

Comparing sequential scanpaths

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Example

- How similar (or different) are two viewing patterns?

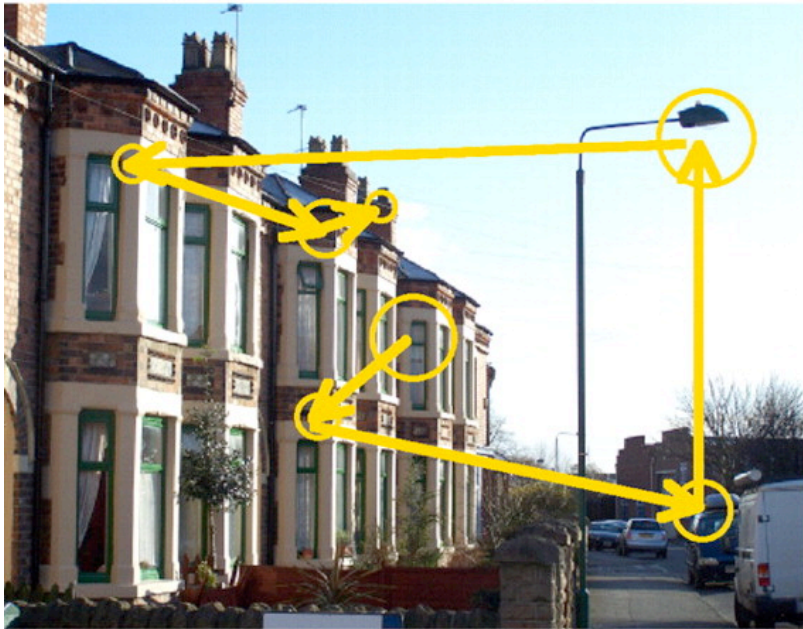


Noton & Stark (1971)

Example

- How similar (or different) are two viewing patterns?

a) Picture at encoding



d) Saliency model scanpath

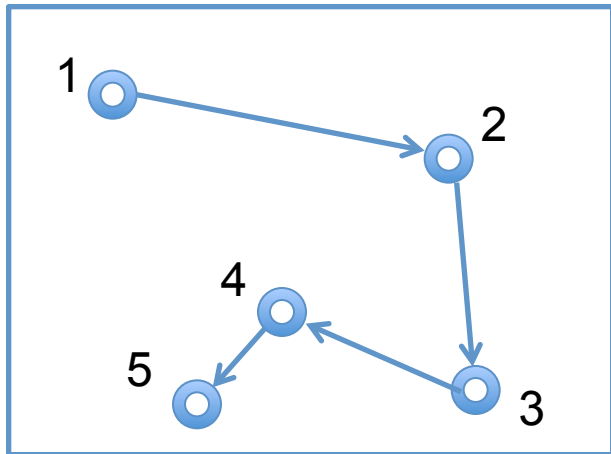


Foulsham & Underwood (2008)

Problem

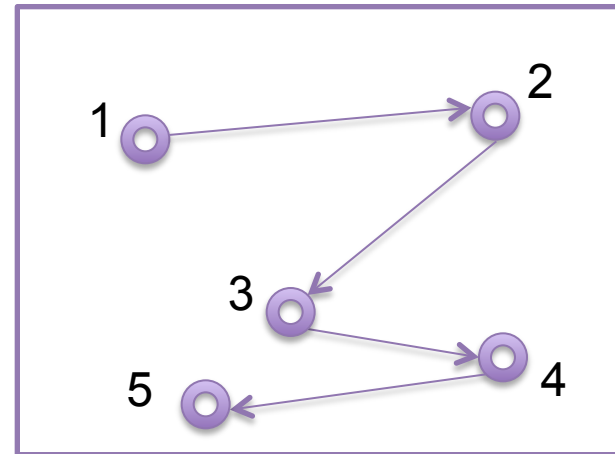
- Can we derive a quantitative measure of scanpath similarity?
- Can we demonstrate similarity is greater than chance?

Linear distance

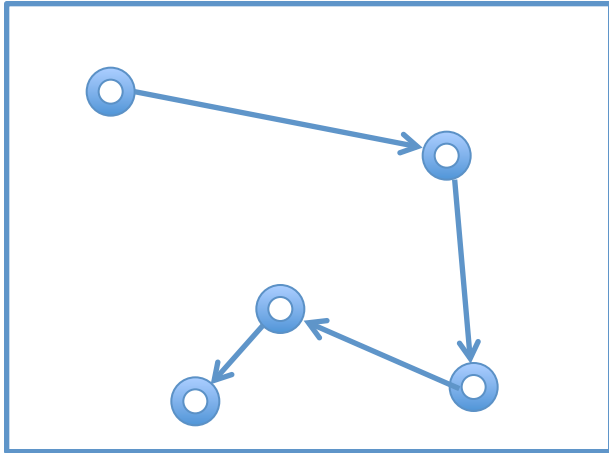


?

