow degree+pageRank
 - Lines are *i: degree=d,pr=v*
- For each edge *i,j*
 - Send to i (in degree/pagerank) table: outlink j
- For each line *i*: degree=*d*,pr=*v*:
 - send to *i*: incrementVBy *c*
 - for each message "outlink j":
 - send to *j*: incrementVBy (1-c)*v/d
- For each line *i*: degree=d,pr=v
 - sum up the incrementVBy messages to compute v'
 - output new row: i: degree=d,pr=v'

One identity mapper with two inputs (edges, degree/ pr table)

Reducer outputs the incrementVBy messages

Two-input mapper + reducer

Control Flow: Streaming PR

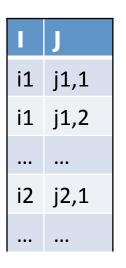


Control Flow: Streaming PR

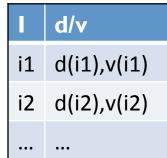
to	delta	I	delta		
i1	С	i1	С	L	v '
j1,1	(1-c)v(i1)/d(i1)	i1	(1-c)v()	i1	~v′(i1)
		i1	(1-c)	i2	~v′(i2)
j1,n1	i			•••	
i2	С	i2	С		
j2,1		i2	(1-c)		-1 <i>1</i>
		i2		•	d/v
i3	С			i1	d(i1),v(i1
				i2	d(i2),v(i2



Control Flow: Streaming PR



and back around for next iteration....





copy or convert to messages

PageRank in Pig

#!/usr/bin/python

from org.apache.pig.scripting import *

```
How to use loops, conditionals, etc?
```

Embed PIG in a real programming language.

Julien Le Dem -Yahoo

```
P = Pig.compile("""
-- PR(A) = (1-d) + d (PR(T1)/C(T1) + ... + PR(Tn)/C(Tn))
previous_pagerank =
   LOAD '$docs_in'
   USING PigStorage('\t')
   AS ( url: chararray, pagerank: float, links:{ link: ( url: chararray ) } );
outbound_pagerank =
   FOREACH previous_pagerank
   GENERATE
    pagerank / COUNT ( links ) AS pagerank,
   FLATTEN ( links ) AS to_url;
new_pagerank =
   FOREACH
        ( COGROUP outbound_pagerank BY to_url, previous_pagerank BY url INNER )
```

GENERATE

```
group AS url,
( 1 - $d ) + $d * SUM ( outbound_pagerank.pagerank ) AS pagerank,
FLATTEN ( previous_pagerank.links ) AS links;
```

```
STORE new_pagerank
INTO '$docs_out'
```

```
USING PigStorage('\t');
```

```
params = { 'd': '0.5', 'docs_in': 'data/pagerank_data_simple' }
```

```
for i in range(10):
```

```
out = "out/pagerank_data_" + str(i + 1)
params["docs_out"] = out
Pig.fs("rmr " + out)
stats = P.bind(params).runSingle()
if not stats.isSuccessful():
    raise 'failed'
```

```
params["docs_in"] = out
```



```
previous_pagerank =
   LOAD '$docs_in'
   USING PigStorage('\t')
   AS ( url: chararray, pagerank: float, links:{ link: ( url: chararray ) } );
```

```
outbound_pagerank =

FOREACH previous_pagerank

GENERATE

pagerank / COUNT ( links ) AS pagerank,

FLATTEN ( links ) AS to_url;
```

```
new_pagerank =
    FOREACH
    ( COGROUP outbound_pagerank BY to_url, previous_pagerank BY url INNER )
    GENERATE
    group AS url,
    ( 1 - $d ) + $d * SUM ( outbound_pagerank.pagerank ) AS pagerank,
    FLATTEN ( previous_pagerank.links ) AS links;
```

