Internet-Scale Alias Resolution with MIDAR

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Introduction

- Goal: We want to produce a router-level map of the Internet using Ark topology data.
  - We need alias resolution.
- Let’s try RadarGun!
  - promising technique by Adam Bender, et al
    - Fixing Ally’s growing pains with velocity modeling (IMC’08)

Outline

- RadarGun
- MIDAR Design
- Measurements
- Toward MAARS

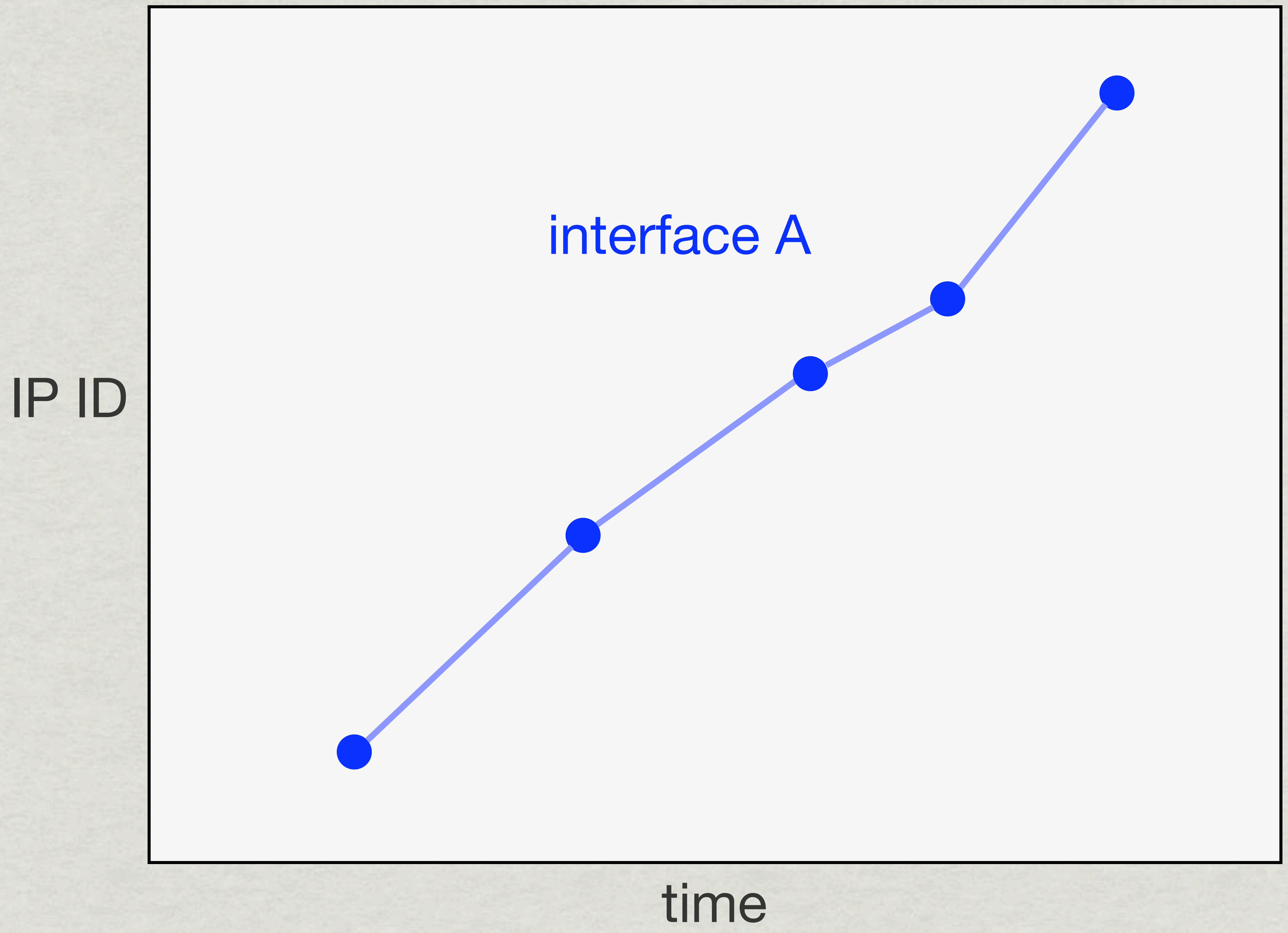
RadarGun

- based on a simple observation:
  - two interfaces belonging to the same router will respond to probes in a similar way
  - specifically, IP ID values in response packets can be used as *fingerprints* to find aliases
    - IP ID is a 16-bit value in the IP header normally used for packet fragmentation and reassembly

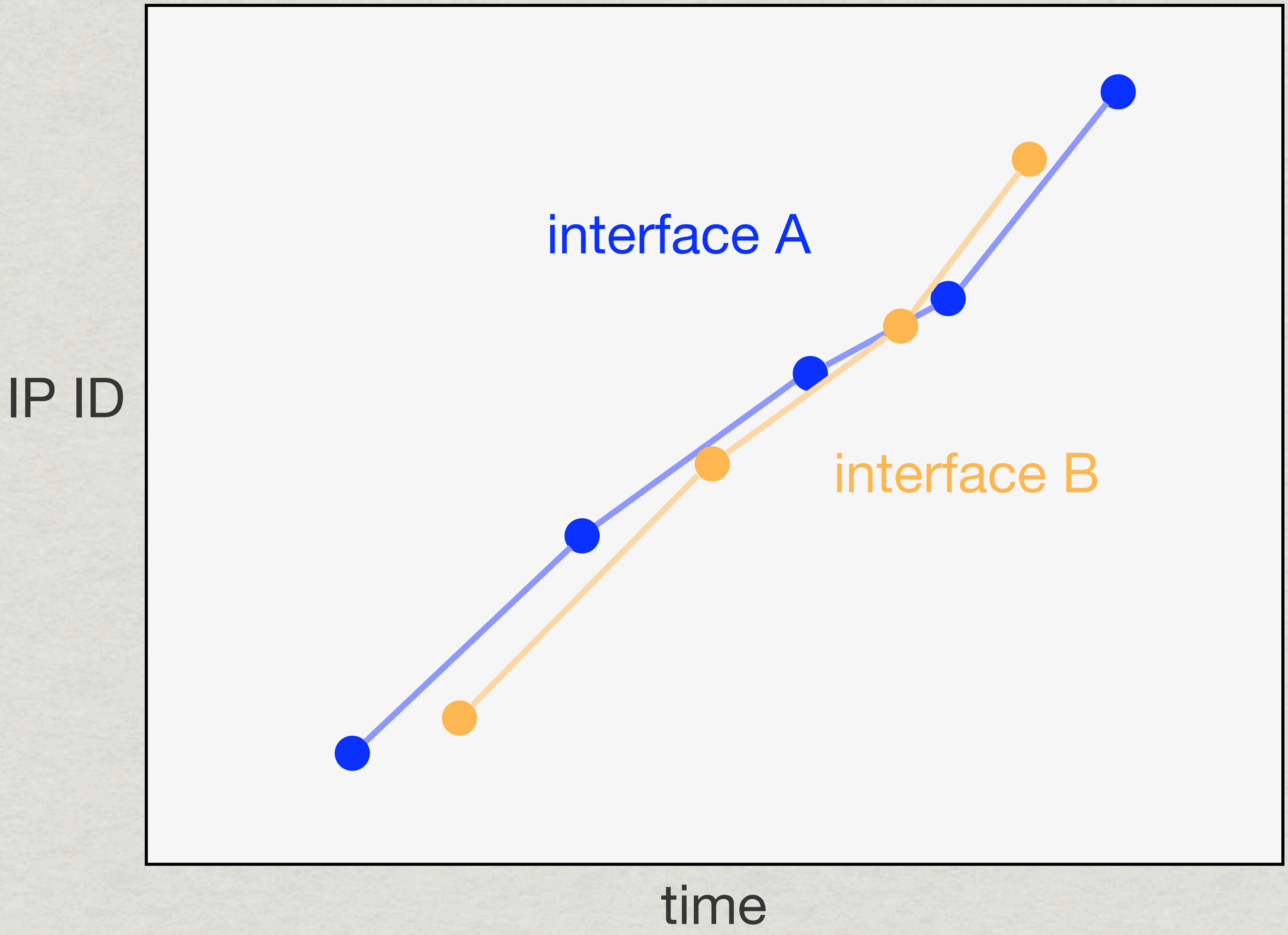
RadarGun

- assumption: a router uses an incrementing system-wide counter to generate IP ID values
  - that is, the router increments the counter whenever it sends out a packet
    - except when merely forwarding packets
- therefore:
  - two interfaces on the same router probed **closely in time** will return similar IP ID values
  - two interfaces on the same router probed repeatedly **over time** will return similar **time series** of IP ID values

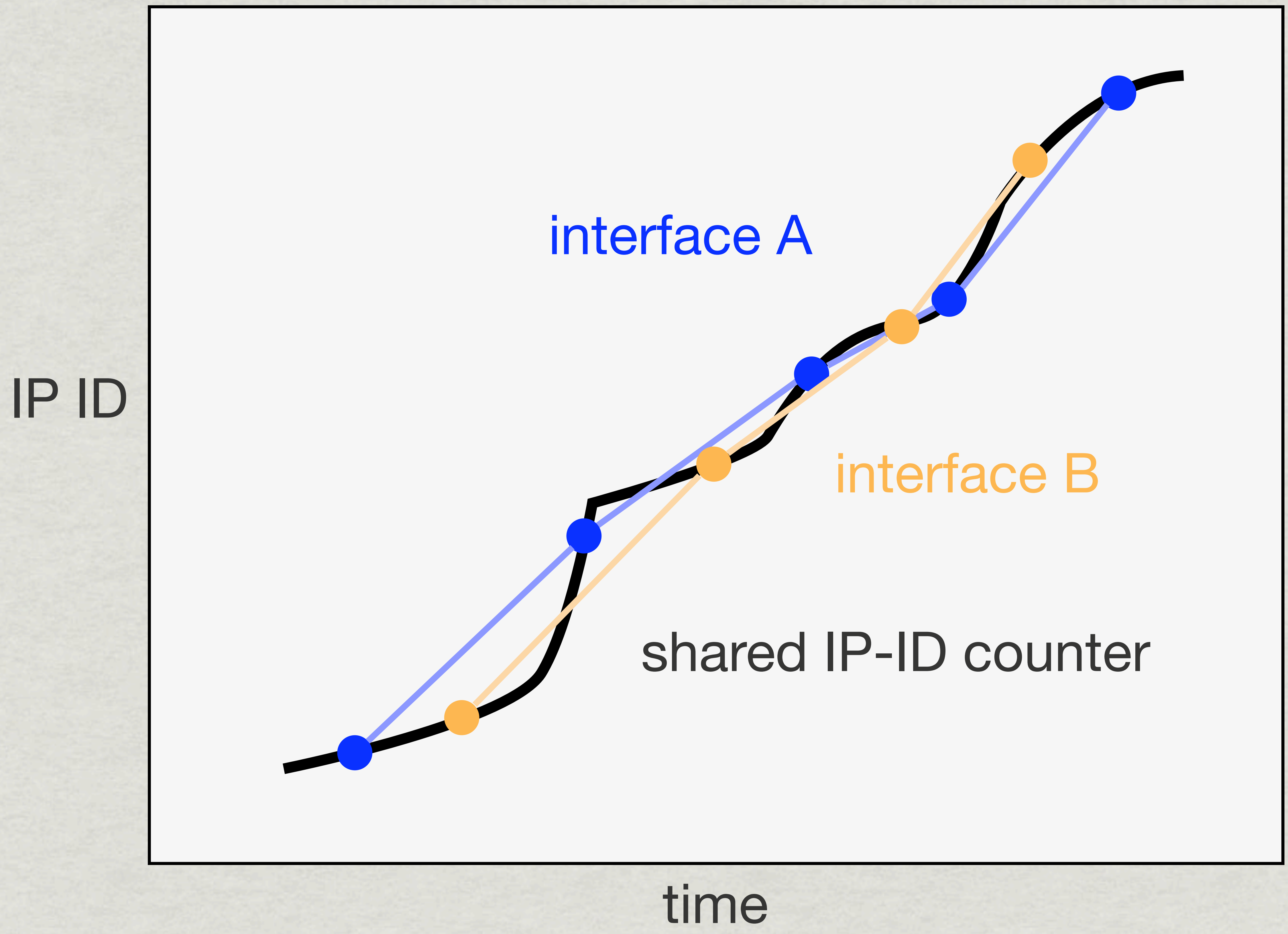
RadarGun



RadarGun



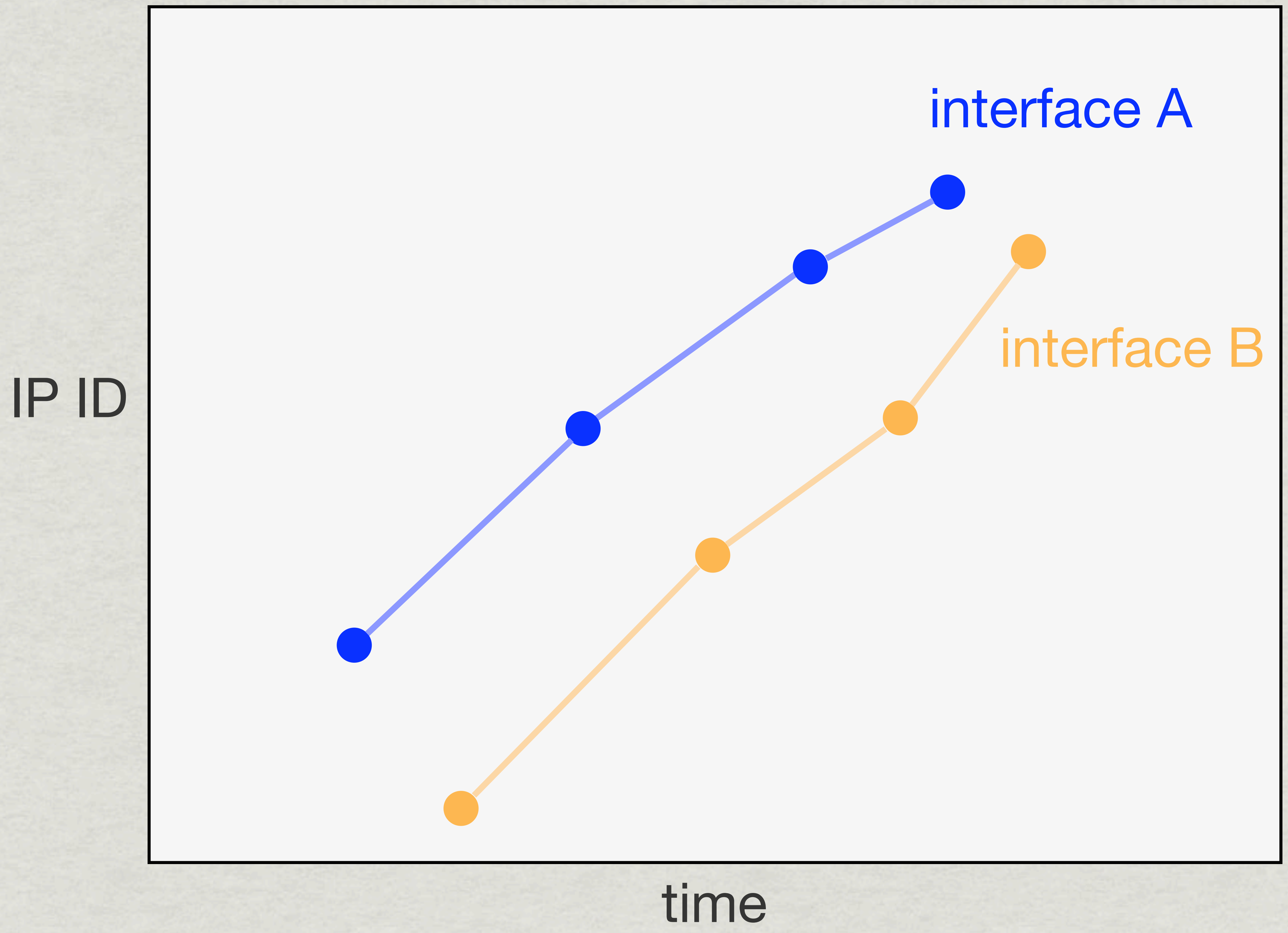
RadarGun



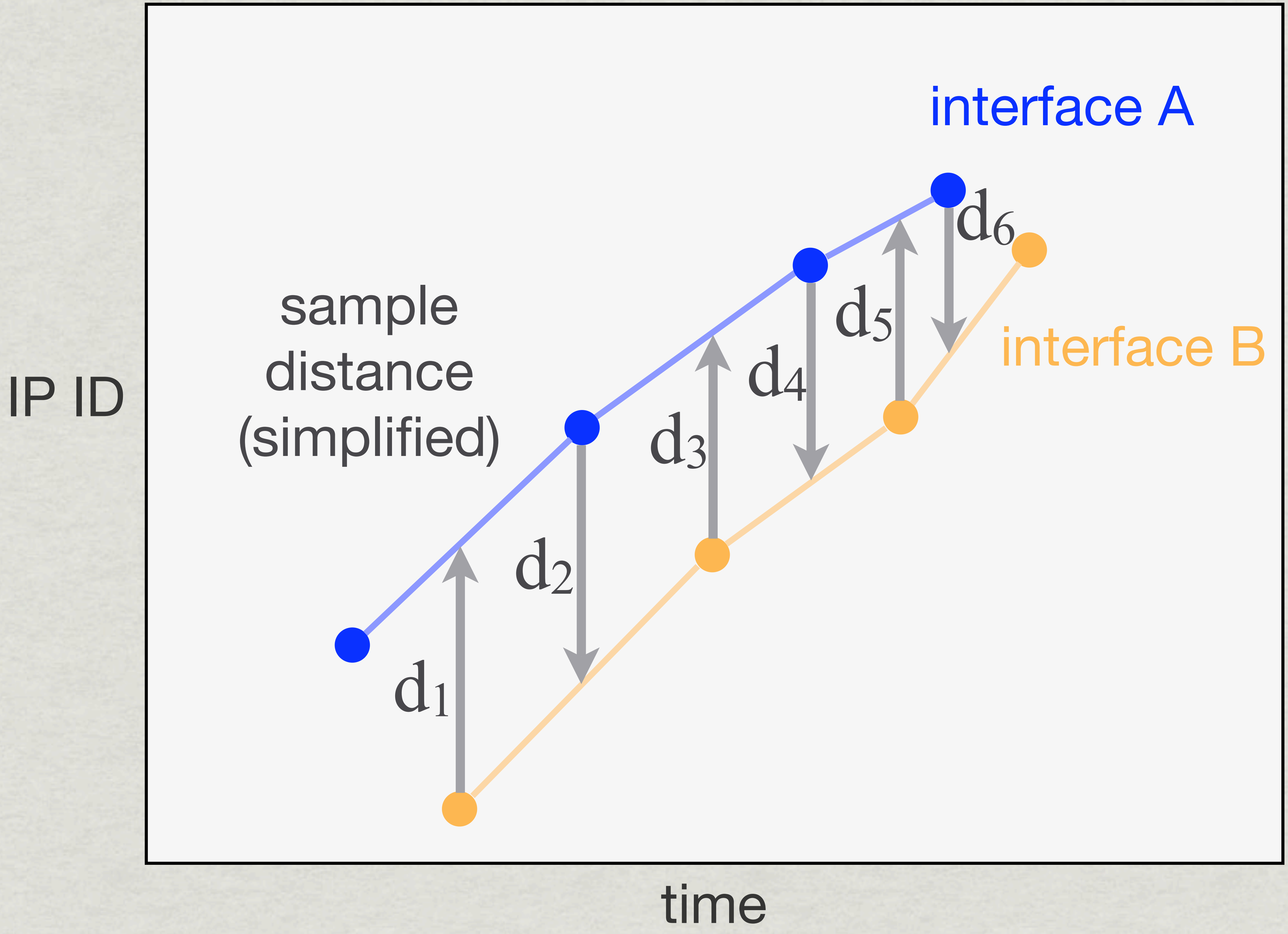
RadarGun

- RadarGun compares the IP-ID time series of two interfaces to determine whether they share a counter
  - share counter => belong to same router
- distance test:
  - compare the distance between two time series
  - if distance is “close”, then the interfaces share a counter