≈

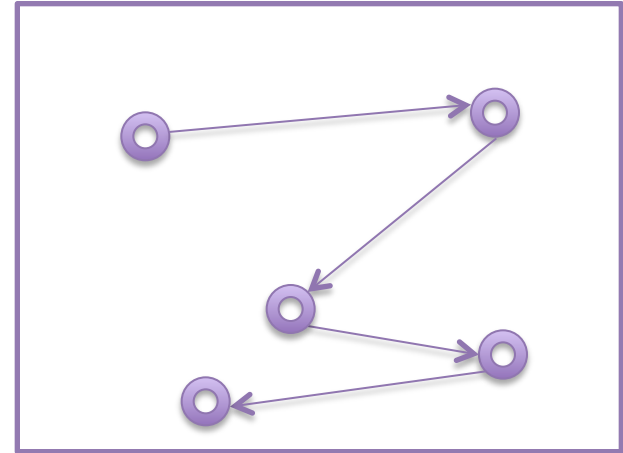


Linear distance



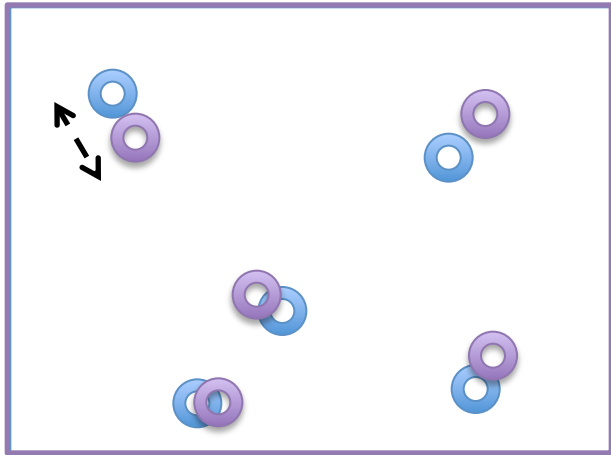
?

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- *Spatial* similarity: the same locations/objects are looked at

Linear distance



?