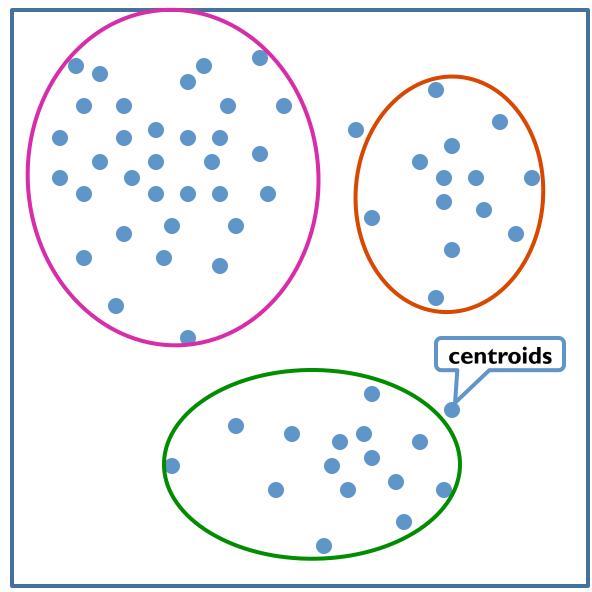
```
STORE new_pagerank
INTO '$docs_out'
USING PigStorage('\t');
```

An example from Ron Bekkerman

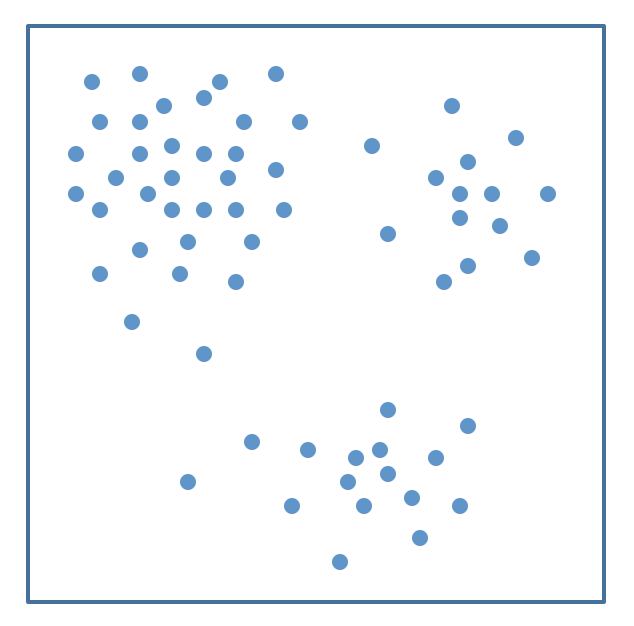
Example: *k*-means clustering

- An EM-like algorithm:
- Initialize *k* cluster centroids
- E-step: associate each data instance with the closest centroid
 - Find expected values of cluster assignments given the data and centroids
- M-step: recalculate centroids as an average of the associated data instances
 - Find new centroids that maximize that expectation