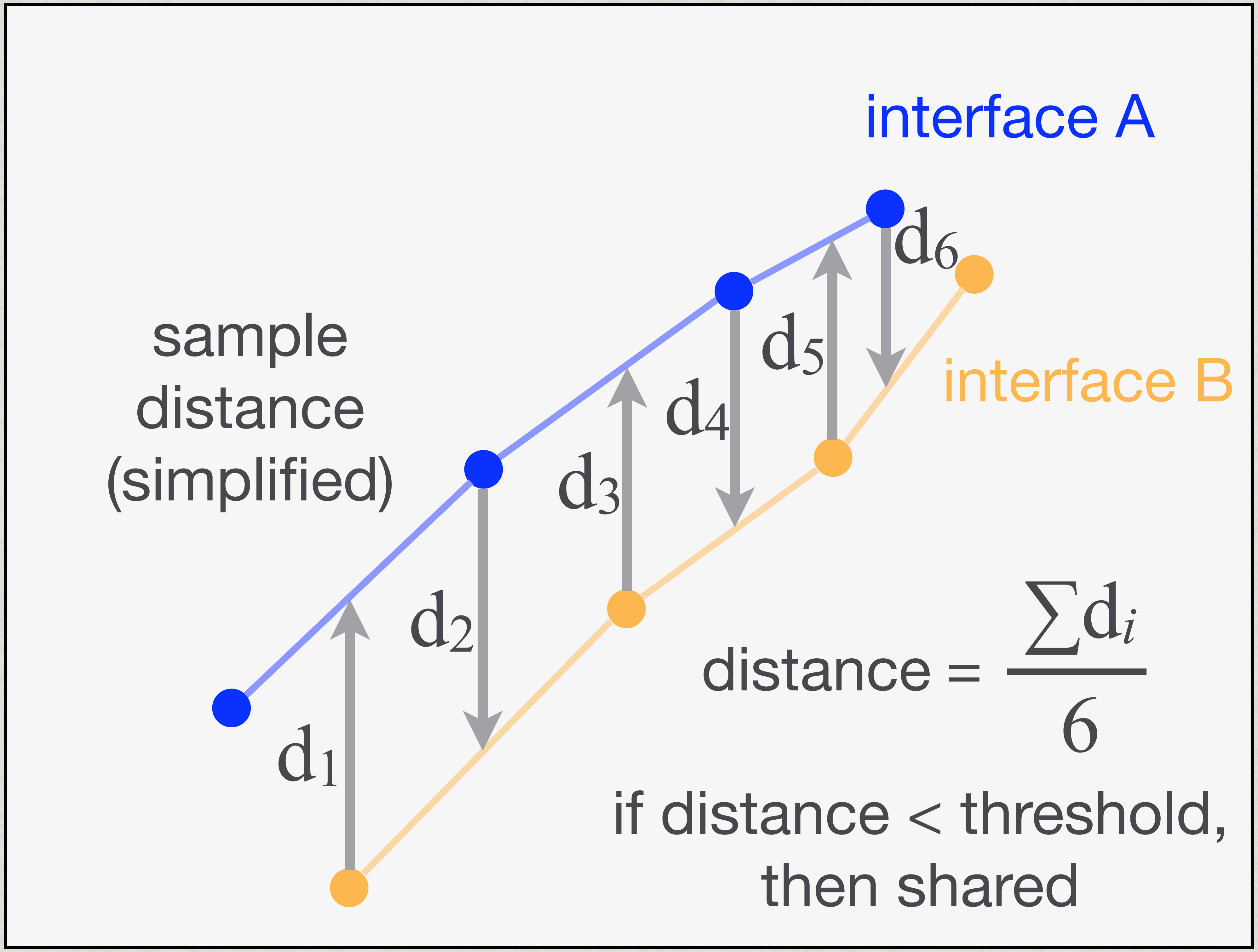
Distance Test



Distance Test



Distance Test

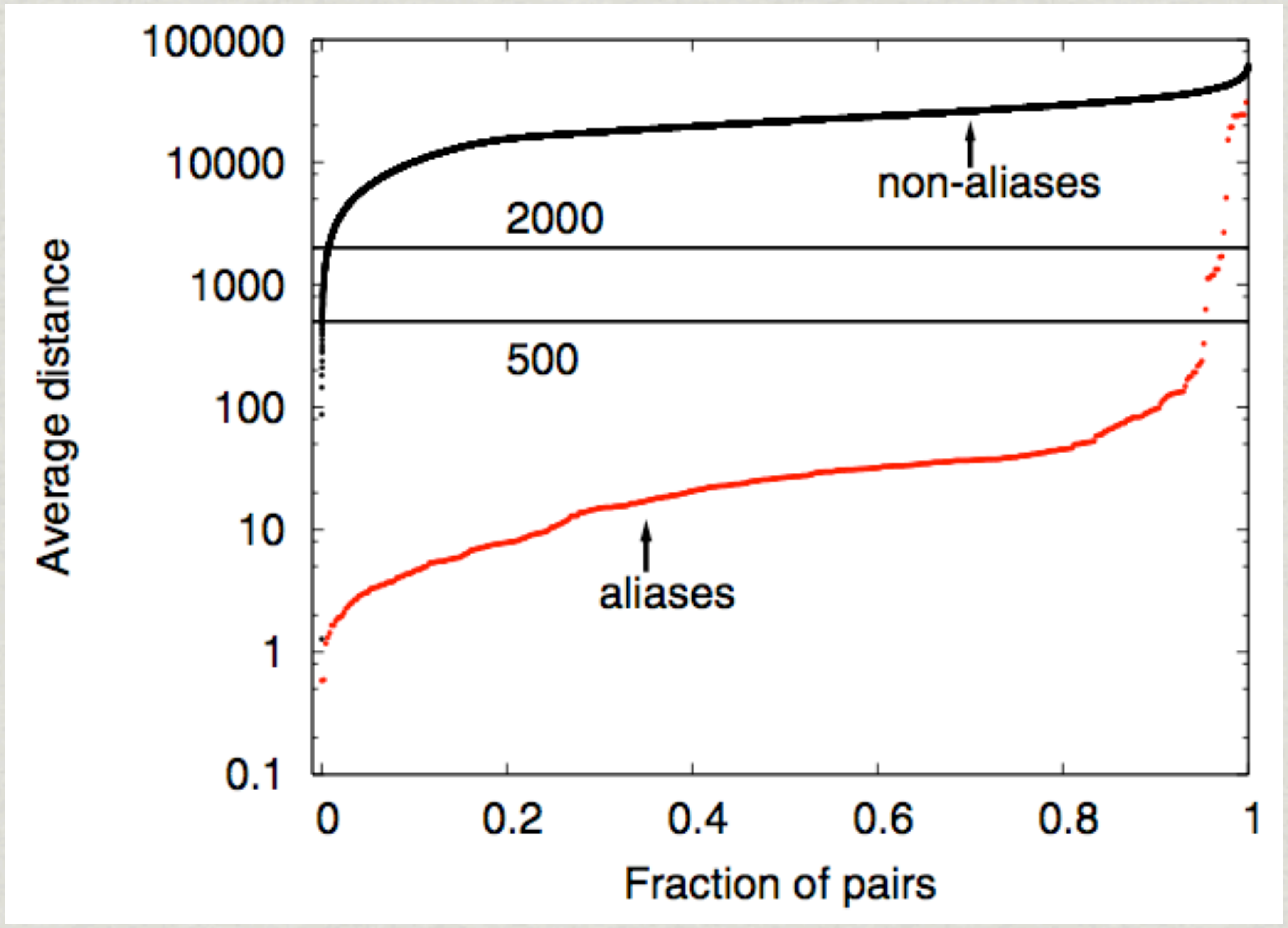


$$\text{distance} = \frac{\sum d_i}{6}$$

if distance < threshold, then shared

Distance Test

- *if distance < **500 IP ID units**, then shared counter*
  - RadarGun authors chose a threshold of 500 based on the distance distribution of alias pairs
    - 932 aliases confirmed with Mercator technique

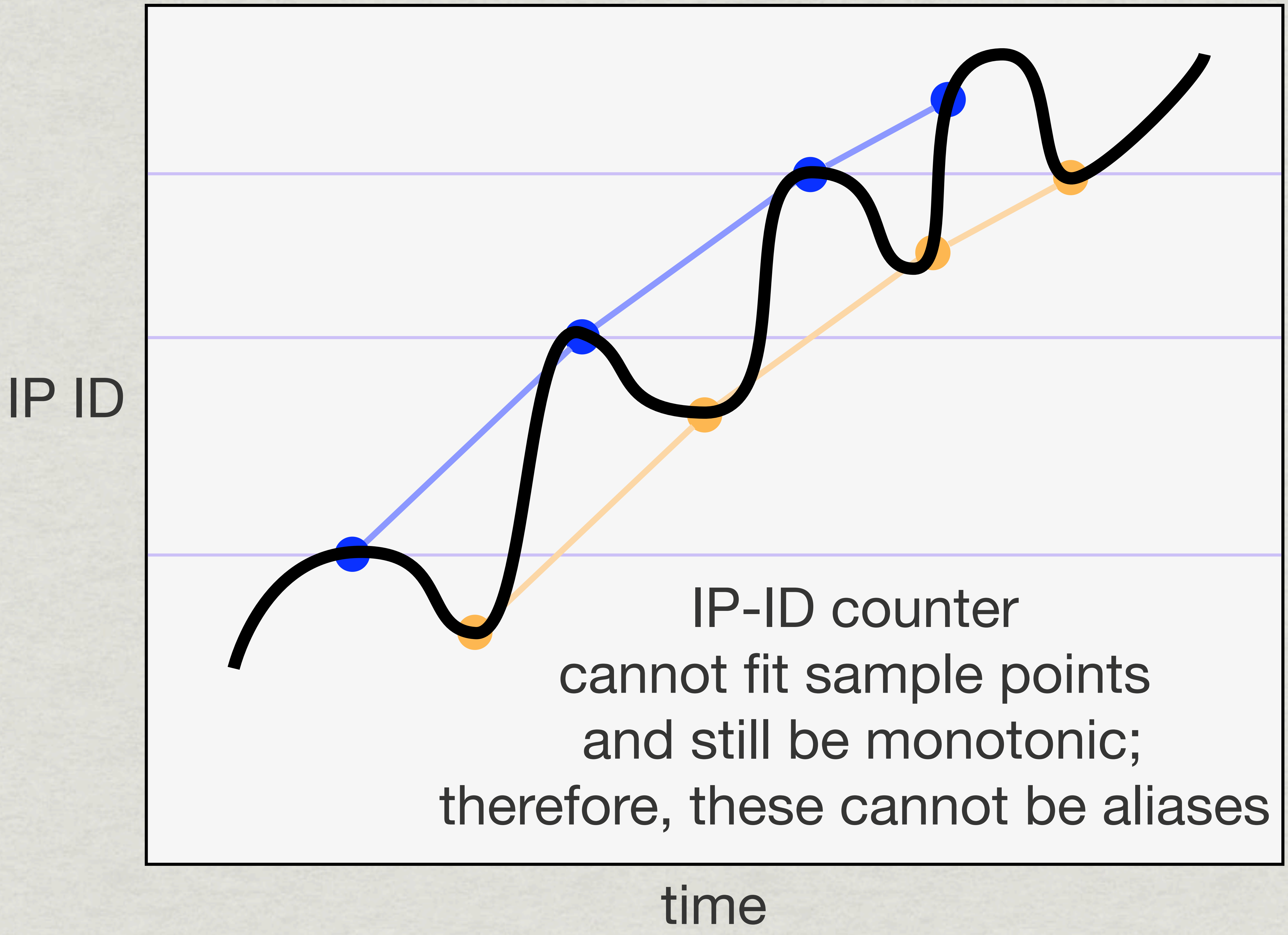


Bender, et al. IMC'08

RadarGun Issues

- RadarGun is groundbreaking work but has both theoretical and practical issues
  - **the distance test for aliases is insufficient**
    - *threshold dependent on underlying dataset*
      - Bender et al used traceroutes between PlanetLab nodes
      - Ark traceroutes are taken to the entire routed space
        - distance distribution noticeably different
    - *threshold doesn't account for velocity*
      - RadarGun *velocity* is the slope of the IP-ID time series
      - setting the threshold high enough to allow high-velocity aliases allows false positives in low-velocity cases
    - *false positives can exist for* ***any*** *chosen threshold*
      - even for a very low threshold

RadarGun false positive for **any** chosen threshold



IP-ID counter
cannot fit sample points
and still be monotonic;
therefore, these cannot be aliases

RadarGun Issues

- **applying RadarGun to 1 million addresses is problematic because RadarGun needs overlapping IP-ID time series for all targets in a short period of time**
    - looks like DDoS attack
    - triggers rate limiting
    - requires high probing rate or large number of machines

RadarGun Issues

$$\frac{\text{interface set size}}{\text{probing rate}} = \text{round duration}$$

or

$$\frac{\text{interface set size}}{\text{round duration}} = \text{probing rate}$$

- probing rate must increase if ...
  - interface set size increases
  - round duration decreases

RadarGun Issues

$$\frac{9{,}056 \text{ interfaces}}{35 \text{ sec}} = 260 \text{ pps}$$

$$\frac{1\text{M interfaces}}{35 \text{ sec}} = 28{,}500 \text{ pps}$$

$$\frac{1\text{M interfaces}}{5 \text{ sec}} = 200{,}000 \text{ pps}$$

- RadarGun’s 35-sec round duration is arbitrary
  - 5 seconds is more appropriate based on the highest actual velocity in our dataset
  - RadarGun needs 769 monitors to probe 1M interfaces with 5-sec duration at 260pps
- 1 week of Ark traces has 1 million interfaces
  - expect possibly 2 million in 1 month of traces
    - possibly 3 million with more monitors

MIDAR

- ***M****onotonic* ***ID****-Based* ***A****lias* ***R****esolution* (MIDAR) is our extension of the RadarGun approach
  - *monotonic bounds test* for accurate testing of pairs
  - *sliding window* for scaling up probing
  - 4 probing methods
  - multiple monitors

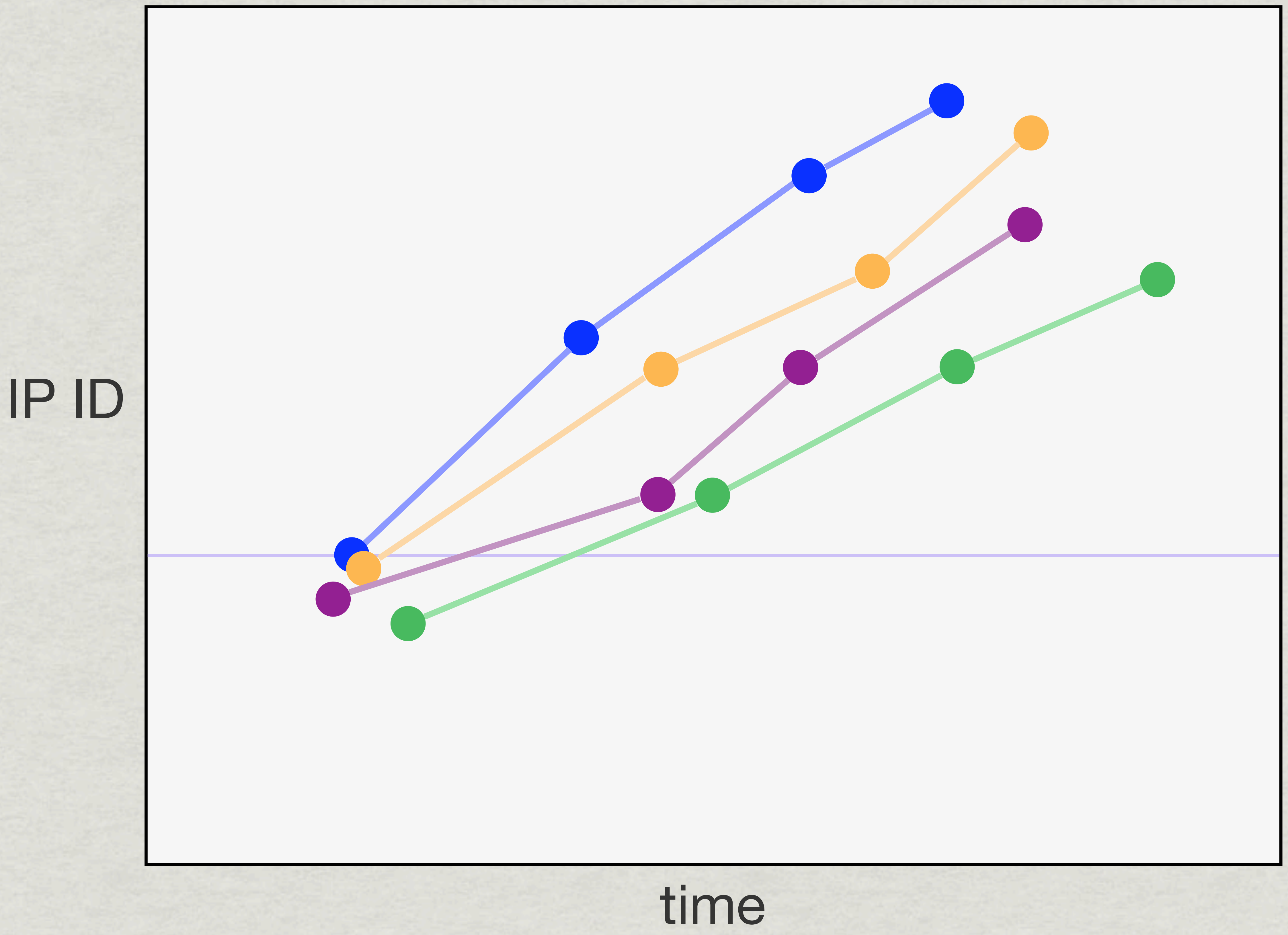
False Positives

- potential for false positives is high when using IP-ID time series for alias resolution
  - IP-ID space has only 2^{16} = 65,536 possibilities
  - birthday paradox (when number of targets < 2^{16}):
    - even with just 9,053 targets, the probability of two targets having the same IP ID value is nearly 1.0
    - only takes 302 targets to have 50% chance for same IP ID
  - pigeonhole principle (when number of targets > 2^{16}):
    - 1 million targets cannot each have unique IP ID values
    - 1 million / 2^{16} = 15 targets per IP ID value on average
  - even worse: nearby IP ID values can cause false positives

