## Pairs Design Pattern

```
map(docID a, doc d)
    for all term w in doc d do
    for all term u NEAR w do
        Emit(pair (w, u), count 1)
reduce(pair p, counts [c1, c2,...])
    sum = 0
    for all count c in counts do
        sum += c
    Emit(pair p, count sum)
```

- Can use combiner or in-mapper combining
- Good: easy to implement and understand
- Bad: huge intermediate-key space (shuffling/sorting cost!)
- Quadratic in number of distinct terms


## Stripes Design Pattern



- Can use combiner or in-mapper combining
- Good: much smaller intermediate-key space
- Linear in number of distinct terms
- Bad: more difficult to implement, Map needs to hold entire stripe in memory


## Beyond Pairs and Stripes

- In general, it is not clear which approach is better
- Some experiments indicate stripes win for cooccurrence matrix computation
- Pairs and stripes are special cases of shapes for covering the entire matrix
- Could use sub-stripes, or partition matrix horizontally and vertically into more square-like shapes etc.
- Can also be applied to higher-dimensional arrays
- Will see interesting version of this idea for joins


## (3) Relative Frequencies

- Important for data mining
- E.g., for each species and color, compute probability of color for that species
- Probability of Northern Cardinal being red, P(color = red | species = N.C.)
- Count $f($ N.C. $)$, the frequency of observations for N.C. (marginal)
- Count f(N.C., red), the frequency of observations for red N.C.'s (joint event)
- $P($ red | N.C. $)=f(N . C .$, red $) / f(N . C$.
- Similarly: normalize word co-occurrence vector for word w by dividing it by w's frequency


## Bird Probabilities Using Stripes

- Use species as intermediate key
- One stripe per species, e.g., stripe[N.C.]
- (stripe[species])[color] stores f(species, color)
- Map: for each observation of (species S, color C) in an observation event, increment (stripe[S])[C]
- Output (S, stripe[S])
- Reduce: for each species $S$, add all stripes for $S$
- Result: stripeSum[S] with total counts for each color for S
- Can get $f(S)$ by adding all stripeSum[S] values together
- Get probability P(color = C $\mid$ species $=\mathrm{S}$ ) as (stripeSum[S])[C] / f(S)


## Discussion, Part 1

- Stripe is great fit for relative frequency computation
- All values for computing the final result are in the stripe
- Any smaller unit would miss some of the joint events needed for computing $f(\mathrm{~S})$, the marginal for the species
- So, this would be a problem for the pairs pattern


## Bird Probabilities Using Pairs

- Intermediate key is (species, color)
- Map produces partial counts for each speciescolor combination in input
- Reduce can compute f(species, color), the total count of each species-color combination
- But: cannot compute marginal f(S)
- Reduce needs to sum f(S, color) for all colors for species S


## Pairs-Based Solution, Take 1

- Make sure all values $f(S$, color) for the same species end up in the same reduce task
- Define custom partitioning function on species
- Maintain state across different keys in same reduce task
- This essentially simulates the stripes approach in the reduce task, creating big reduce tasks when there are many colors
- Can we do better?


## Discussion, Part 2

- Pairs-based algorithm would work better, if marginal $f(S)$ was known already
- Reducer computes f(species, color) and then outputs f(species, color) / f(species)
- We can compute the species marginals f(species) in a separate MapReduce job first
- Better: fold this into a single MapReduce job
- Problem: easy to compute f(S) from all f(S, color), but how do we compute $f(S)$ before knowing $f(S$, color $)$ ?


## Bird Probabilities Using Pairs, Take 2

- Map: for each observation event, emit ((species S, color C), 1) and ((species S, dummyColor), 1) for each species-color combination encountered
- Use custom partitioner that partitions based on the species component only
- Use custom key comparator such that ( S , dummyColor) is before all (S, C) for real colors C
- Reducer computes $f(S)$ before the $f(S, C)$
- Reducer keeps $f(\mathrm{~S})$ in state for duration of entire task
- Reducer then computes $f(S, C)$ for each $C$, outputting $f(S, C)$ / f(S)
- Advantage: avoids having to manage all colors for a species together


## Order Inversion Design Pattern

- Occurs surprisingly often during data analysis
- Solution 1: use complex data structures that bring the right results together
- Array structure used by stripes pattern
- Solution 2: turn synchronization into ordering problem
- Key sort order enforces computation order
- Partitioner for key space assigns appropriate partial results to each reduce task
- Reducer maintains task-level state across Reduce invocations
- Works for simpler pairs pattern, which uses simpler data structures and requires less reducer memory


## (4) Secondary Sorting

- Recall the weather data: for simplicity assume observations are (date, stationID, temperature)
- Goal: for each station, create a time series of temperature measurements
- Per-station data: use stationID as intermediate key
- Problem: reducers receive huge number of (date, temp) pairs for each station
- Have to be sorted by user code