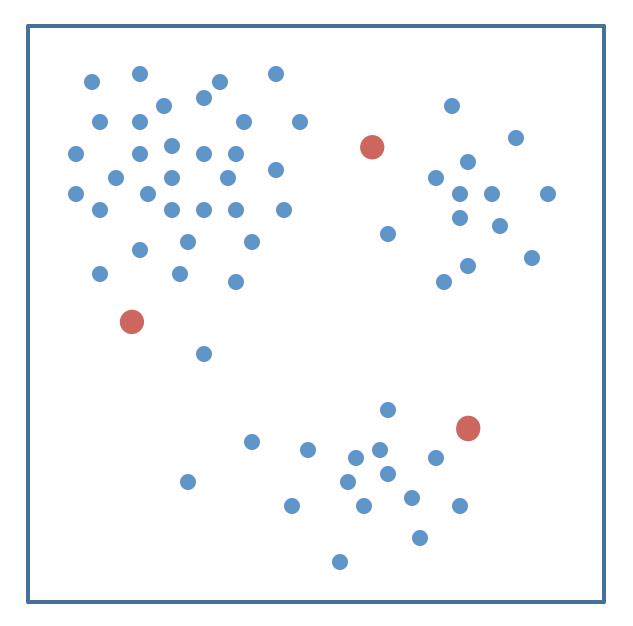
k-means Clustering



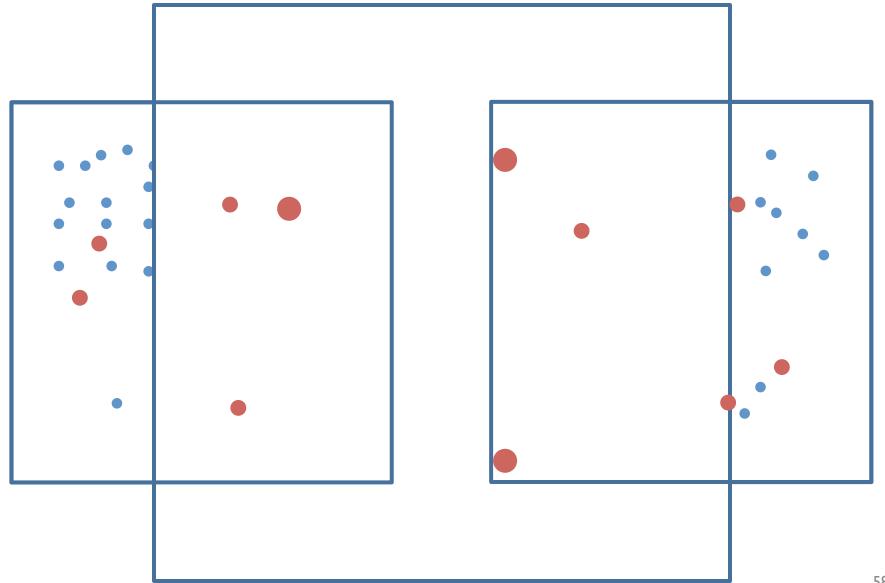
Parallelizing k-means



Parallelizing k-means



Parallelizing k-means



k-means on MapReduce

Panda et al, Chapter 2

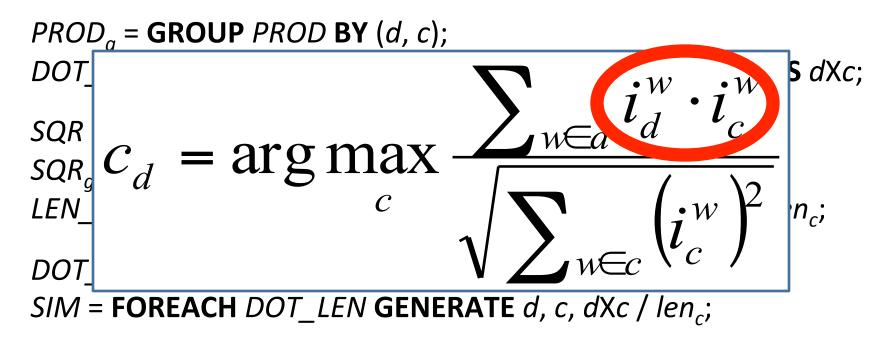
- Mappers read data portions and centroids
- Mappers assign data instances to clusters
- Mappers compute new local centroids and local cluster sizes
- Reducers aggregate local centroids (weighted by local cluster sizes) into new global centroids
- Reducers write the new centroids

k-means in Apache Pig: input data

- Assume we need to cluster documents
 - Stored in a 3-column table *D*:

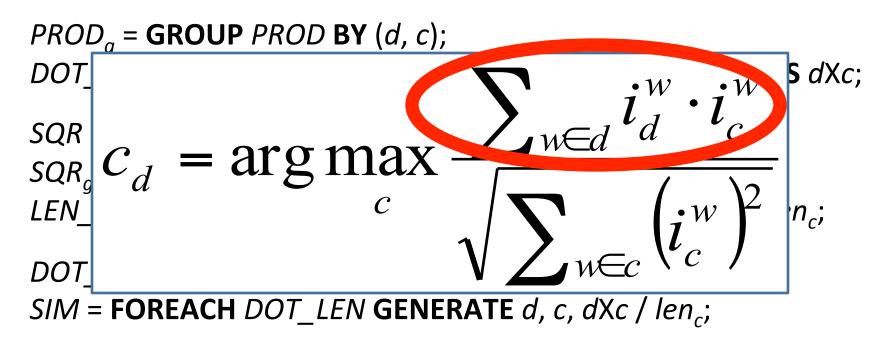
Document	Word	Count
docl	Carnegie	2
docl	Mellon	2

 $D_C =$ **JOIN** C **BY** w, D **BY** w; PROD =**FOREACH** D_C **GENERATE** d, c, $i_d * i_c$ **AS** $i_d i_c$;

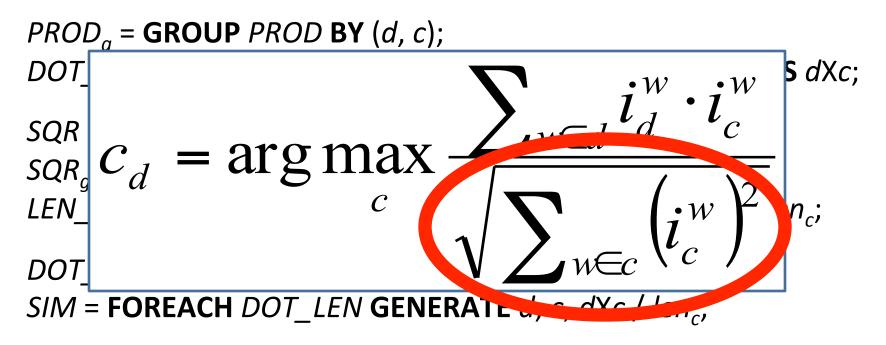


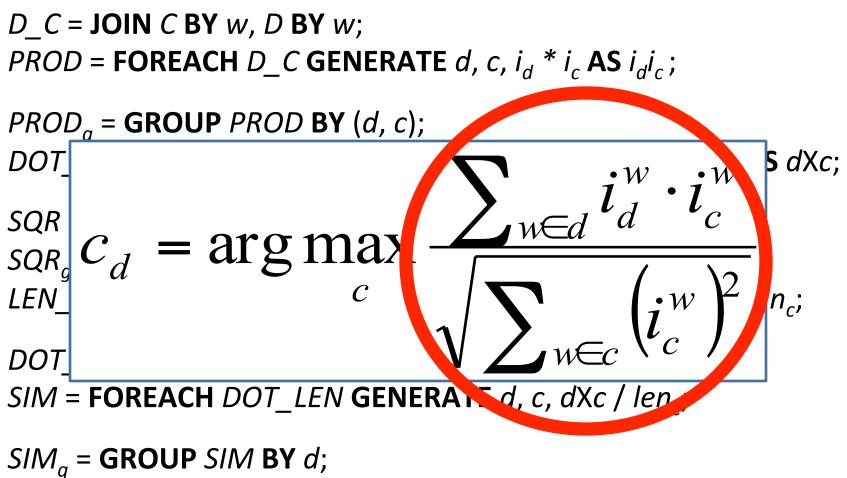
```
D_C = JOIN C BY w, D BY w;

PROD = FOREACH D_C GENERATE d, c, i_d * i_c AS i_d i_c;
```