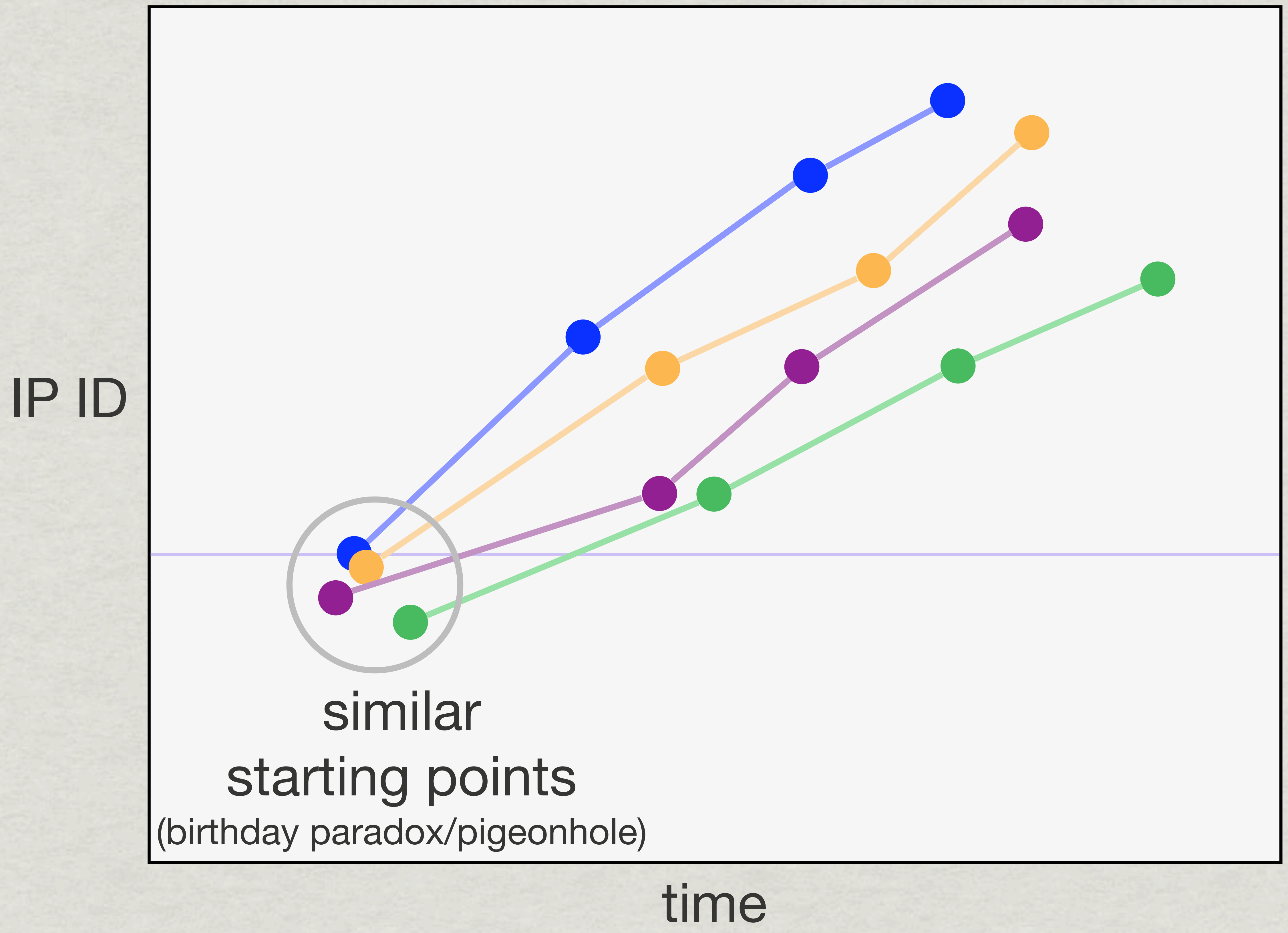
False Positives

- we compare time series, not just individual sample points, for alias resolution
- however, the potential for false positives is still high because the velocity distribution of targets is heavily skewed
  - not much variability (or entropy) in practice
  - ~80% of targets have velocity of 10 IDs/sec or less
  - ~50% have velocity of 1 IDs/sec or less

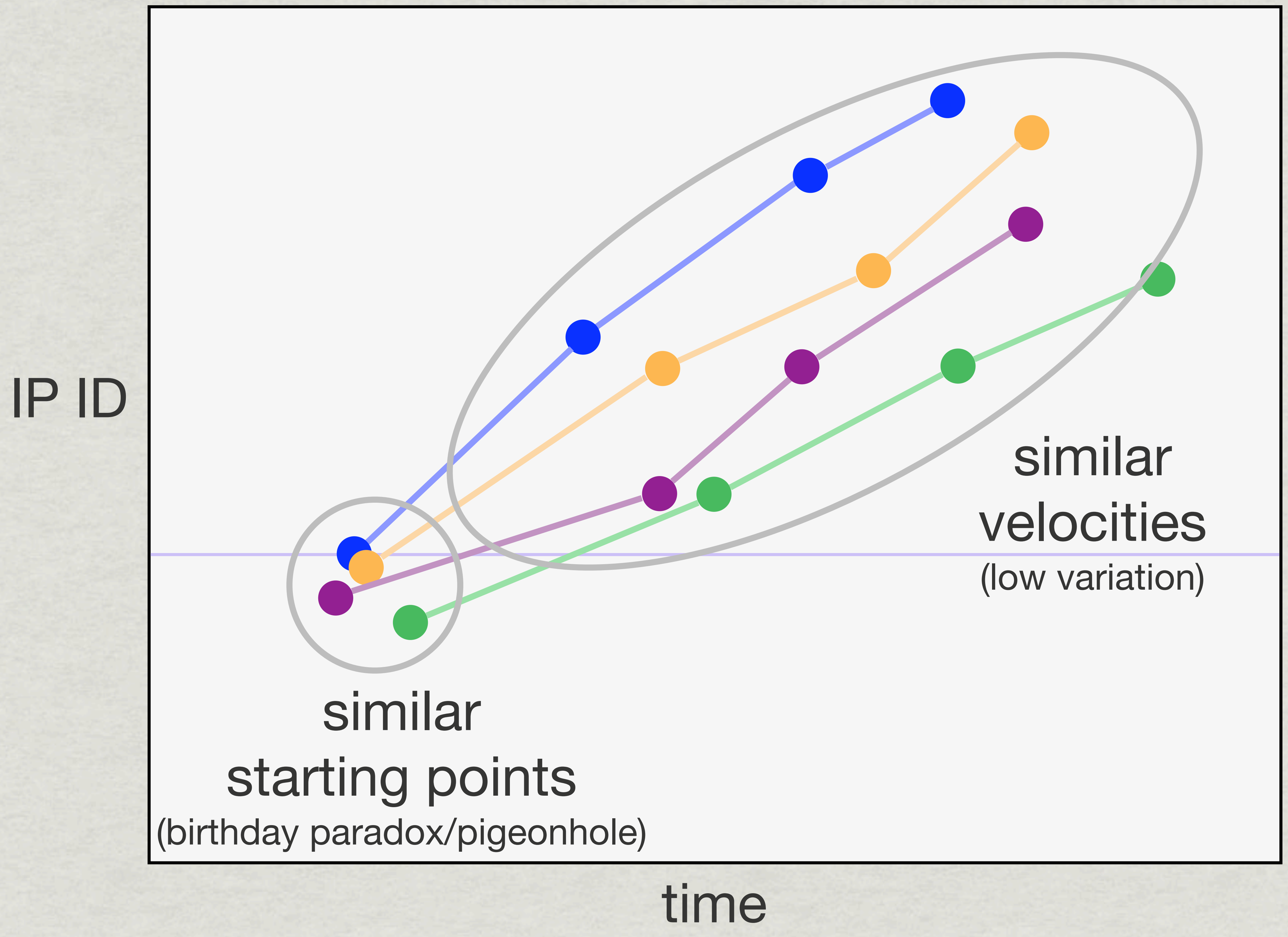
False Positives



False Positives



False Positives



False Positives

- an accurate shared counter test is critical
  - the number of true alias pairs is low
    - with N addresses:
      - number of true aliases is $O(N)$
      - number of false positives is a fraction of total pairs, or $O(N^2)$

addrs	all pairs	true alias pairs[1]	
10k	50M	245k	0.490%
100k	5G	2.5M	0.049%
1M	500G	25M	0.005%

[1] alias pairs extrapolated from tier 1 ISP

  - false positives are amplified when combining alias pairs into routers with transitive closure

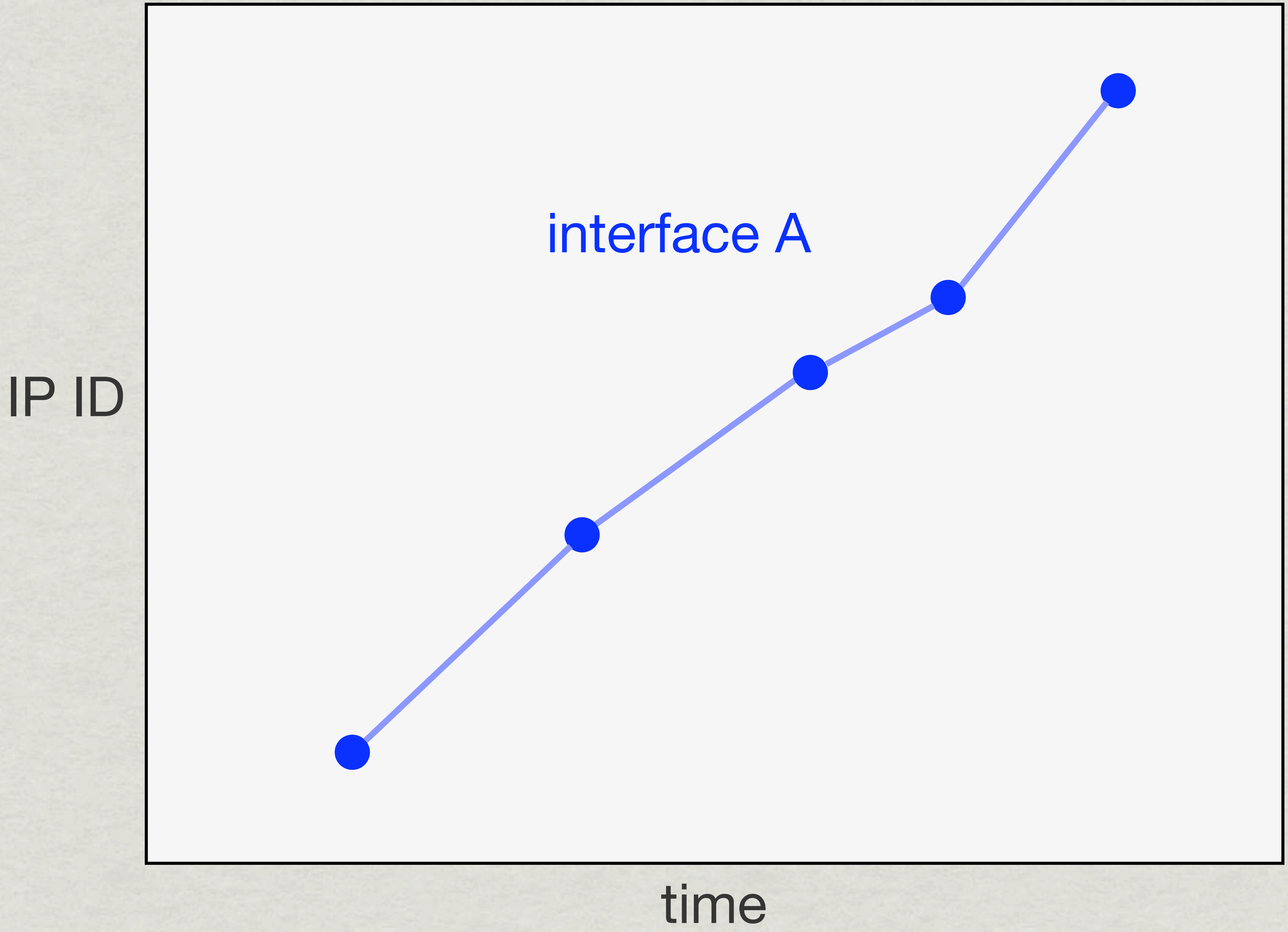
MIDAR

- MIDAR uses the *monotonic bounds test*:
  - based on a **necessary** condition, not an arbitrary threshold
  - failing the test means definitively “not a shared counter”
    - that is, provides *negative* information
    - “not shared” is not as strong as “not alias” but still useful
  - extremely low false positives when repeated

Monotonic Bounds Test

- the *monotonic bounds test* rationale:
  - if two interfaces use a shared counter for their IP-ID values, then they are aliases
    - the same observation underlying RadarGun
    - careful: converse not true; aliases need not share a counter
      - so time-series analysis can only detect aliases that share a counter (which applies to RadarGun & MIDAR equally)
  - if two interfaces share a counter, then their IP-ID time series must form a strictly increasing sequence (“must be monotonic”) when merged together
    - therefore, having a monotonic combined time series is a **necessary** condition for being a shared counter and thus a necessary condition for being a **detectable** alias

Monotonic Bounds Test



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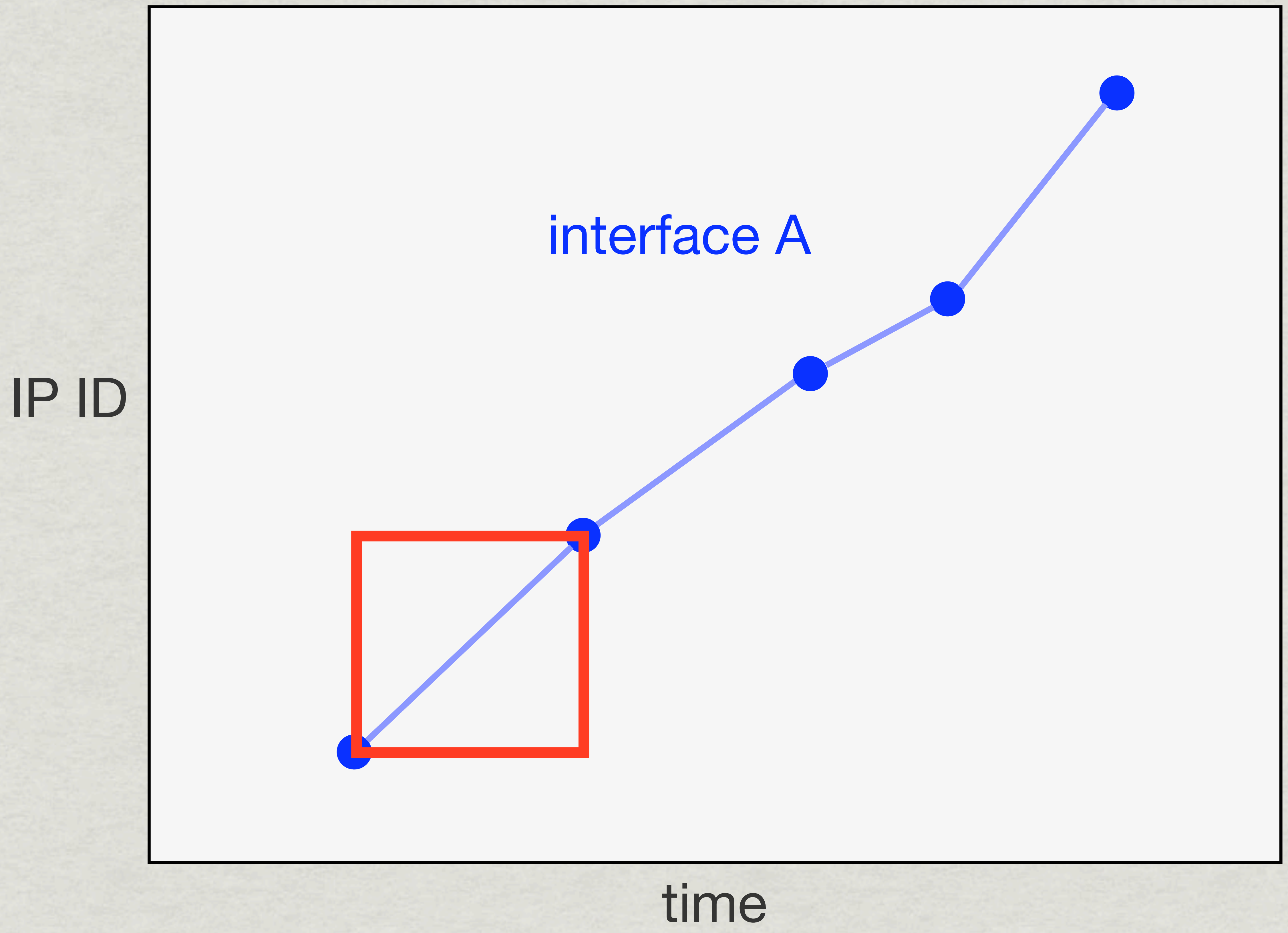

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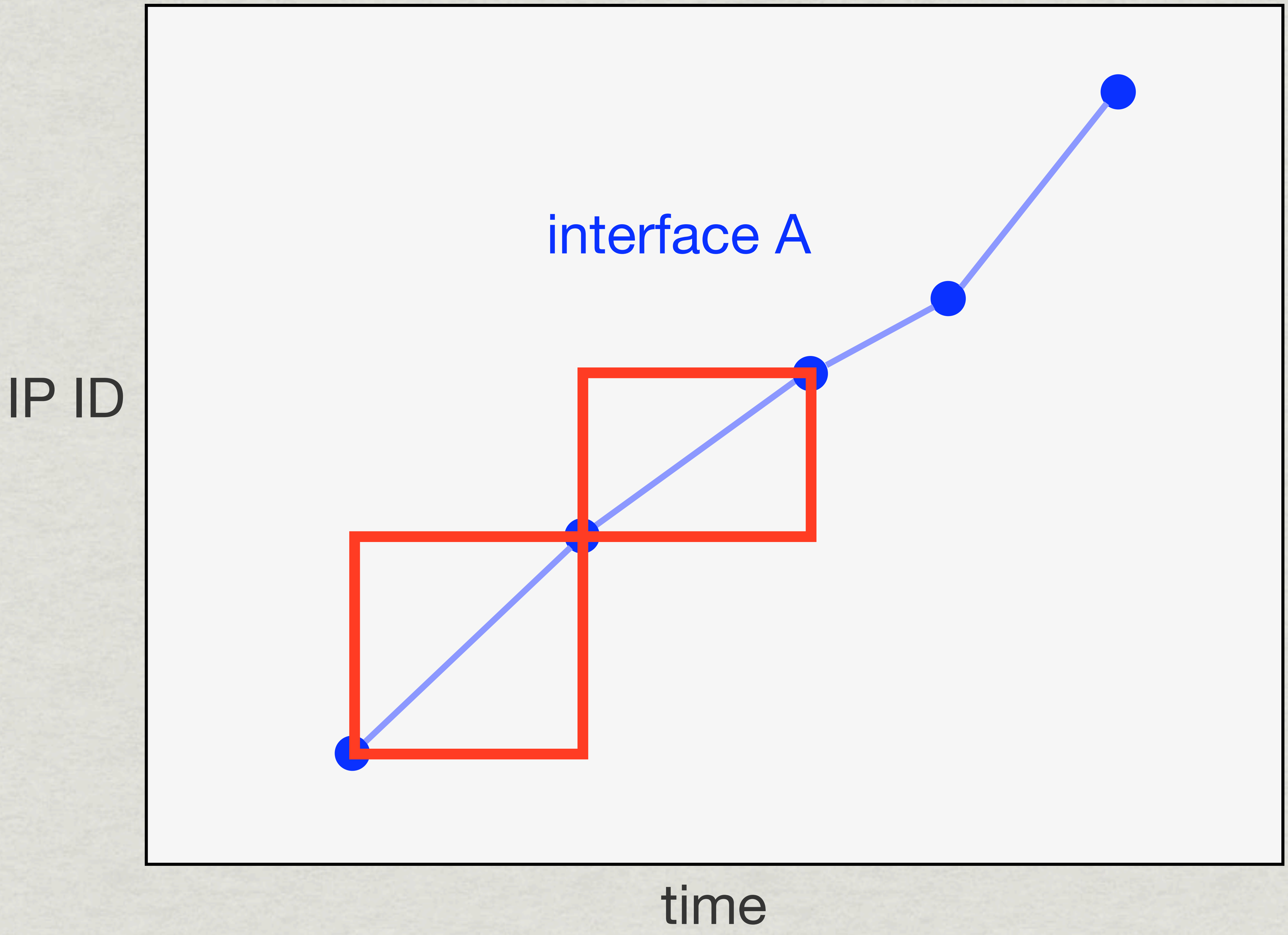