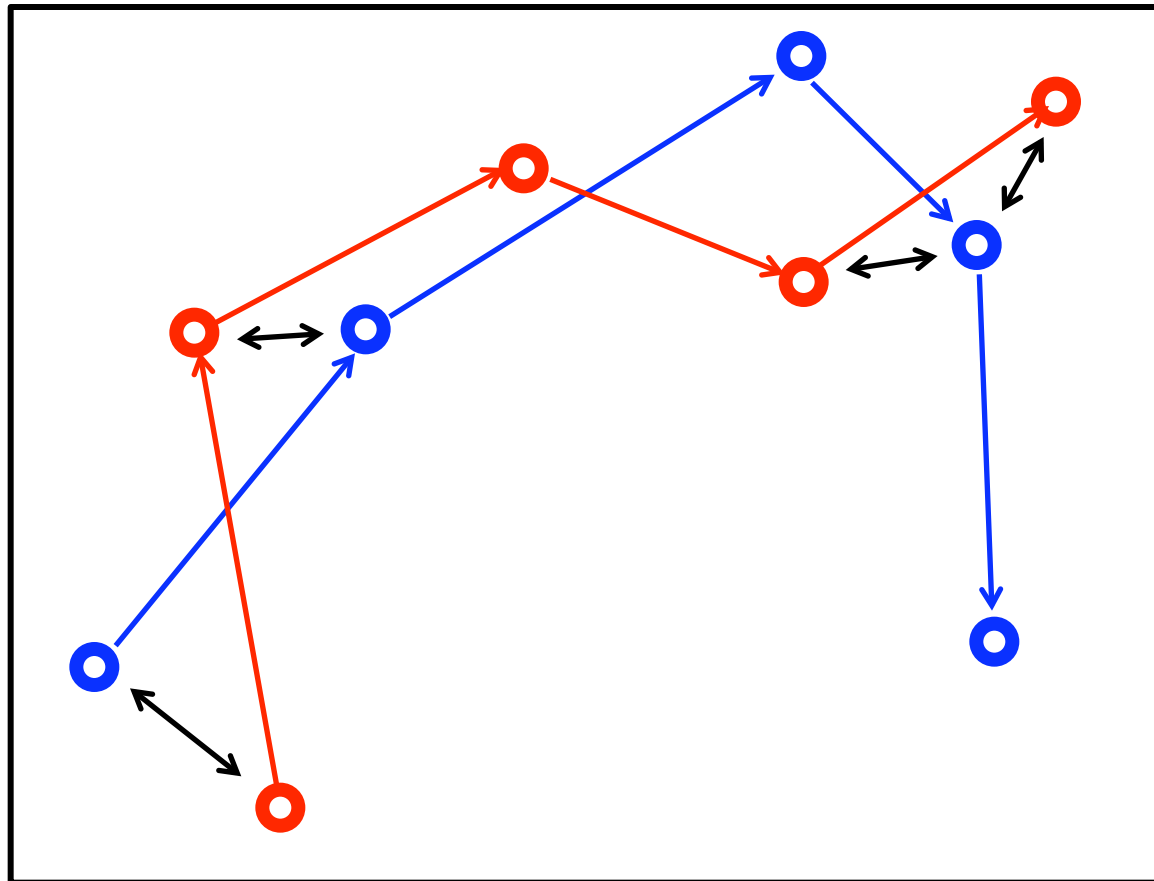
≈

- *Spatial* similarity: the same locations/objects are looked at

Linear distance

- Calculate the Euclidian distance between pairs of fixations
- Mannan et al (1995)
 - calculate linear distance between each fixation and the nearest fixation in the other scanpath
 - average across all fixations
 - standardize across the display size and the distance expected from randomly generated scanpaths, to give a “similarity index” 0-100.