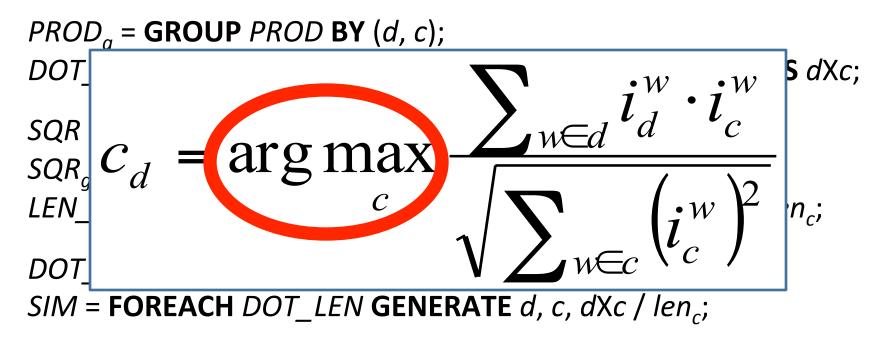
 $D_C =$ **JOIN** C **BY** w, D **BY** w; PROD =**FOREACH** D_C **GENERATE** d, c, $i_d * i_c$ **AS** $i_d i_c$;

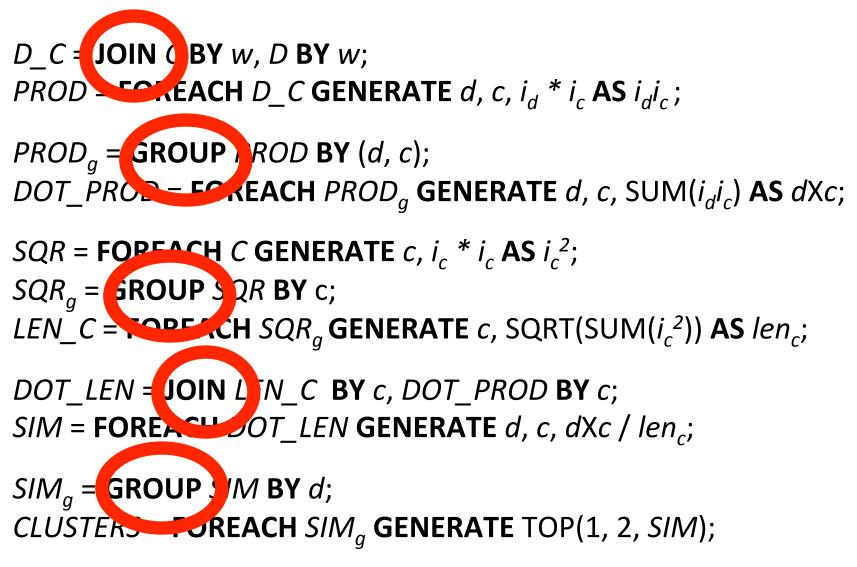


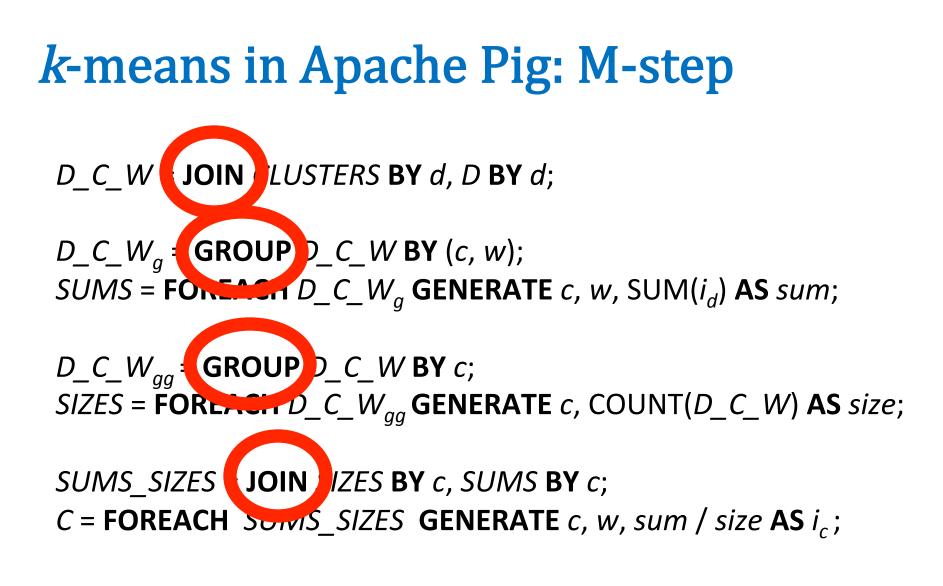


CLUSTERS = FOREACH SIM_g GENERATE TOP(1, 2, SIM);