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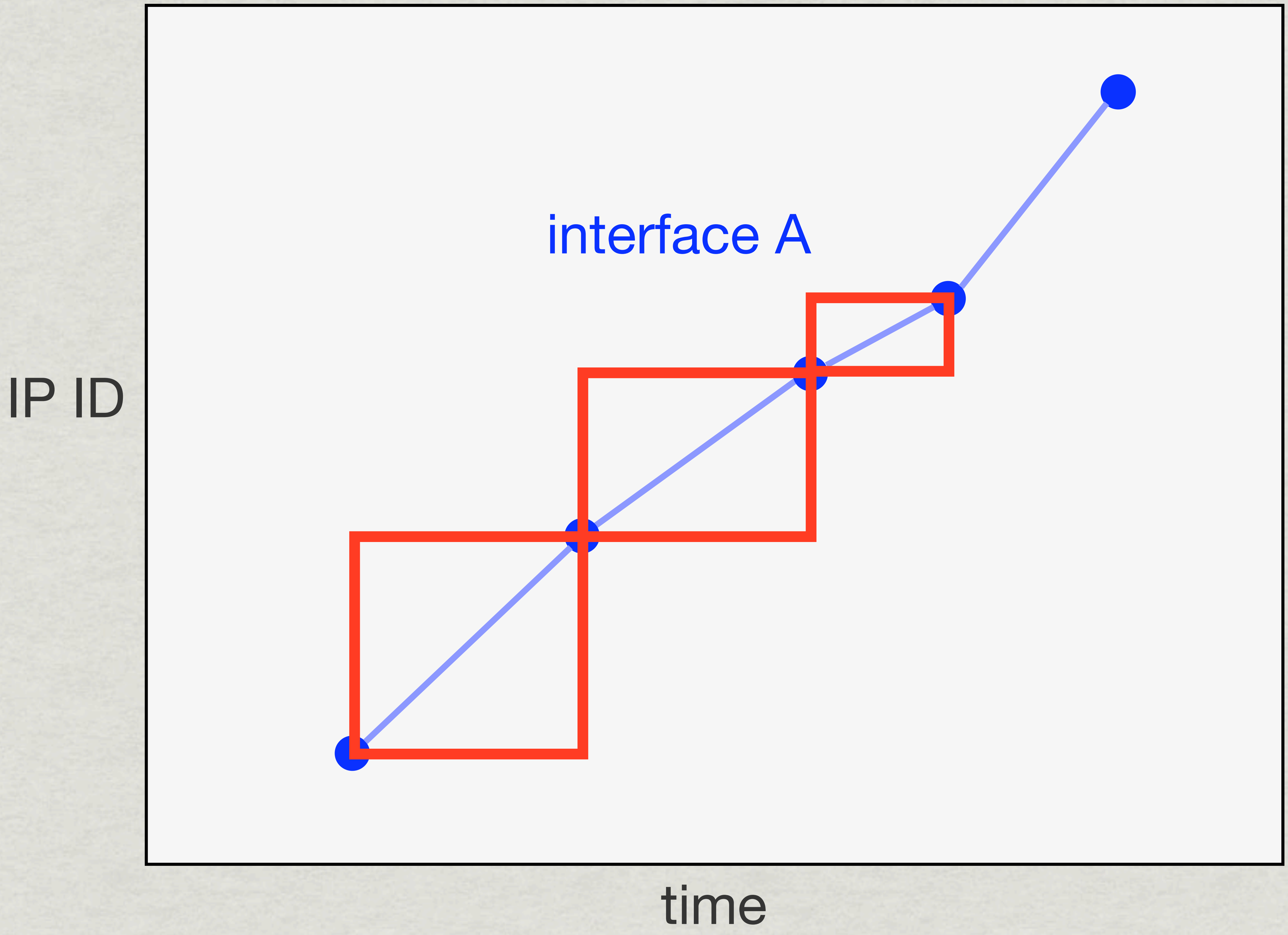

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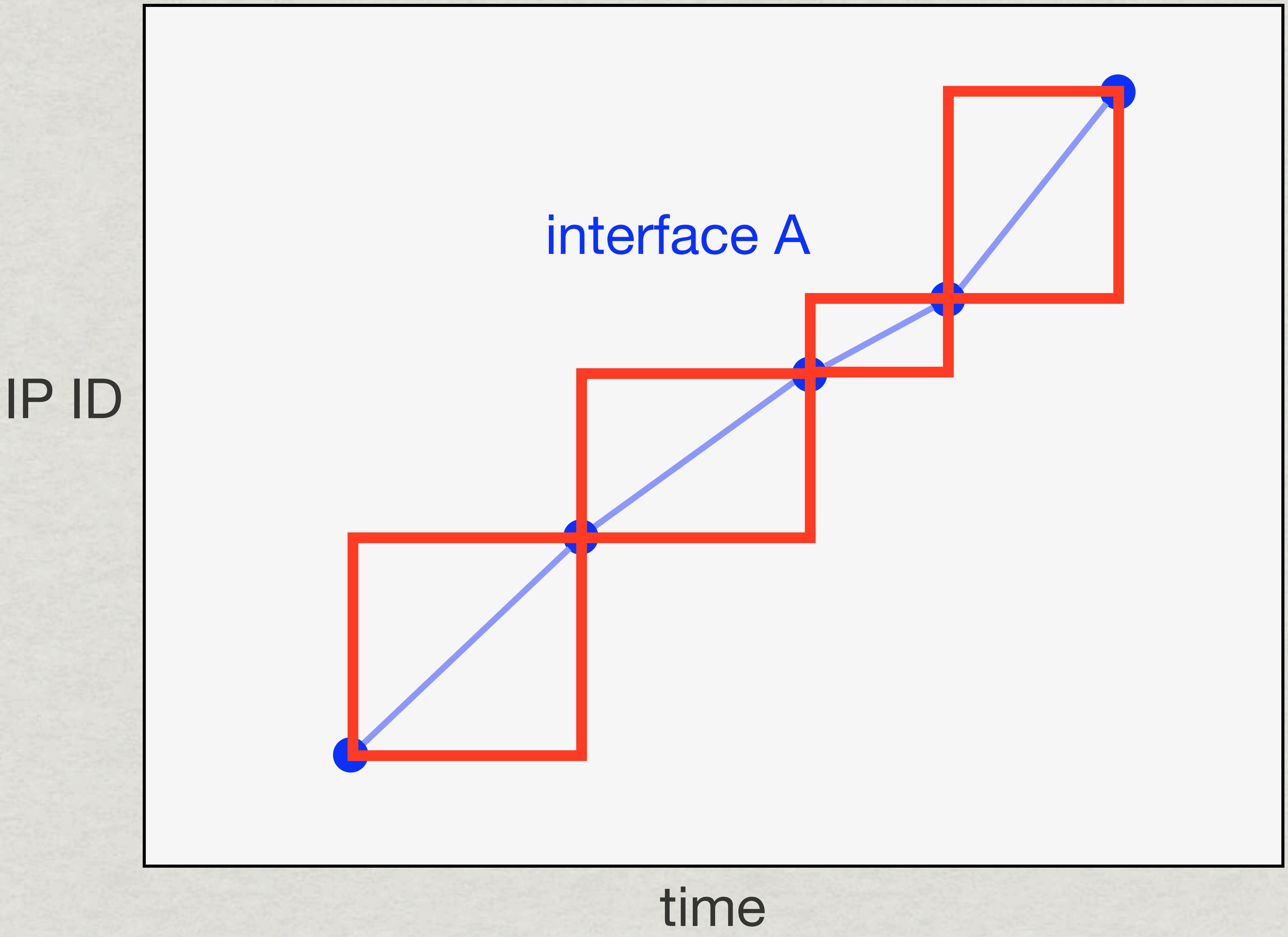

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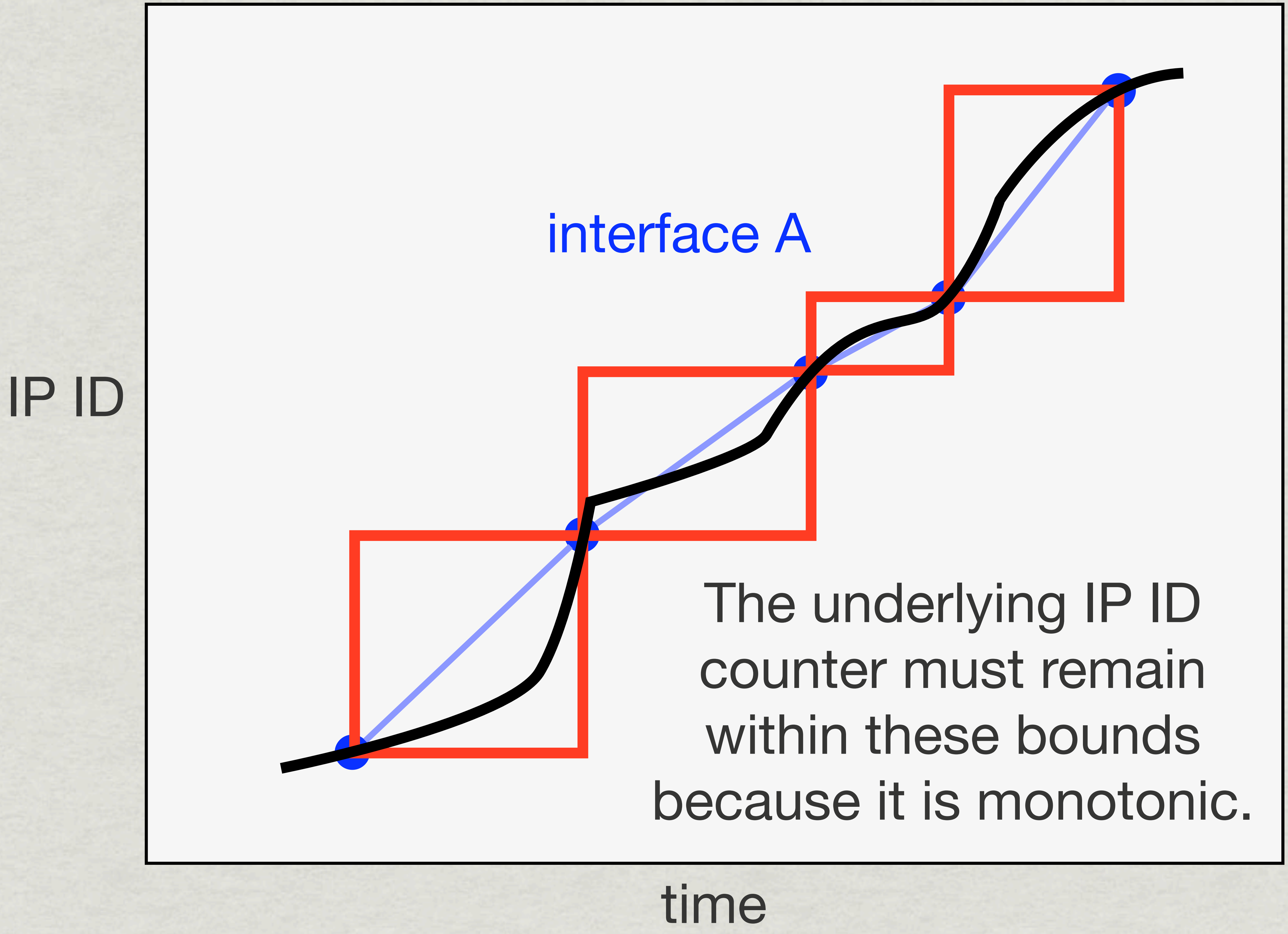
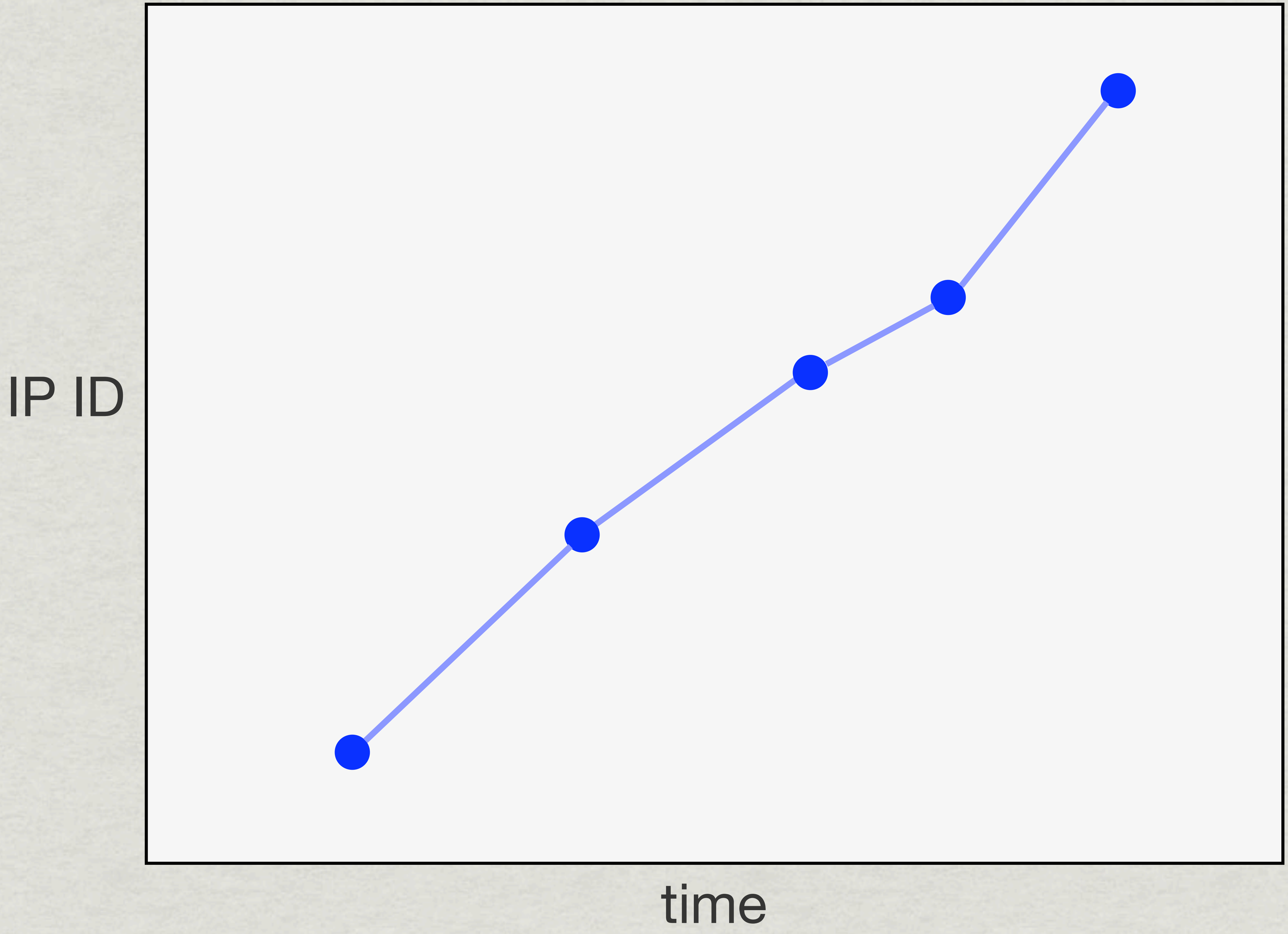


The underlying IP ID counter must remain within these bounds because it is monotonic.

Monotonic Bounds Test



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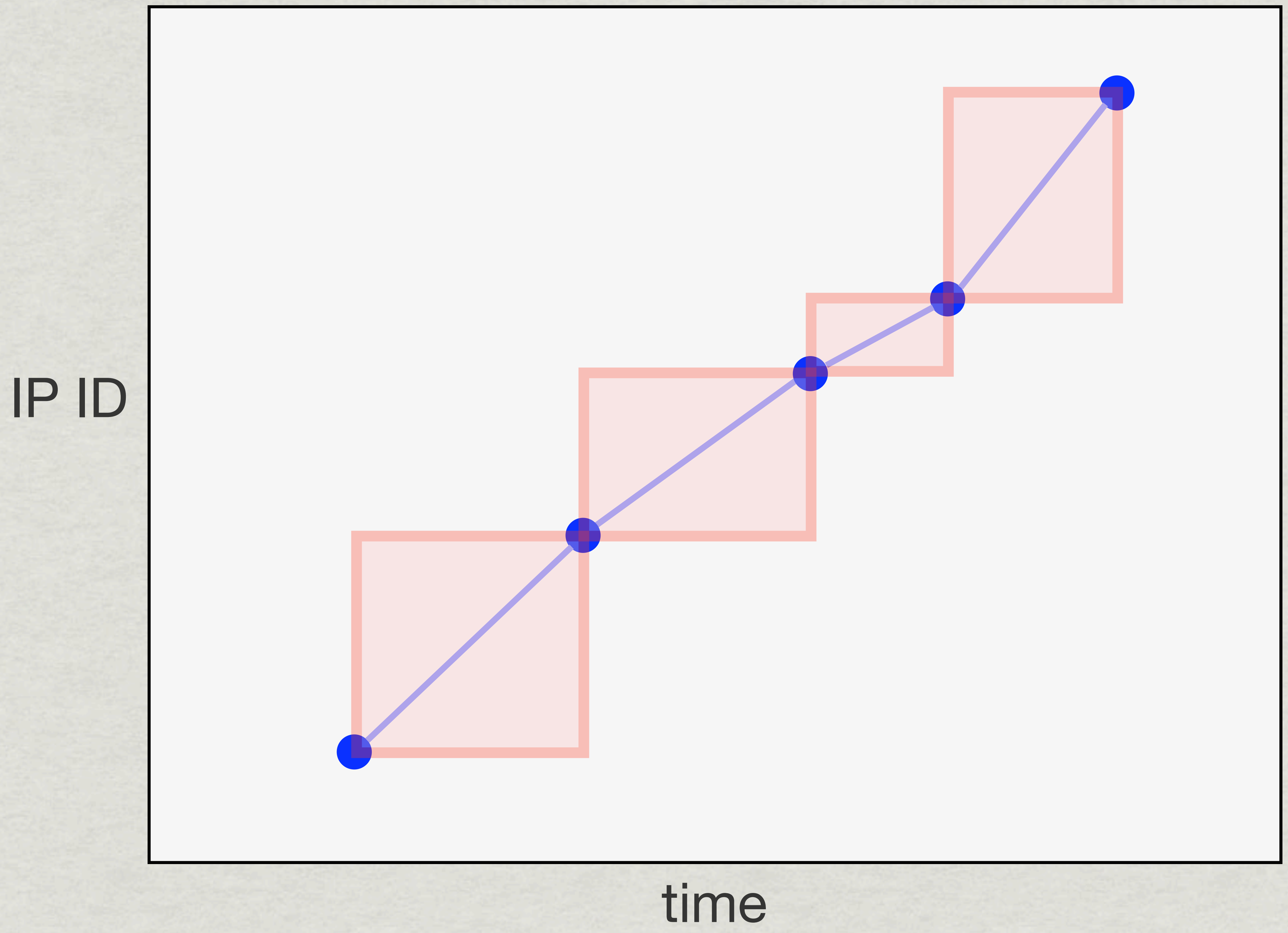