## Can Hadoop Do The Sorting?

- Use (stationID, date) as intermediate key
- Problem: records for the some station might end up in different reduce tasks
- Solution: custom partitioner, using only stationID component of key for partitioning
- General value-to-key conversion design pattern
- To partition by X and then sort each X -group by Y , make $(\mathrm{X}, \mathrm{Y})$ the key
- Define key comparator to order by composite key (X, Y)
- Define partitioner and grouping comparator for ( $X, Y$ ) to consider only X for partitioning and grouping
- Grouping part is necessary if all dates for a station should be processed in the same Reduce invocation (otherwise each stationdate combination ends up in a different Reduce invocation)


## Design Pattern Summary

- In-mapper combining: do work of combiner in mapper
- Pairs and stripes: for keeping track of joint events
- Order inversion: convert sequencing of computation into sorting problem
- Value-to-key conversion: scalable solution for secondary sorting, without writing own sort code


## Tools for Synchronization

- Cleverly-constructed data structures for key and values to bring data together
- Preserving state in mappers and reducers, together with capability to add initialization and termination code for entire task
- Sort order of intermediate keys to control order in which reducers process keys
- Custom partitioner to control which reducer processes which keys


## Issues and Tradeoffs

- Number of key-value pairs
- Object creation overhead
- Time for sorting and shuffling pairs across the network
- Size of each key-value pair
- (De-)serialization overhead
- Local aggregation
- Opportunities to perform local aggregation vary
- Combiners can make a big difference
- Combiners vs. in-mapper combining
- RAM vs. disk vs. network

Now that we have seen important design patterns and MapReduce algorithms for simpler problems, let's look at some more complex problems.

## Joins in MapReduce

- Data sets $S=\left\{s_{1}, \ldots, s_{|S|}\right\}$ and $T=\left\{t_{1}, \ldots, t_{|T|}\right\}$
- Find all pairs $\left(\mathrm{s}_{\mathrm{i}}, \mathrm{t}_{\mathrm{j}}\right)$ that satisfy some predicate
- Examples
- Pairs of similar or complementary function summaries
- Facebook and Twitter posts by same user or from same location
- Typical goal: minimize job completion time


## Function-Join Pattern

- Find groups of summaries with certain properties of interest
- Similar trends, opposite trends, correlations
- Groups not known a priori, need to be discovered



## Existing Join Support

- Hadoop has some built-in join support, but our goal is to design our own algorithms
- Built-in support is limited
- We want to understand important algorithm design principles
- "Join" usually just means equi-join, but we also want to support other join predicates
- Note: recall join discussion from earlier lecture


## Joining Large With Small

- Assume data set $T$ is small enough to fit in memory
- Can run Map-only join
- Load T onto every mapper
- Map: join incoming S-tuple with T, output all matching pairs
- Can scan entire T (nested loop) or use index on T (index nested loop)
- Downside: need to copy T to all mappers
- Not so bad, since $T$ is small


## Distributed Cache

- Efficient way to copy files to all nodes processing a certain task
- Use it to send small T to all mappers
- Part of the job configuration
- Hadoop still needs to move the data to the worker nodes, so use this with care
- But it avoids copying the file for every task on the same node


## Recall: Standard Equi-Join Algorithm

- Join condition: S.A=T.A
- $\operatorname{Map}(\mathrm{s})=(\mathrm{s} . \mathrm{A}, \mathrm{s}) ; \operatorname{Map}(\mathrm{t})=(\mathrm{t} . \mathrm{A}, \mathrm{t})$
- Reduce combines S-tuples and T-tuples with same key
DFS nodes Mappers Reducers DFS nodes



## Problems With Standard Approach

- Degree of parallelism limited by number of distinct A-values
- Data skew
- If one A -value dominates, reducer processing that key will become bottleneck
- Does not generalize to other joins


## Reducer-Centric Cost Model

- Difference between join implementations starts with Map output


Receive Mapper output

Sort input by key

Read Run join input algorithm

Send join output


## Optimization Goal: Minimal Job Completion time

- Assume all reducers are similarly capable
- Processing time at reducer is approximately monotonic in input and output size
- Hence need to minimize:
- Max-reducer-input and/or
- Max-reducer-output
- Join problem classification
- Input-size dominated: minimize max-reducer-input
- Output-size dominated: minimize max-reducer-output
- Input-output balanced: minimize combination of both


## Join Model

- Join-matrix $\mathrm{M}: \mathrm{M}(\mathrm{i}, \mathrm{j})=$ true, if and only if $\left(\mathrm{s}_{\mathrm{i}}, \mathrm{t}_{\mathrm{j}}\right)$ in join result
- Cover each true-valued cell by exactly one reducer



abs(S.A - T.A) < 2
S.A >= T.A