 $D_C =$ **JOIN** C **BY** w, D **BY** w; PROD =**FOREACH** D_C **GENERATE** d, c, $i_d * i_c$ **AS** $i_d i_c$;







Finally - embed in Java (or Python or) to do the looping

#!/usr/bin/python

from org.apache.pig.scripting import *

```
How to use loops,
conditionals, etc?
```

Embed PIG in a real programming language.

h/t Julien Le Dem -Yahoo

```
P = Pig.compile("""
-- PR(A) = (1-d) + d (PR(T1)/C(T1) + ... + PR(Tn)/C(Tn))
previous_pagerank =
   LOAD '$docs_in'
   USING PigStorage('\t')
   AS ( url: chararray, pagerank: float, links:{ link: ( url: chararray ) } );
outbound_pagerank =
    FOREACH previous_pagerank
```

```
GENERATE
   pagerank / COUNT ( links ) AS pagerank,
```

params["docs_in"] = out

```
FLATTEN ( links ) AS to_url;
```

```
new_pagerank =
    FOREACH
       ( COGROUP outbound_pagerank BY to_url, previous_pagerank BY url INNER )
   GENERATE
       group AS url,
       (1 - $d) + $d * SUM (outbound_pagerank.pagerank) AS pagerank,
       FLATTEN ( previous_pagerank.links ) AS links;
STORE new_pagerank
   INTO '$docs_out'
   USING PigStorage('\t');
(""")
params = { 'd': '0.5', 'docs_in': 'data/pagerank_data_simple' }
for i in range(10):
   out = "out/pagerank_data_" + str(i + 1)
   params["docs_out"] = out
   Pig.fs("rmr " + out)
   stats = P.bind(params).runSingle()
   if not stats.isSuccessful():
       raise 'failed'
```



The problem with k-means in Hadoop

I/O costs

Data is read, and model is written, with every iteration

Panda et al, Chapter 2

- Mappers read data portions and centroids
- Mappers assign data instances to clusters
- Mappers compute new local centroids and local cluster sizes
- Reducers aggregate local centroids (weighted by local cluster sizes) into new global centroids
- Reducers write the new centroids

Spark

Spark

- Too much typing

 programs are not concise
- Too low level
 - missing abstractions
 - hard to specify a workflow
- Not well suited to iterative operations
 - E.g., E/M, k-means clustering, ...
 - -Workflow and memory-loading issues

Sharded files are replaced by "RDDs" – resiliant distributed datasets

RDDs can be cached in *cluster* memory and recreated to recover from error

Set of concise dataflow operations ("transformation")