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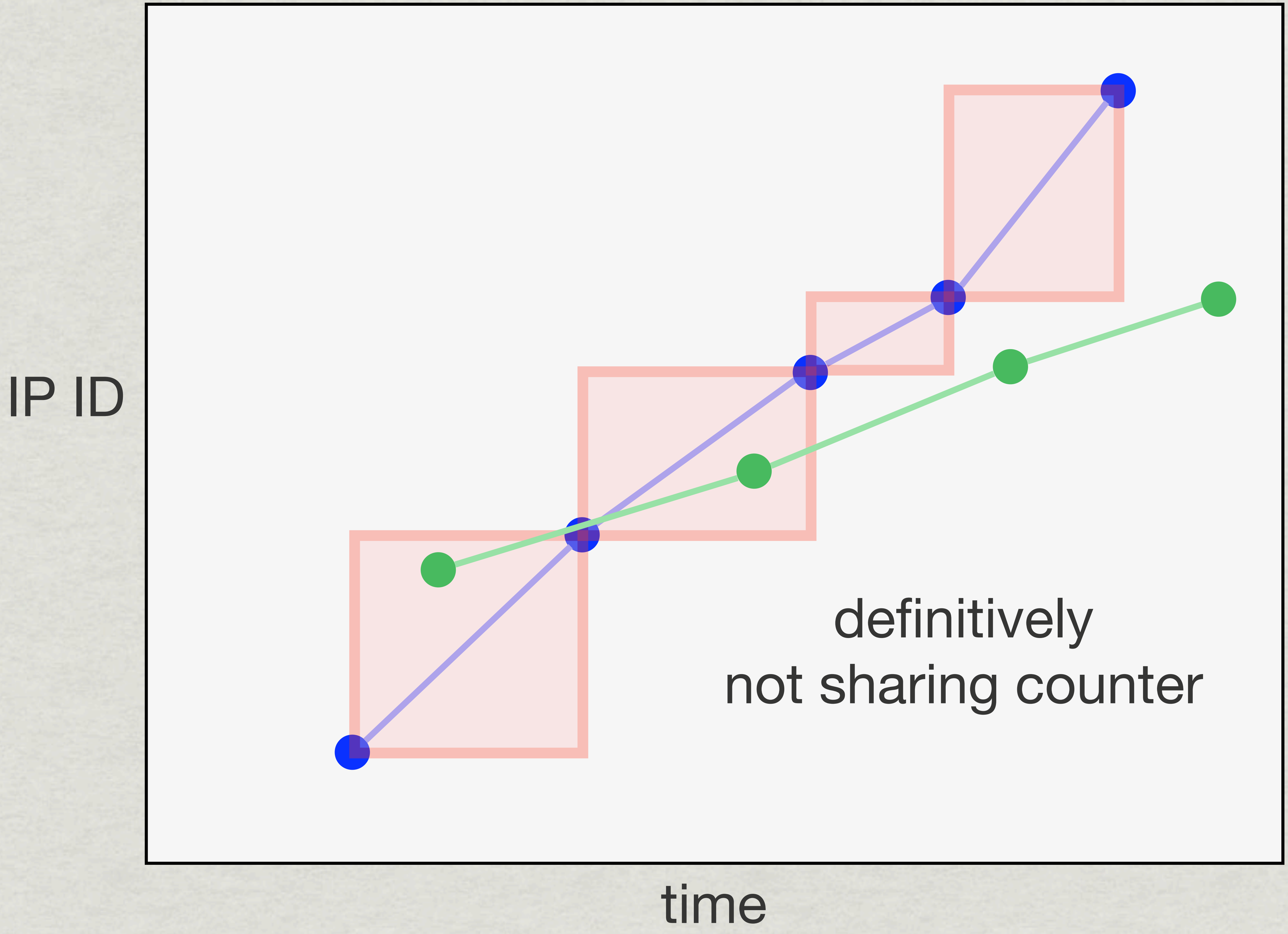

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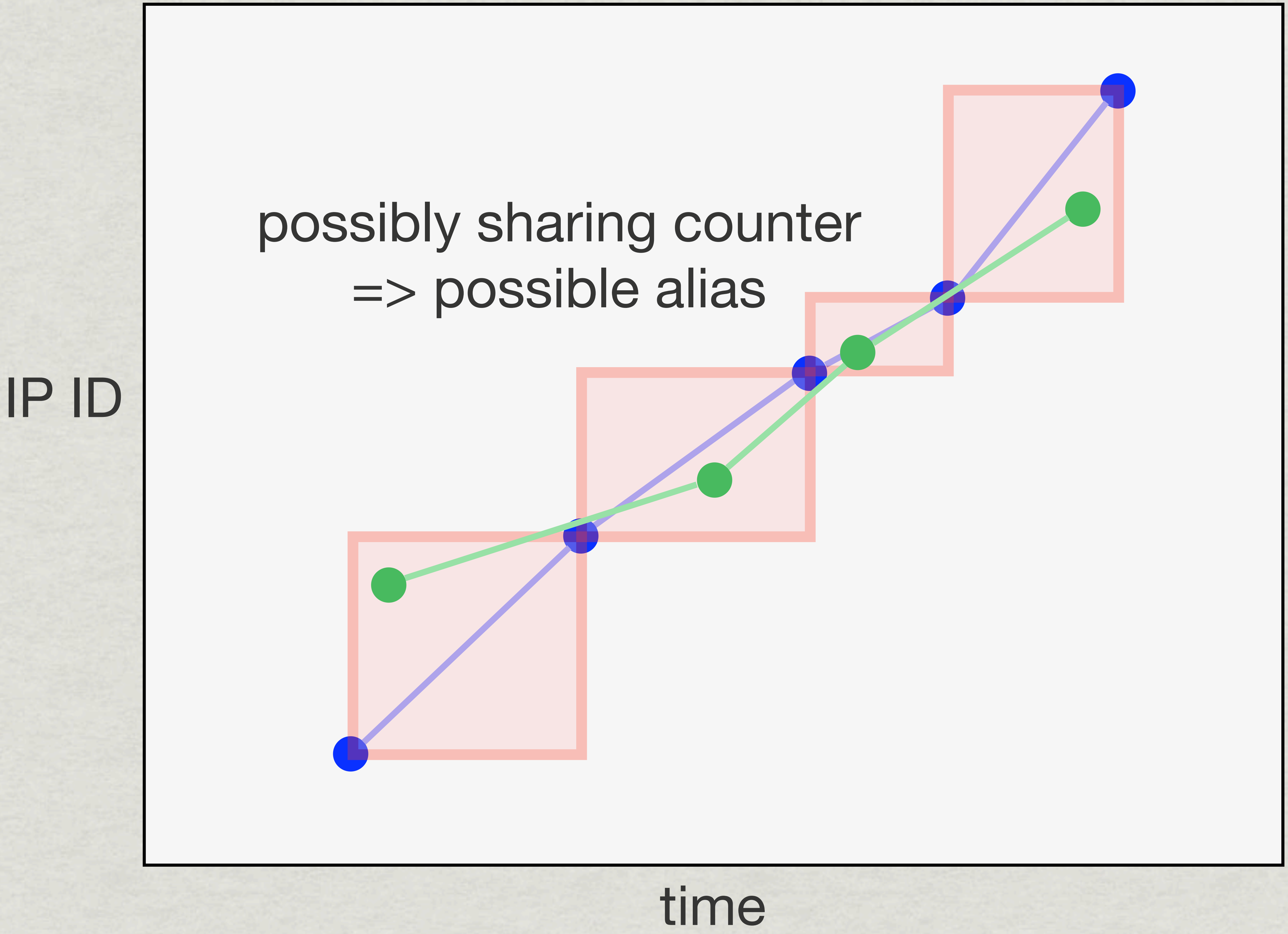


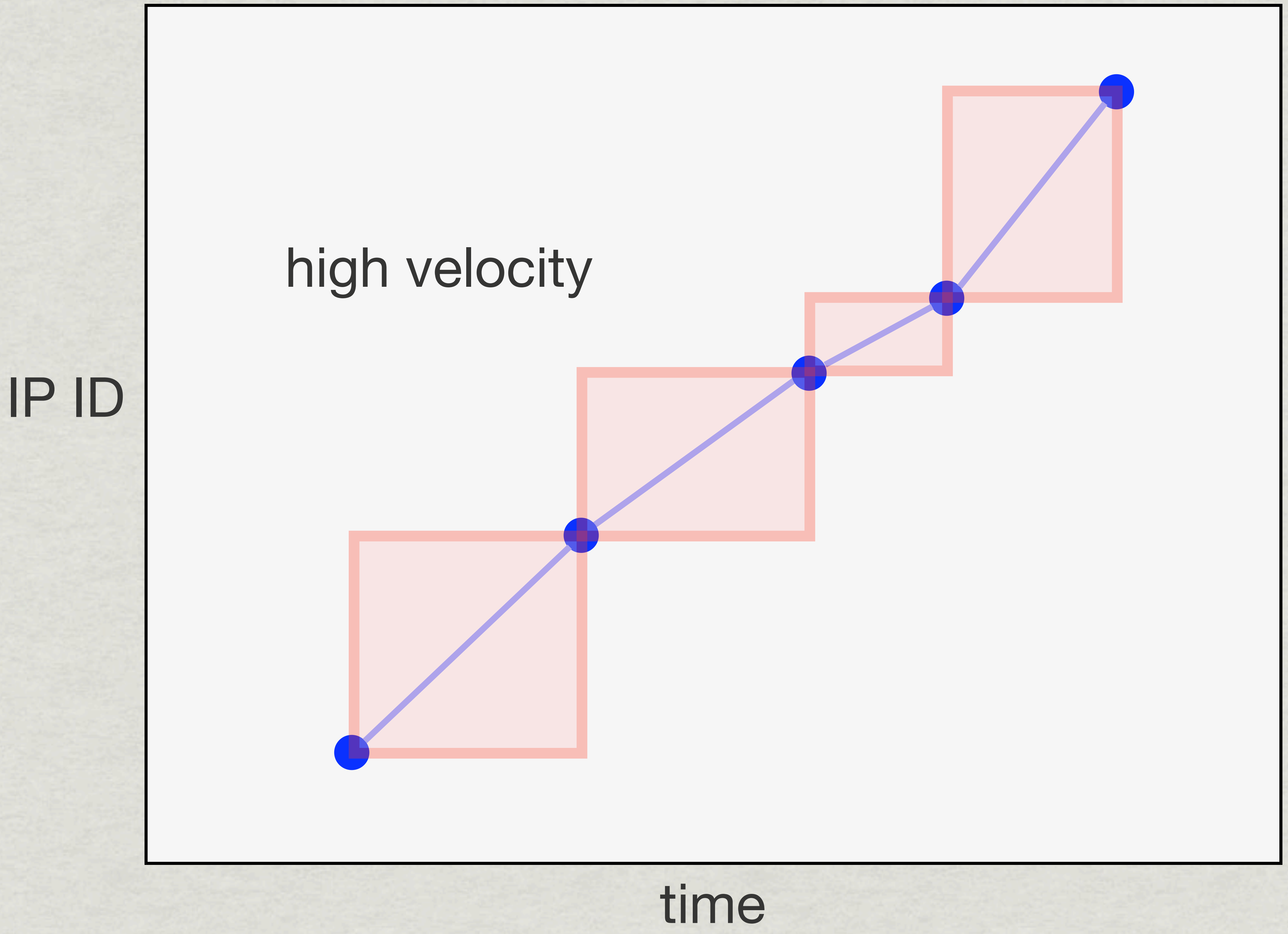
Monotonic Bounds Test

- passing the monotonic bounds test is not a **sufficient** condition for sharing a counter
  - false positives from chance alignment, just as with the distance test
  - but **crucial** point:
    - the monotonic bounds test guarantees the **necessary** condition for sharing a counter
    - we can exploit this guarantee to ensure sufficiency

Monotonic Bounds Test

- we can improve confidence by repeating the test at a later time after non-shared counters have had a chance to diverge
  - each application of the monotonic bounds test only removes false positives
    - never rejects real aliases (that is, does not create false negatives)
    - so repetition is helpful and never harmful
  - the test converges quickly and with high confidence to the set of true positives with repetition
    - because the test takes advantage of varying velocities and probe spacing

Monotonic Bounds Test



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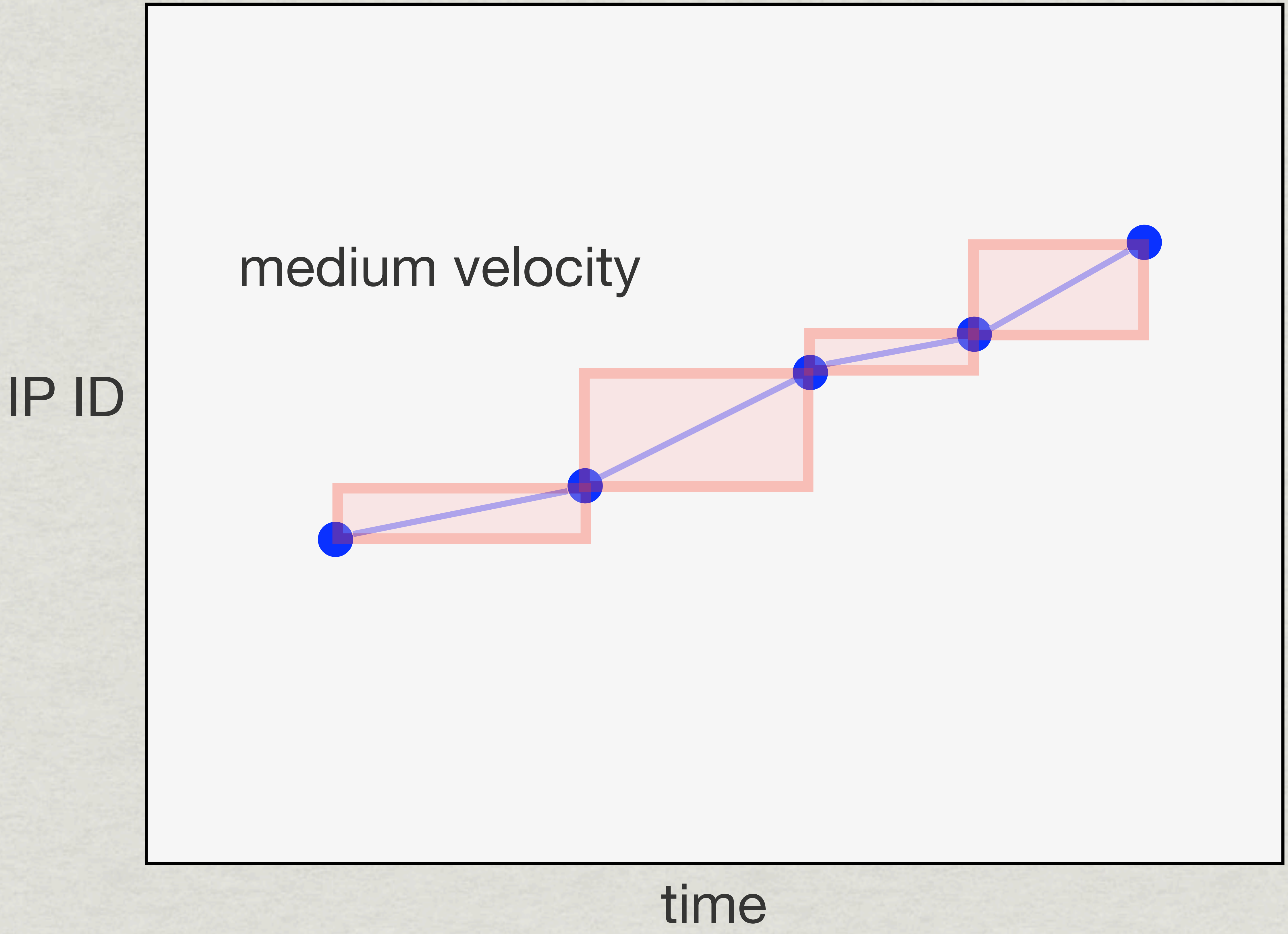

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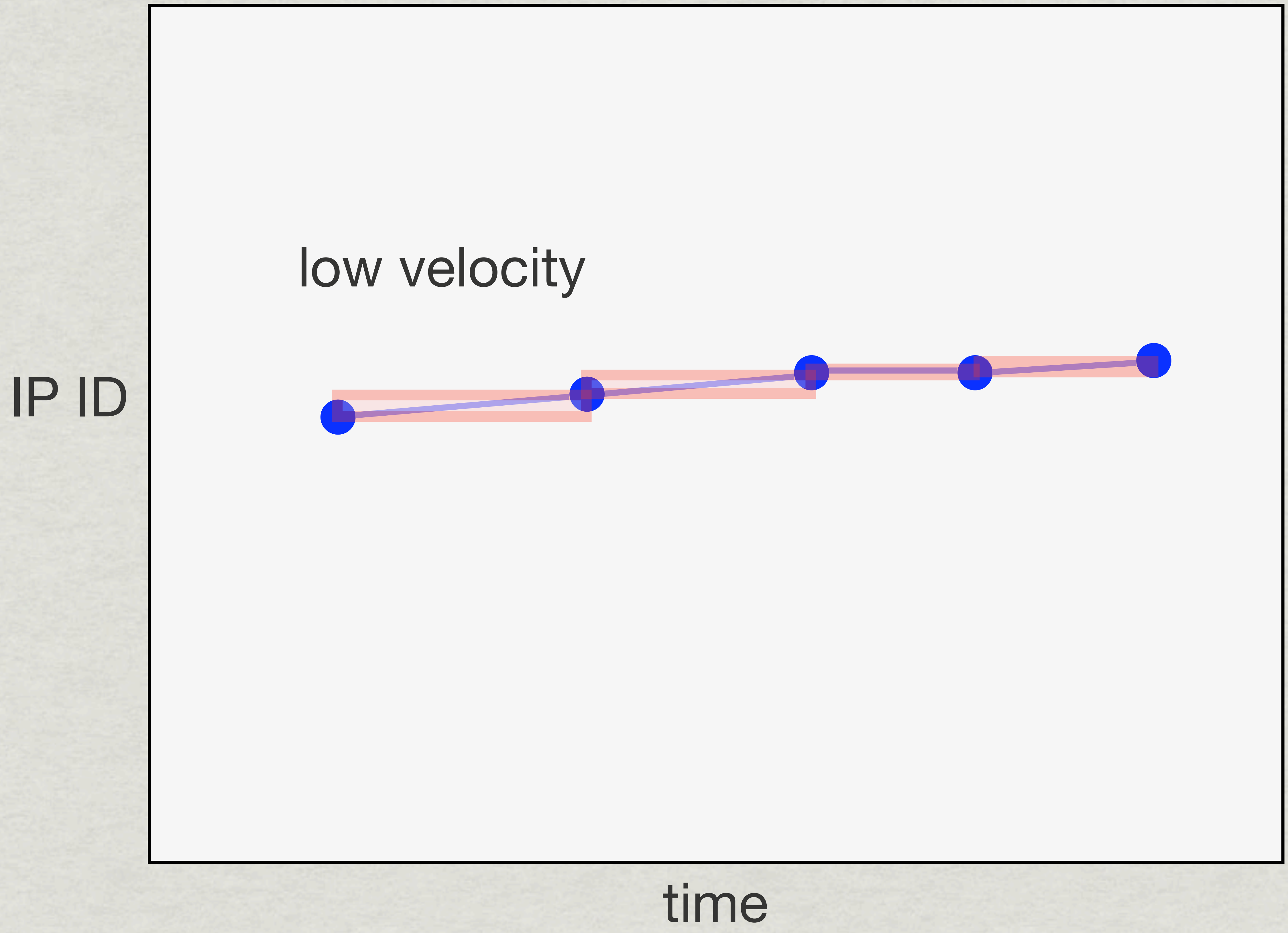

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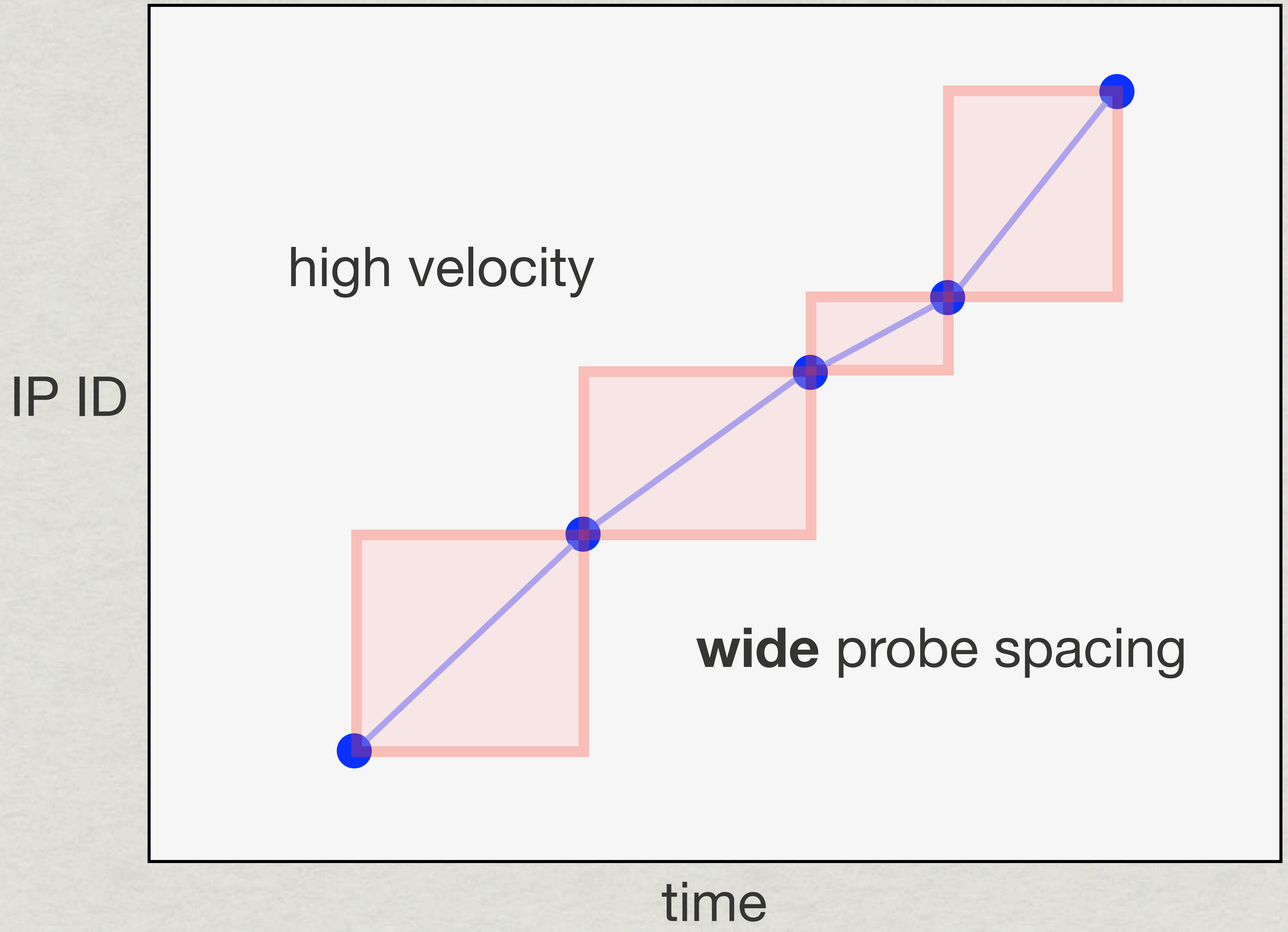

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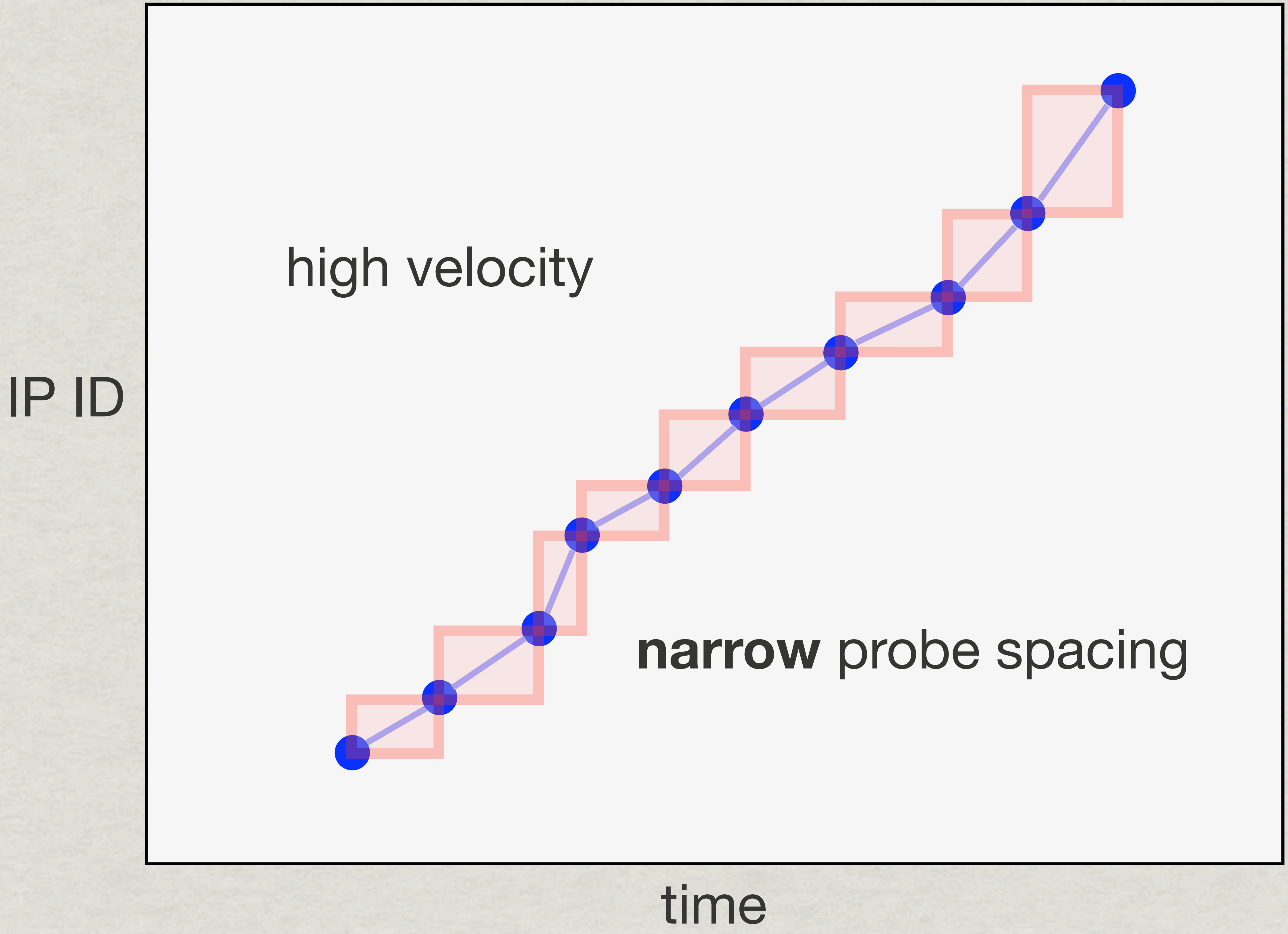
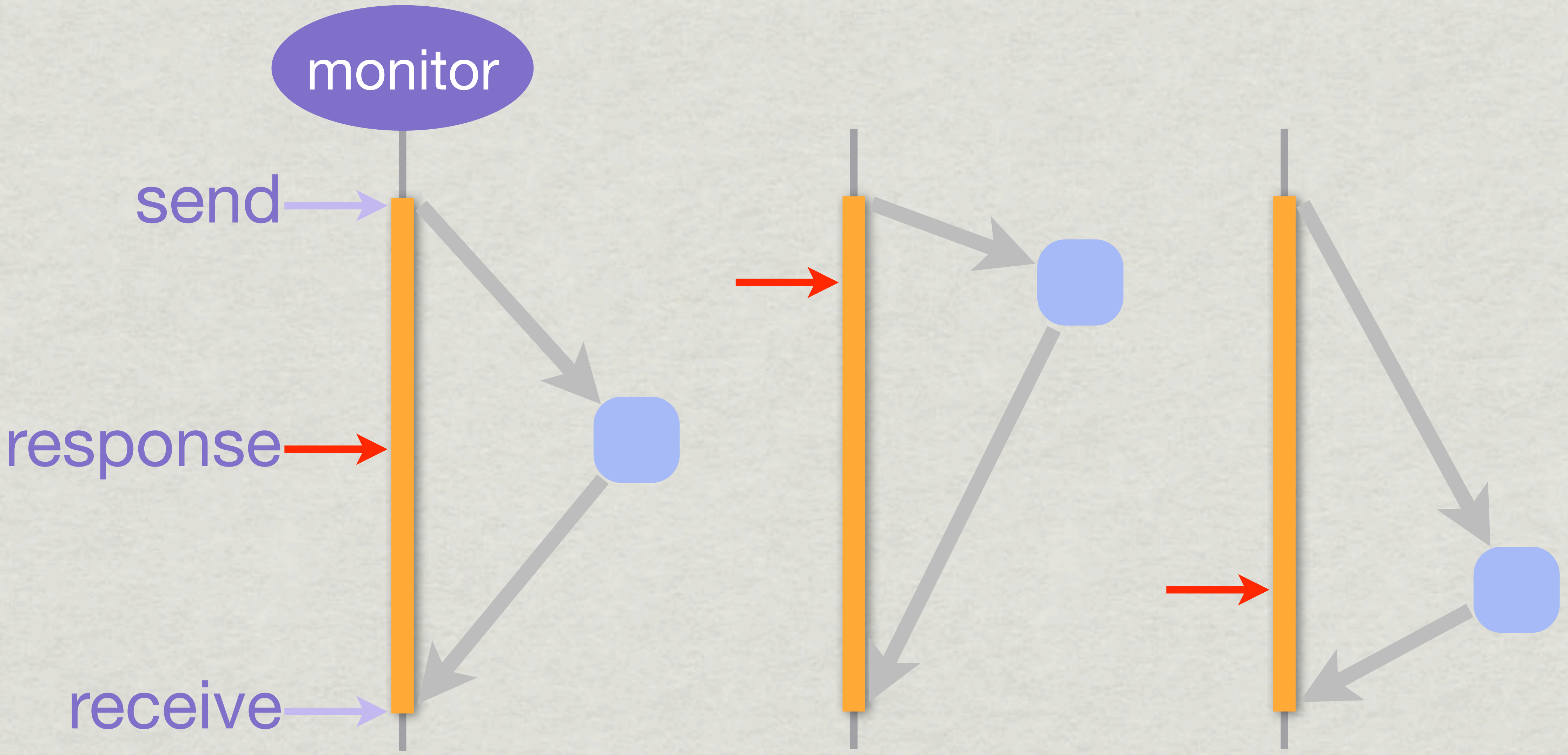


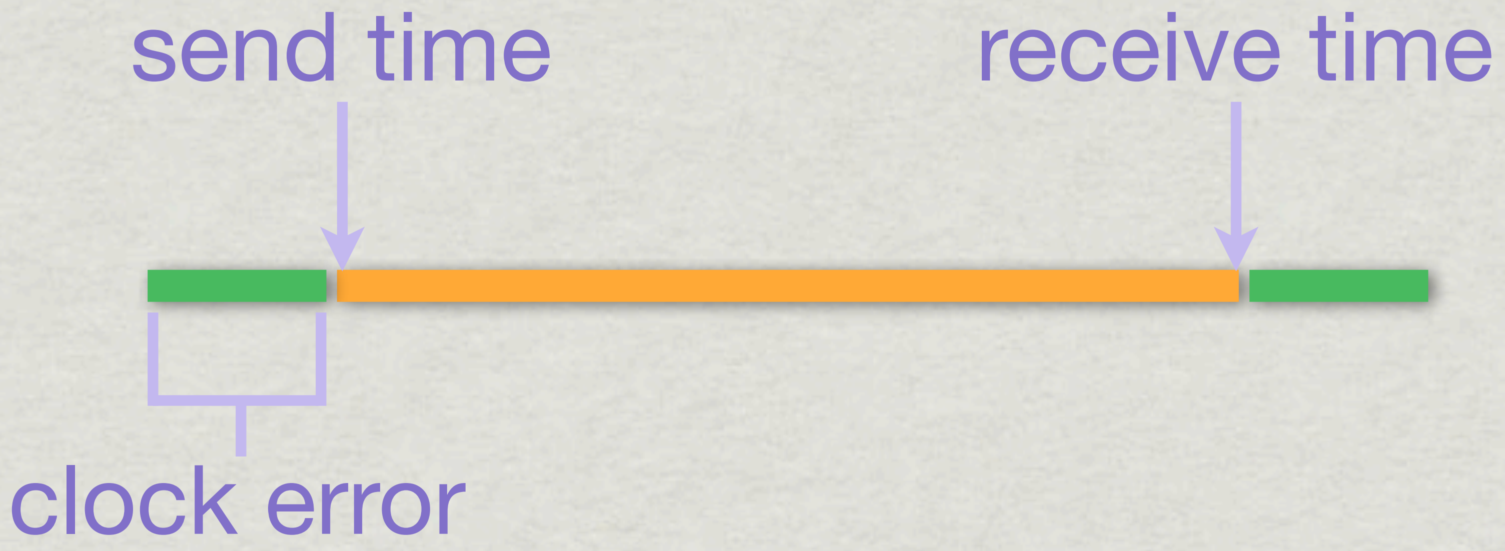
Monotonic Bounds Test

- the monotonic bounds test is slightly more complicated in practice
  - first, exact time of response unknown:



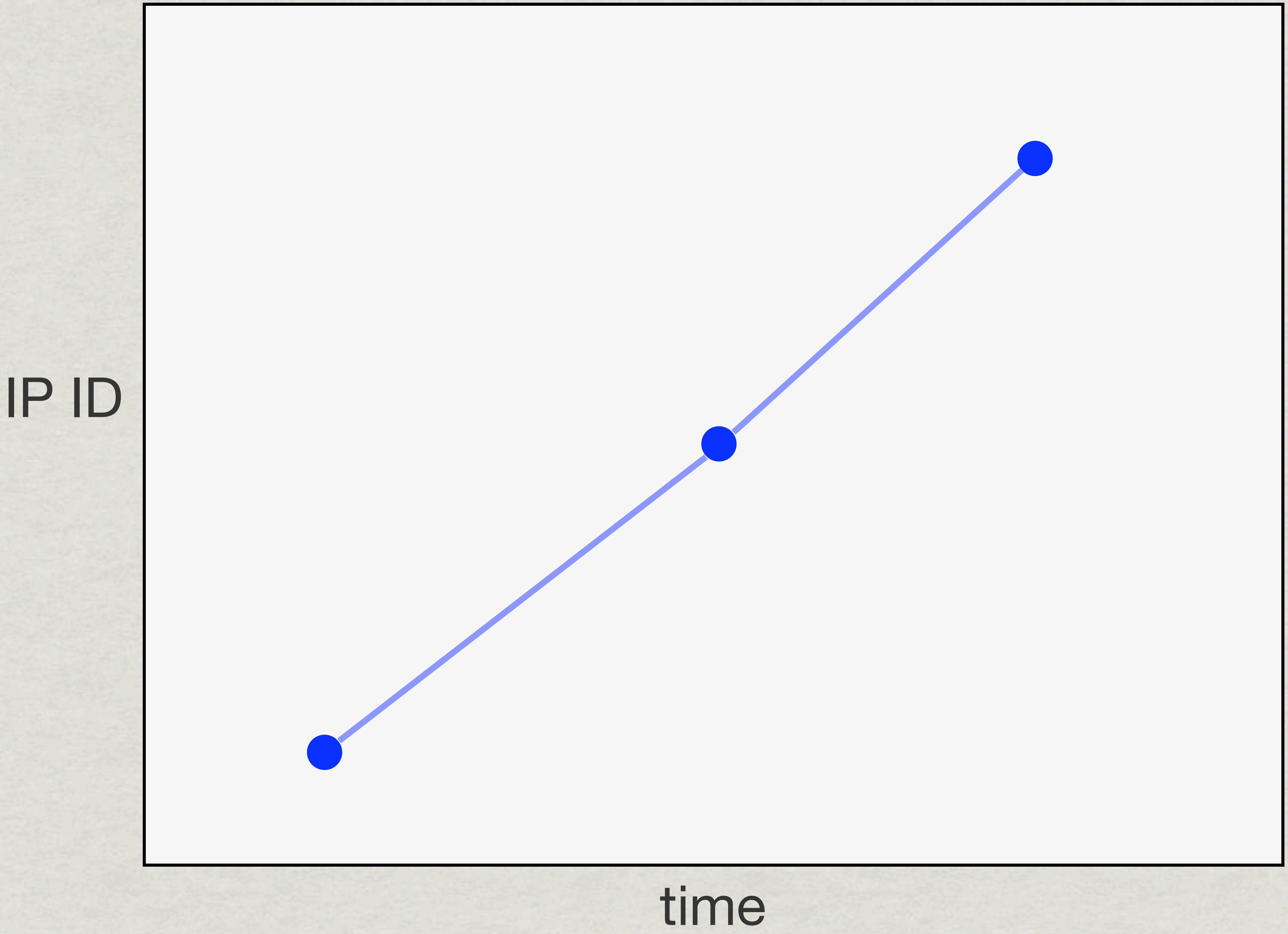
Monotonic Bounds Test

- second, clocks are not perfectly synchronized across monitors
  - only matters when comparing data from multiple monitors



- we can accommodate uncertainties in both the response time and clock offset without compromising the rigor of the monotonic bounds test

Monotonic Bounds Test



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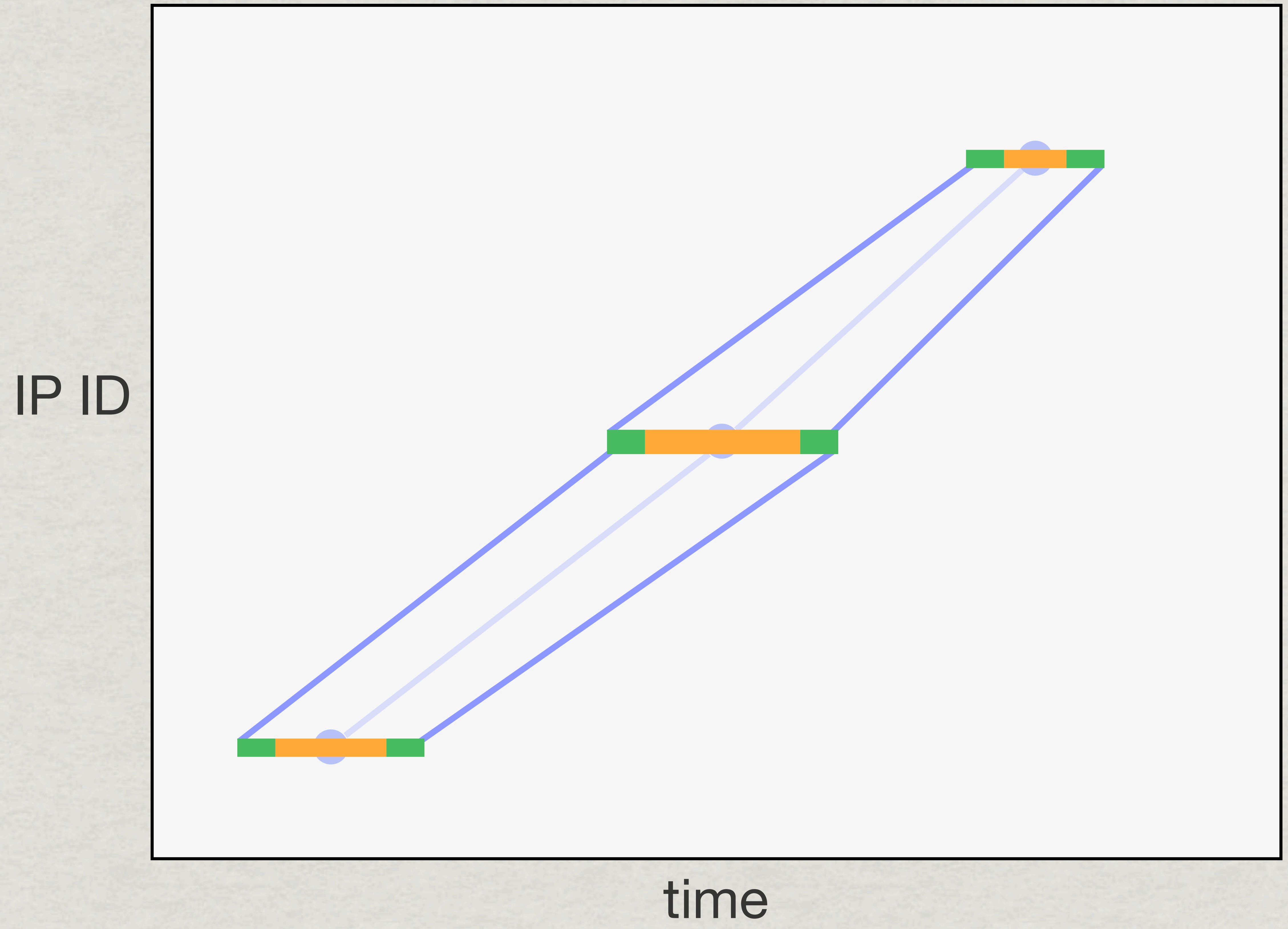
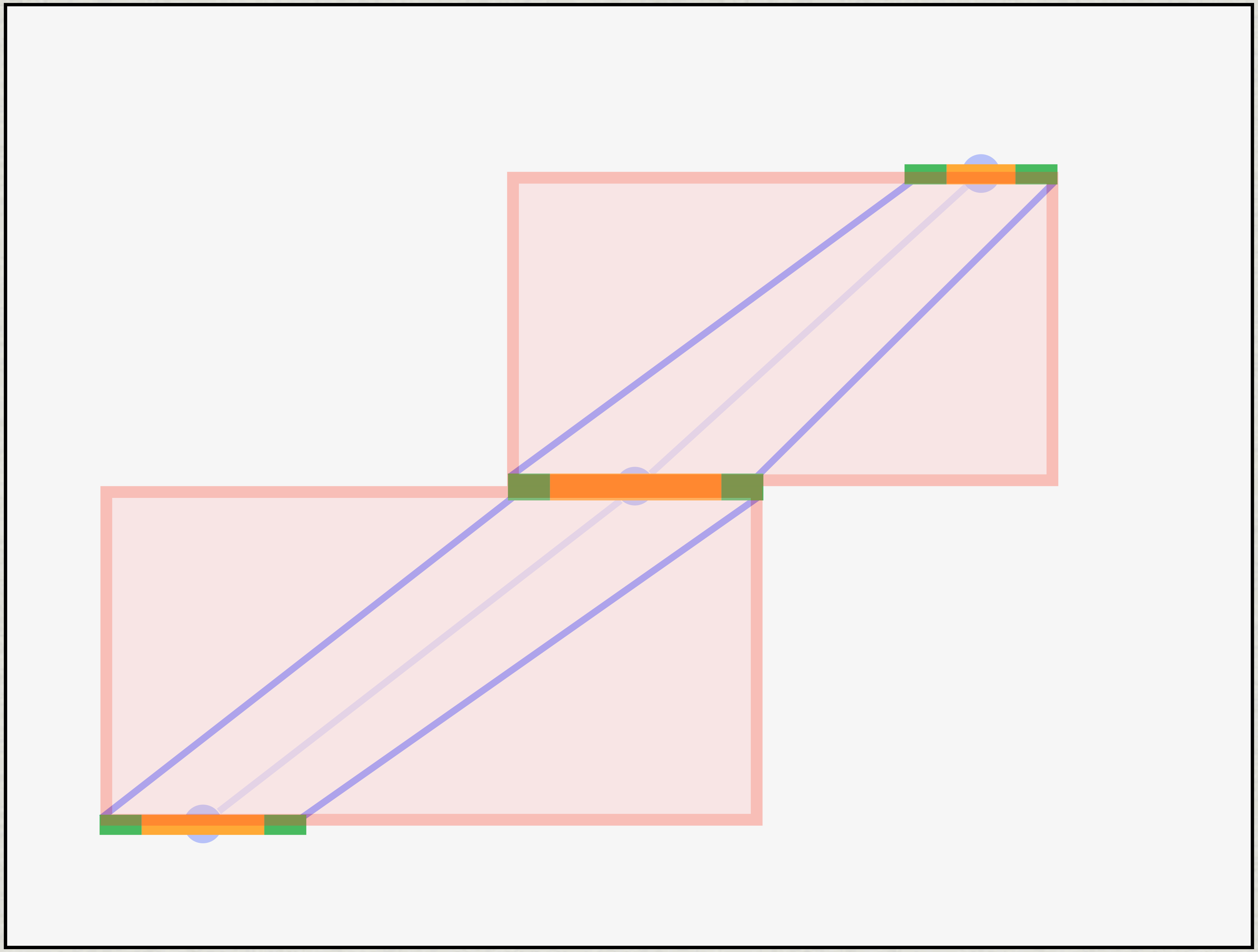