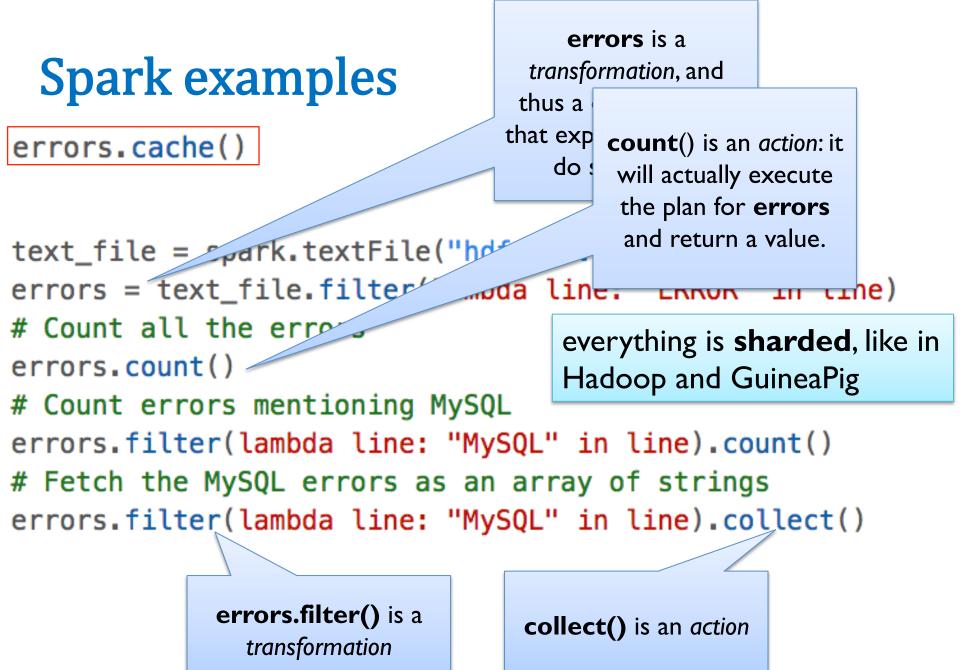
Dataflow operations are embedded in an API together with "actions"

Spark examples

errors.cache()

spark is a spark context object

text_file = spark.textFile("hdfs://...")
errors = text_file.filter(lambda line: "ERROR" in line)
Count all the errors
errors.count()
Count errors mentioning MySQL
errors.filter(lambda line: "MySQL" in line).count()
Fetch the MySQL errors as an array of strings
errors.filter(lambda line: "MySQL" in line).collect()



Spark examples

everything is **sharded** ... and the shards are stored in *memory* of worker machines not local *disk* (if possible)

- text_file = spark.textFile("hdfs://...")
- errors = text_file.filter(lambda line: "ERROR" in line)
 errors.cache() # modify errors to be stored in cluster memory
 errors.count()
- # Count errors mentioning MySQL
 errors.filter(lambda line "MySQL" in line).count()
 # Fetch the MySQL errors as ray of strings
 errors.filter(lambda line: "MySQL

You can also **persist()** an RDD on disk, which is like marking it as opts(stored=True) in GuineaPig. Spark's *not* smart about persisting data. subsequent actions will be much faster

Spark examples: wordcount

```
text_file = spark.textFile("hdfs://...")
counts = text_file.flatMap(lambda line: line.split(" ")) \
                .map(lambda word: (word, 1)) \
                .reduceByKey(lambda a, b: a + b)
counts.saveAsTextFile( hdfs://...")
```

the action

transformation on (key,value) pairs , which are special

```
points = spark.textFile(...).map(parsePoint).cache()
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)))) - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
   w -= gradient
print "Final parating plane: %s" % w
                                            p.x and w are vectors,
                 reduce is an action –
                                          from the numpy package.
                  it produces a numby
                                              Python overloads
                         vector
                                           operations like * and +
                                                 for vectors.
```

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```
points = spark.textFile(...).map(parsePoint).cache()
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)))) - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
    w -= gradient
print "Final separating plane: %s" % w
```

Important note: numpy vectors/matrices are not just "syntactic sugar".

- They are *much more compact* than something like a list of python floats.
- numpy operations like **dot**, *, + are calls to optimized C code
- a little python logic around a lot of numpy calls is pretty efficient

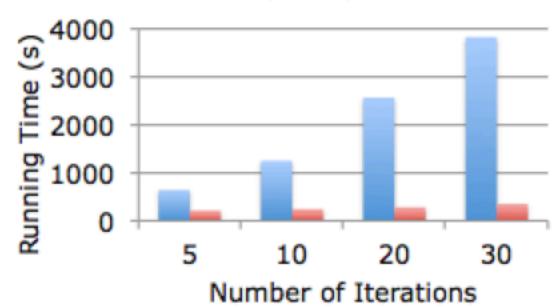
```
points = spark.textFile(...).map(parsePoint).cache()
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)))) - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
    w -= gradient
print "Final separating plane: %s" w
```

So: python builds a *closure* – code including the *current value* of **w** – and Spark ships it off to each worker. So **w** is *copied*, and must be *read-only*. w is defined *outside* the lambda function, but used *inside* it