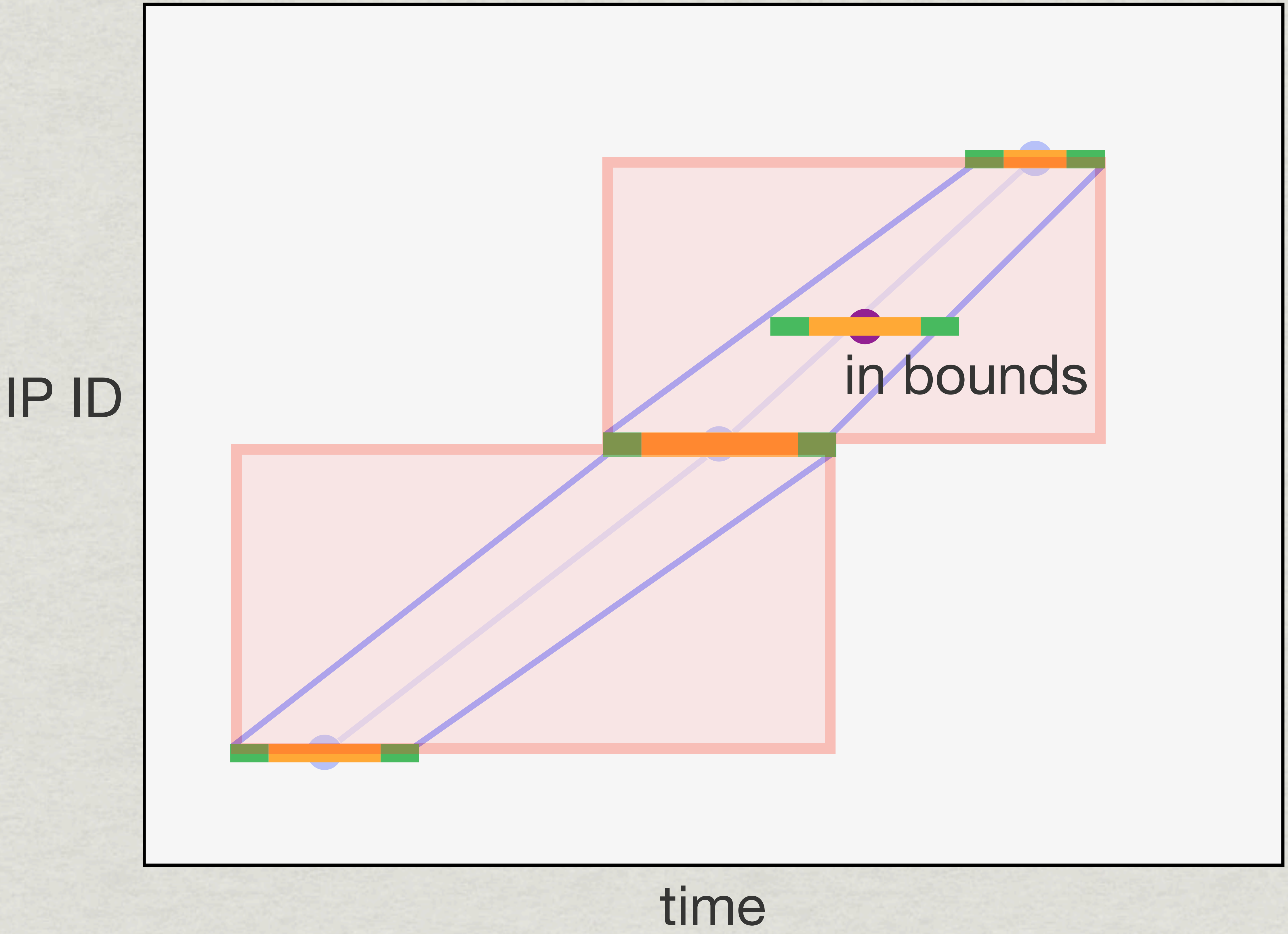
Monotonic Bounds Test

IP ID



time

Monotonic Bounds Test



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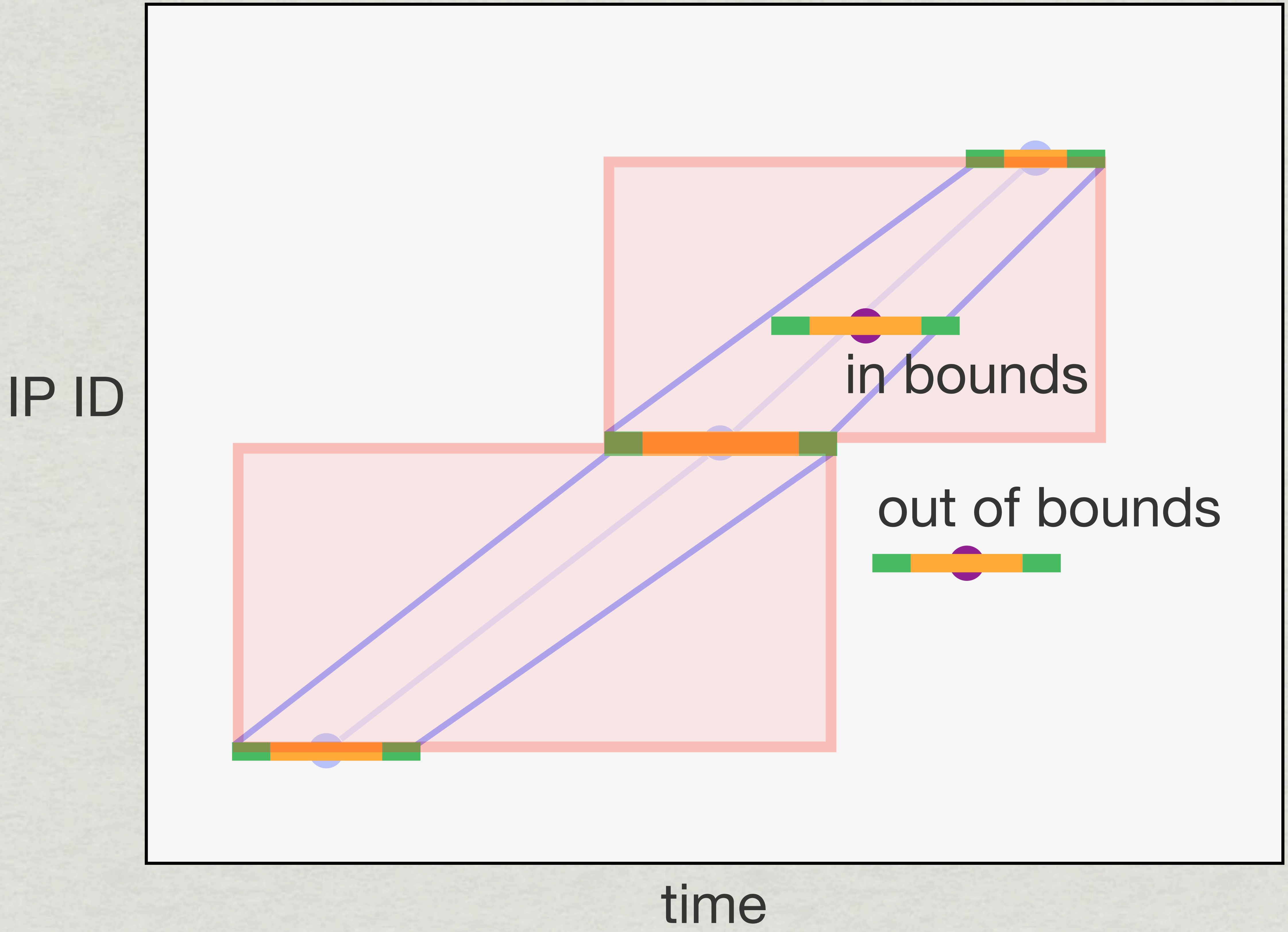

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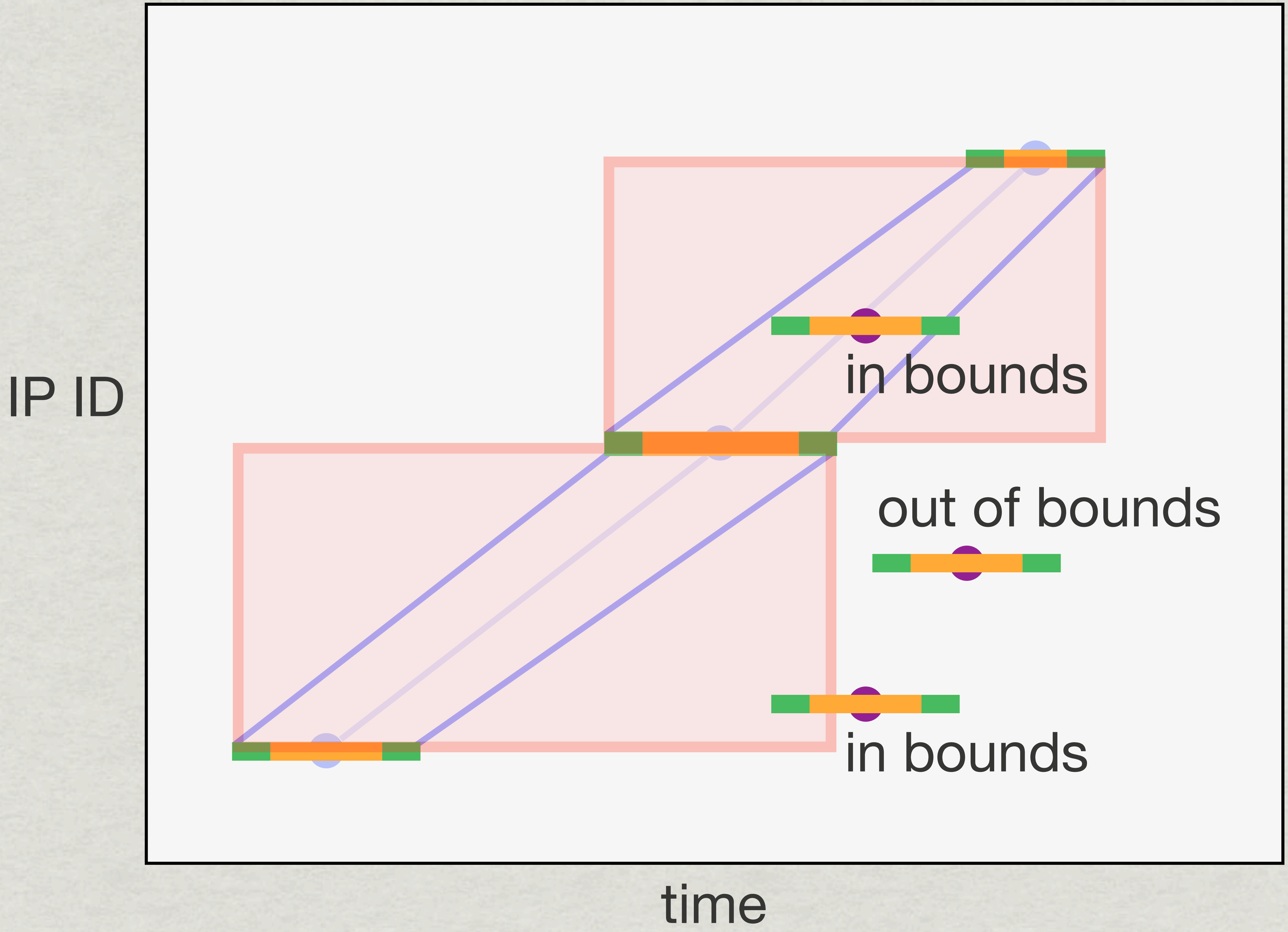

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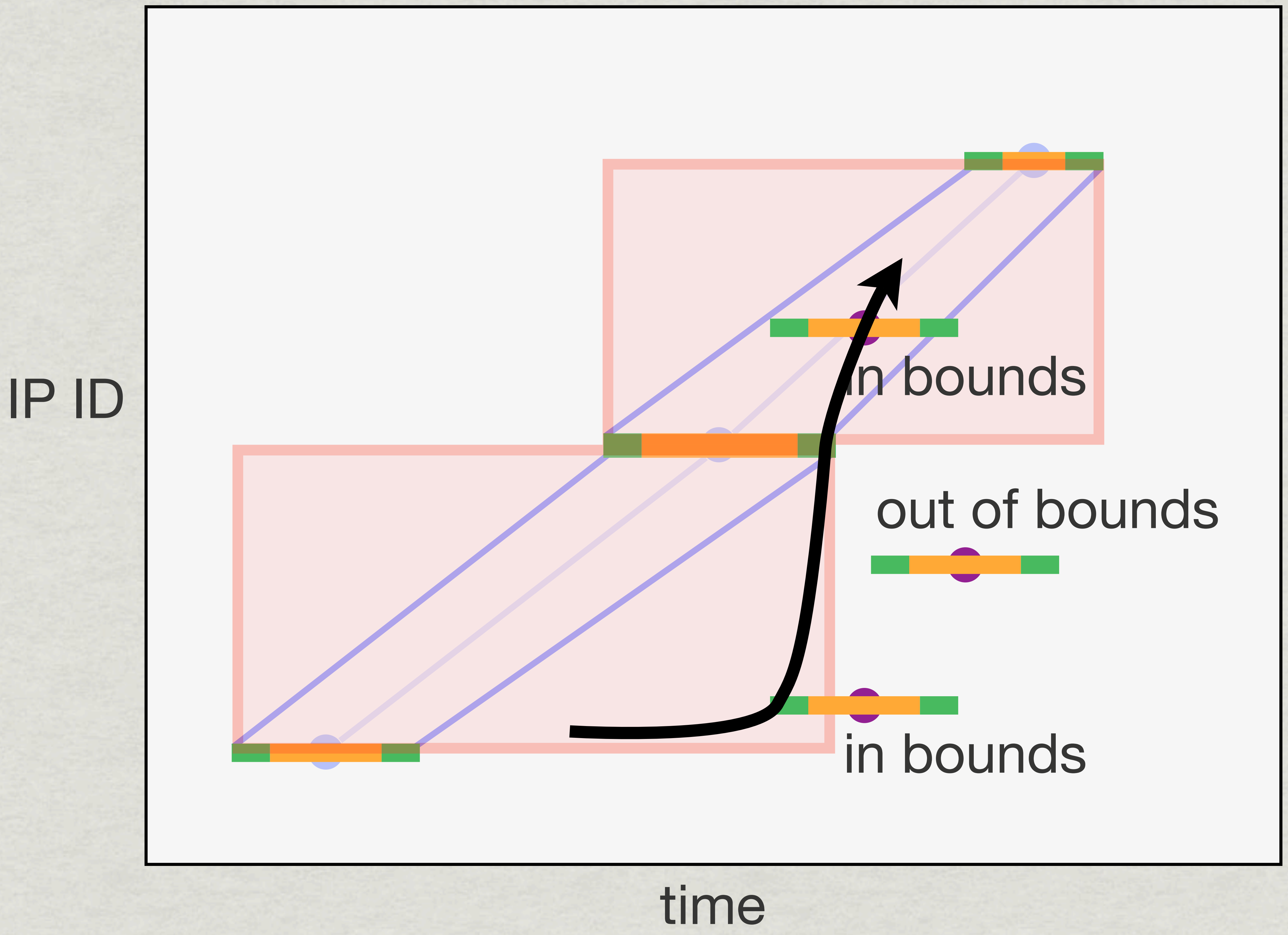


Monotonic Bounds Test

- summary: the monotonic bounds test provides a high-confidence test of a shared counter, and ultimately of aliases
  - based on a necessary condition that ensures convergence to the true positives
    - difference of kind, not just of degree, with RadarGun’s distance test
  - very low false positive rate minimizes further errors caused by taking the transitive closure of alias pairs

MIDAR

- MIDAR probes with a *sliding window* for scalability
  - scales up gracefully
    - can accommodate varying numbers of monitors
    - use “what you have”, not “what you **must** have”
  - reduces chances of rate limiting
- we ran MIDAR on 1 million interfaces with just 27 monitors at 100pps/monitor