```
points = spark.textFile(...).map(parsePoint).cache()
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)
                                                    - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
   w -= gradient
print "Final separating plane: %s" % w
                                                dataset of points is
                                                 cached in cluster
                                               memory to reduce i/o
```

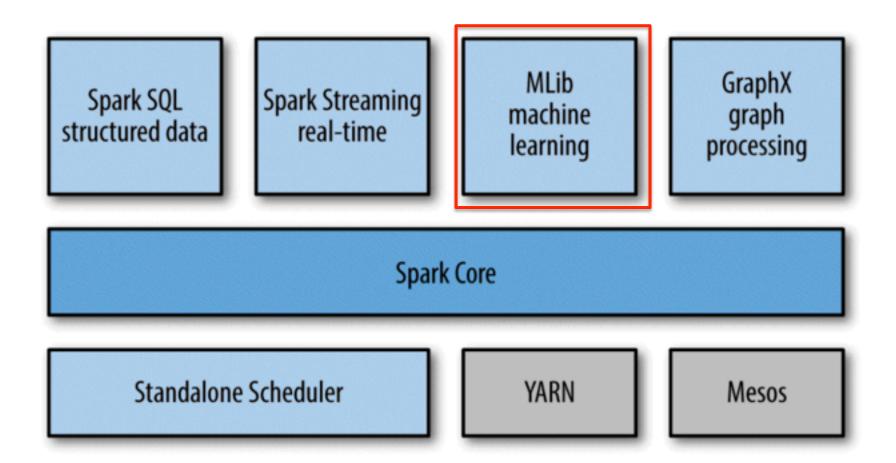
Spark logistic regression example

The graph below compares the performance of this Spark program against a Hadoop implementation on 30 GB of data on an 80-core cluster, showing the benefit of in-memory caching:



Hadoop Spark

Spark



Spark details: broadcast

```
points = spark.textFile(...).map(parsePoint).cache()
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)))) - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
    w -= gradient
print "Final separating plane: 9 6 w
```

So: python builds a *closure* – code including the *current value* of **w** – and Spark ships it off to each worker. So **w** is *copied*, and must be *read-only*.

Spark details: broadcast

little penalty for distributing something that's not used by all

```
points = spark.textFile(...).map(parsePoint).cac workers
w = numpy.random.ranf(size = D) # current separating plane
for i in range(ITERATIONS):
    gradient = points.map(
        lambda p: (1 / (1 + exp(-p.y*(w.dot(p.x)))) - 1) * p.y * p.x
    ).reduce(lambda a, b: a + b)
    w -= gradient
print "Final separating plane: %
    what's sent is a small
pointer to w (e.g., the
```

alternative: create a broadcast variable, e.g.,

- w_broad = spark.broadcast(w)
 which is accessed by the worker via
- w_broad.value()

what's sent is a *small* pointer to **w** (e.g., the name of a file containing a serialized version of **w**) and when **value** is called, some clever allreduce like machinery is used to reduce network load.

Spark details: mapPartitions

```
class WordProb(Planner):
```

Common issue:

- map task requires loading in some small shared value
- more generally, map task requires some sort of *initialization* before processing a shard
- GuineaPig:
 - special Augment ... sideview ... pattern for shared values
 - can kludge up any initializer using Augment
- Raw Hadoop: mapper.configure() and mapper.close() methods

Spark details: mapPartitions

```
class WordProb(Planner):
```

Spark:

- rdd.mapPartitions(f): will call f(iteratorOverShard) once per shard, and return an iterator over the mapped values.
- f() can do any setup/close steps it needs

Also:

• there are transformations to partition an RDD with a user-selected function, like in Hadoop. Usually you partition and persist/cache.