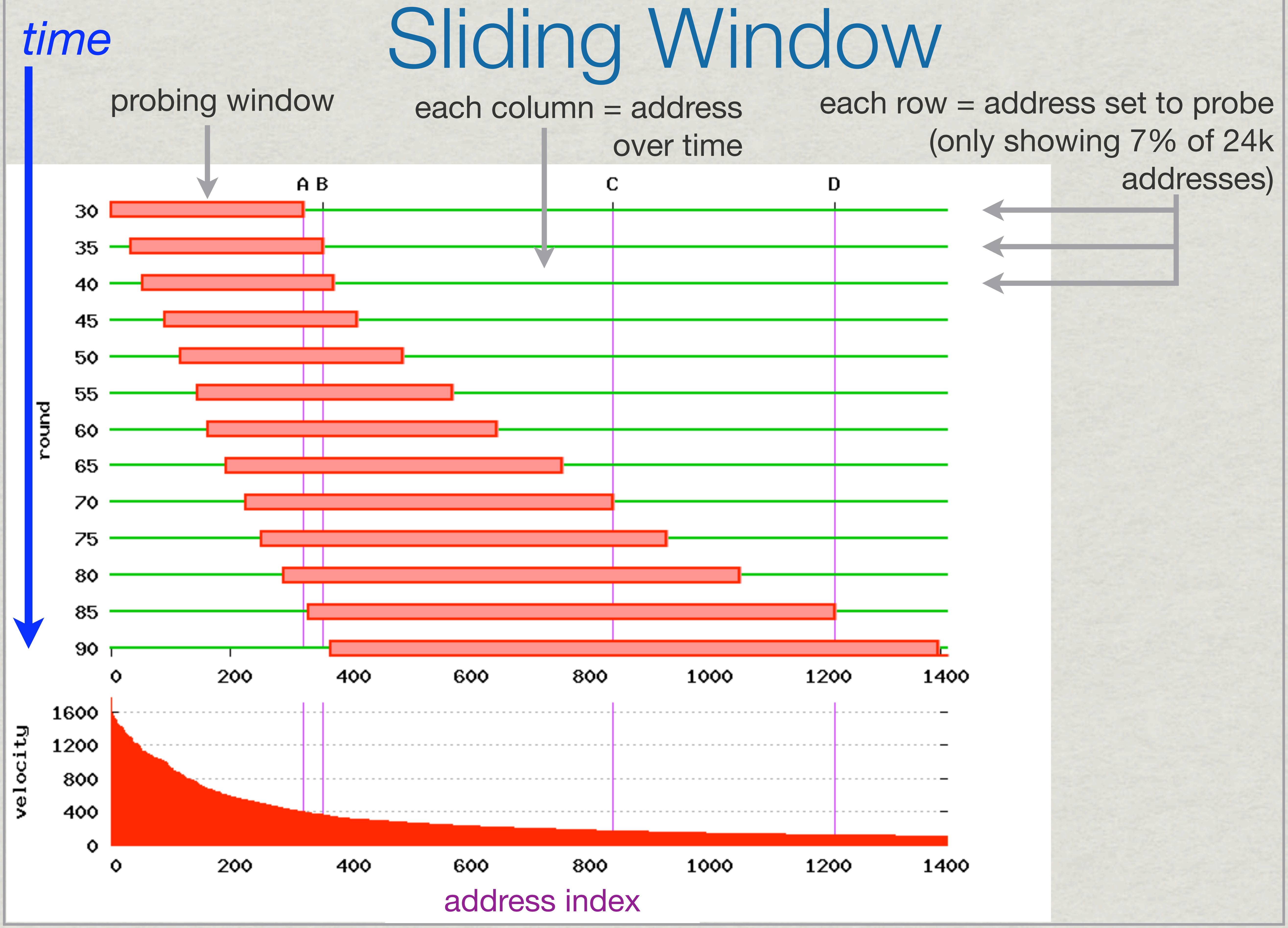
Sliding Window

- the *sliding window* rationale:
  - two interfaces that share a counter will have similar time series and thus similar velocities
    - that is, interfaces with very different velocities cannot be shared, and so we do not need to probe such interfaces closely in time
  - high velocity targets should be probed with tighter probe spacing than low velocity targets
    - need to reduce the bounds in the monotonic bounds test
    - need to be able to detect random IP ID’s
  - low velocity targets can be probed with wide probe spacing because their IP-ID counter changes slowly

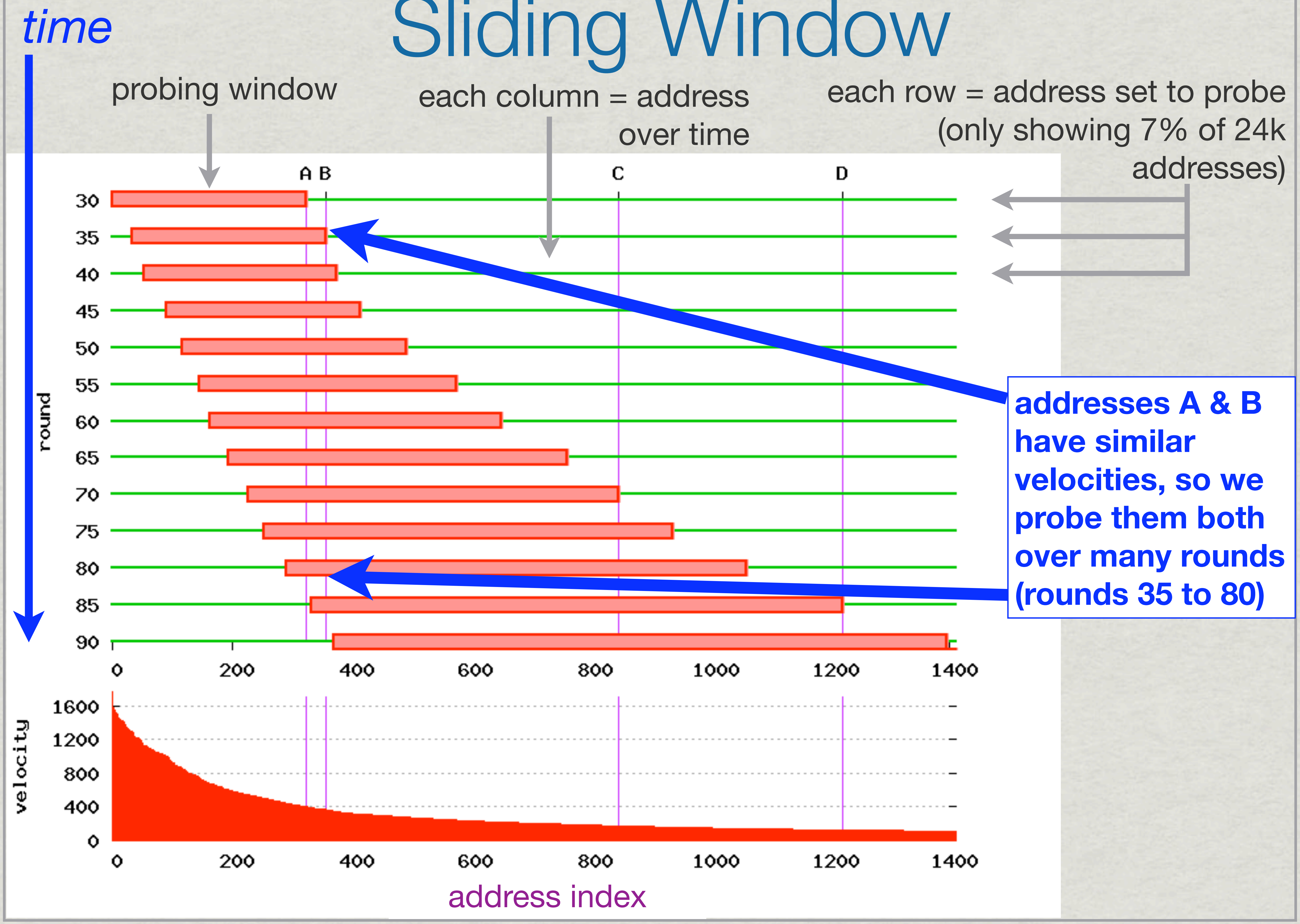
Sliding Window

- implementation:
  - sort targets by descending velocity
  - set up a *window* over an initial segment of the target list
  - loop:
    - probe each address in the window
    - slide window forward (to lower velocity targets) by a small fraction of its size, and increase window size by a small fraction

Sliding Window



Sliding Window



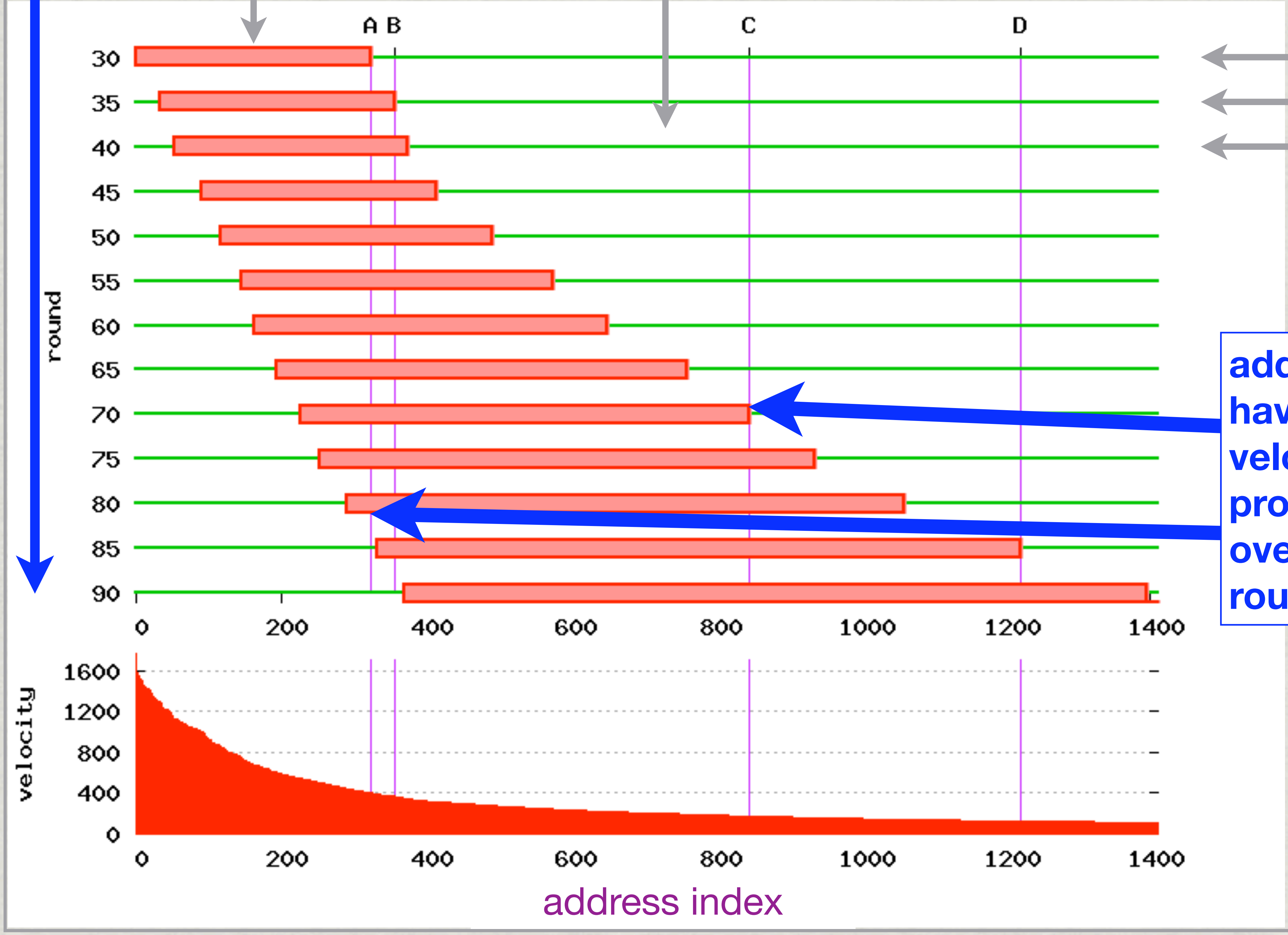
Sliding Window

time

probing window

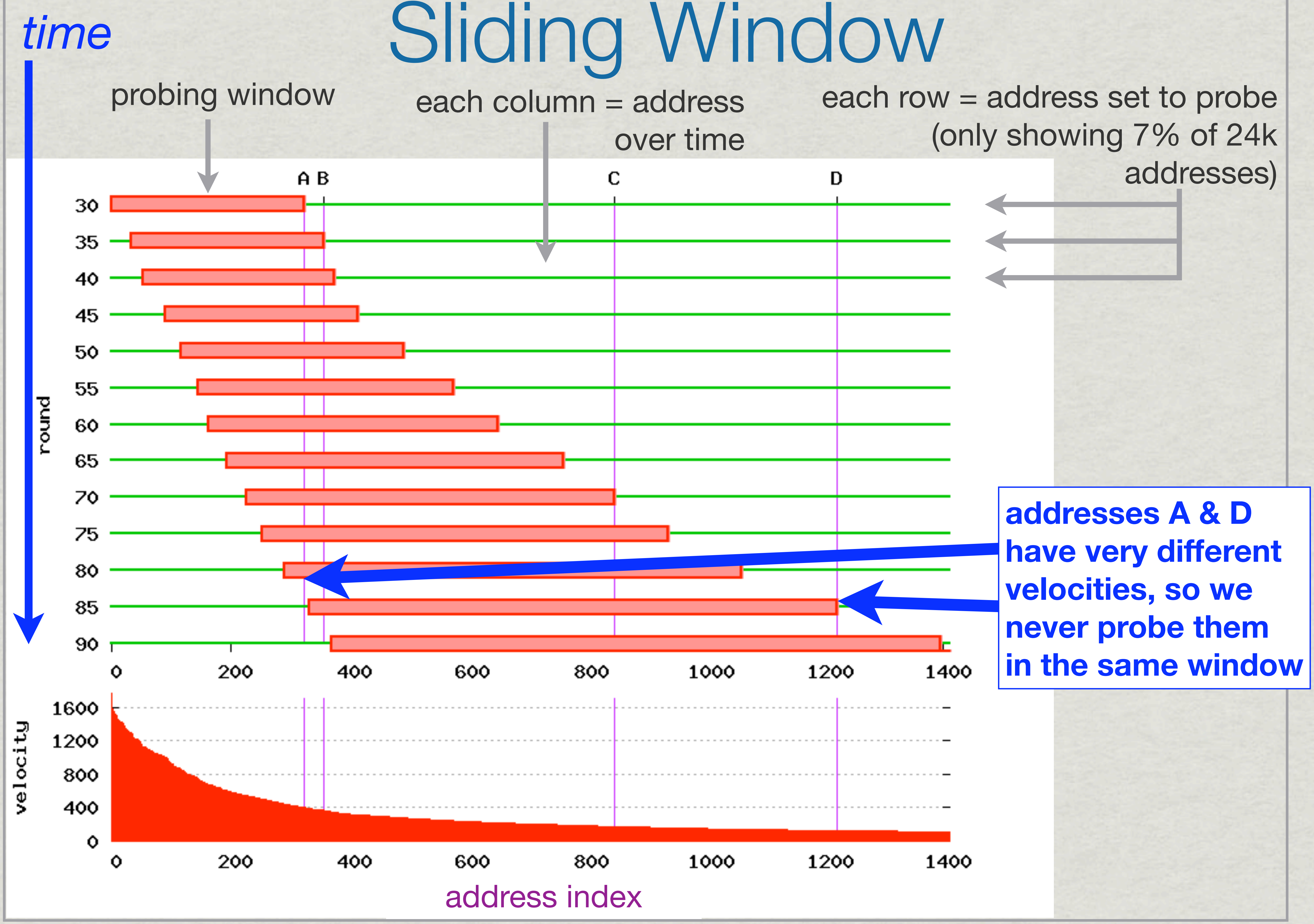
each column = address over time

each row = address set to probe (only showing 7% of 24k addresses)



addresses A & C have different velocities, so we probe them both over only a few rounds (70 to 80)

Sliding Window



addresses A & D have very different velocities, so we never probe them in the same window

More Probe Methods

- MIDAR uses 4 probing methods:
  - TCP ACK (same as RadarGun), UDP, ICMP, and *indir*
    - *indir* reproduces the conditions of the original traceroute used to obtain an interface address
- using additional methods improves response rate

methods				responsive		monotonic	
tcp				747,408	66.57%	481,999	42.93%
	udp			664,742	59.21%	645,103	57.46%
		icmp		953,562	84.94%	390,827	34.81%
			indir	973,199	86.69%	838,826	74.72%
tcp	**udp**	**icmp**	**indir**	1,088,572	96.96%	1,014,999	90.41%

responsive = target responded to at least 75% of probes
monotonic = target's IP-ID time series is monotonic

Counter Sharing

- addresses that respond to multiple methods frequently share counters across methods:

	udp	icmp	indir
tcp	94.97%	87.05%	90.57%
udp		96.15%	95.91%
icmp			95.84%

- cross-method comparison of different addresses may be useful
    - but negative results should not be treated as conclusive
        - caused by per-method or per-interface counter

MIDAR Execution

- **discovery stage**: find candidate alias pairs
- **corroboration stage**: confirm candidates

Discovery Stage

- estimation run
  - find velocities needed for sliding window
  - identify each target's best probe method
    - prefer in descending order TCP, UDP, ICMP, indir
  - can probe each target independently of others
- sliding window run
  - discover candidate alias pairs, including many false positives

Corroboration Stage

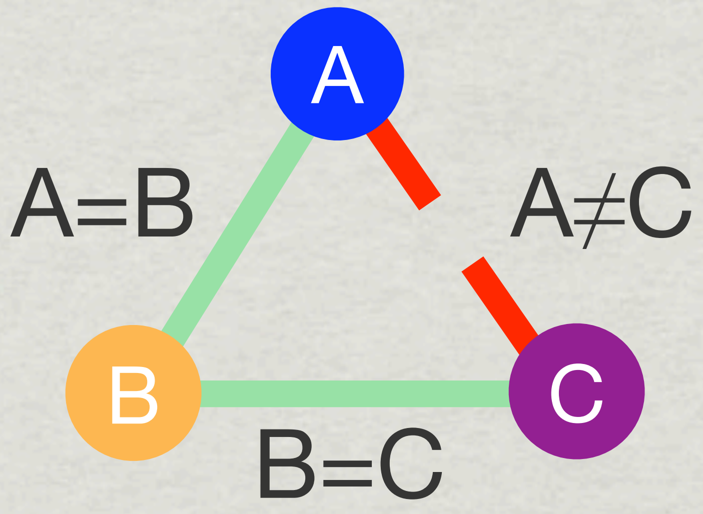
- goal: eliminate all false positives
- probing several hours after discovery stage gives non-shared counters time to diverge
- naive implementation: repeat sliding window run
  - unnecessarily tests pairs that we have already rejected
- optimized implementation:
  - only compare pairs in the transitive closure of the potential alias pairs found in the discovery stage
  - probe alias set members one at a time, with smallest possible spacing that doesn't trigger rate limiting (>500ms)
    - tight spacing reduces false positives

MIDAR Results

- discovery stage (sliding window):
  - probed 1.0 million addresses
  - 486 **billion** pairs compared
  - shared pairs found: 1.6 million (0.00093%)
  - 55k alias sets containing 497k addrs
- corroboration stage:
  - shared pairs found: 428k (26% of discovery stage)
    - not actually 1.2 million false positives; inflated by human error
  - 69k alias sets containing 186k addrs
    - stable across multiple corroboration runs

MIDAR Results

- consistency check: out of 69k sets,187k addrs, 428k pairs after corroboration ...
  - every pair inferred by transitive closure was tested with the monotonic bounds test at least once and passed every time
  - all but 80 pairs were tested at least twice and passed every time
  - only 12 sets (49 addrs) contained transitive *closure conflicts:*



We suspect real network change caused these conflicts and not false positives.

MIDAR Validation

- we compared MIDAR results to ground truth for a tier 1 ISP
  - for comparison, we only consider routers that appear with multiple interfaces in Ark traces
    - observed multi-interface routers (OMIRs)
- **0 false positives**

	full ISP topology	**OMIRs**	**MIDAR**
routers	1,986	983	434
addresses	24,429	4,008	1,284
pairs	611,407	16,900	2,133

Future Work

- MIDAR improvements
  - adapt corroboration spacing to responsiveness
- MAARS: Multi-Approach Alias Resolution System
  - combine MIDAR, kapar, iffinder (and others?)
  - How to use MIDAR negatives to reduce false positives in kapar?