Linear distance example

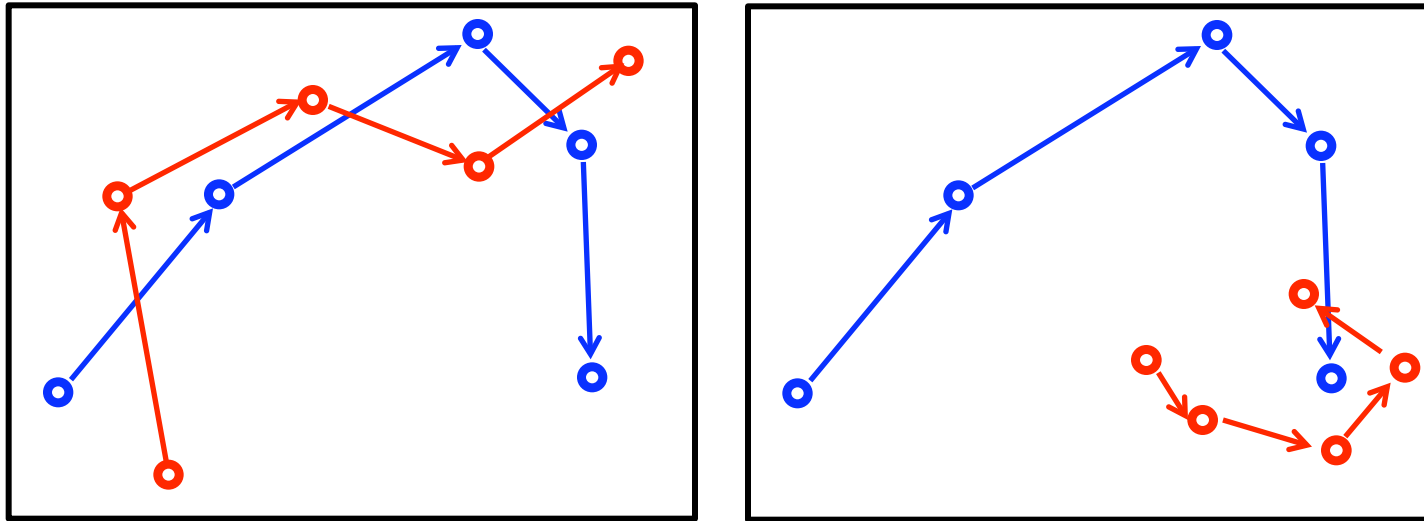


A1 vs B1 = 200 px

A2 vs B2 = 150 px

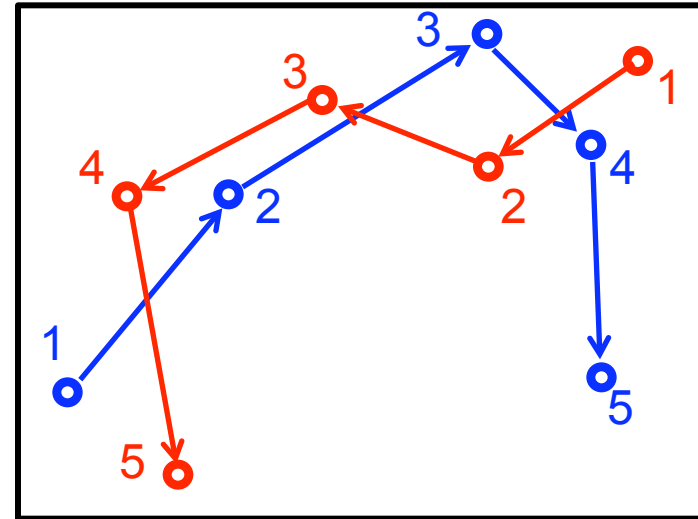
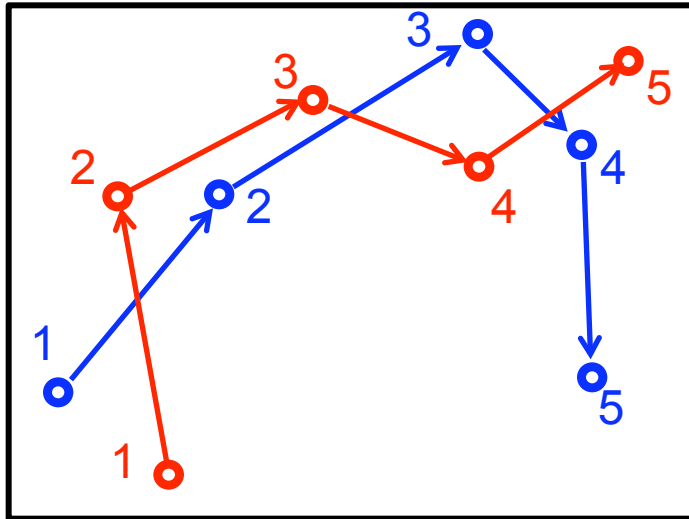
...

Problems with linear distance methods



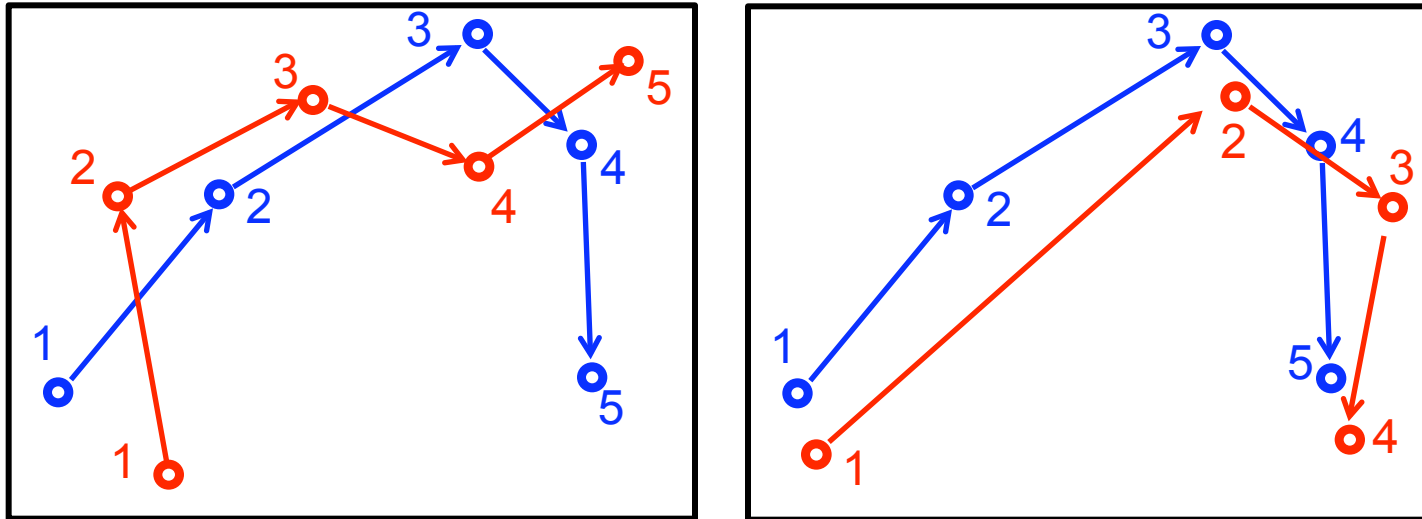
Similarity is skewed by large differences in the distributions of the scanpaths

Problems with linear distance methods



Similarity does not take into account sequential order.

Problems with linear distance methods

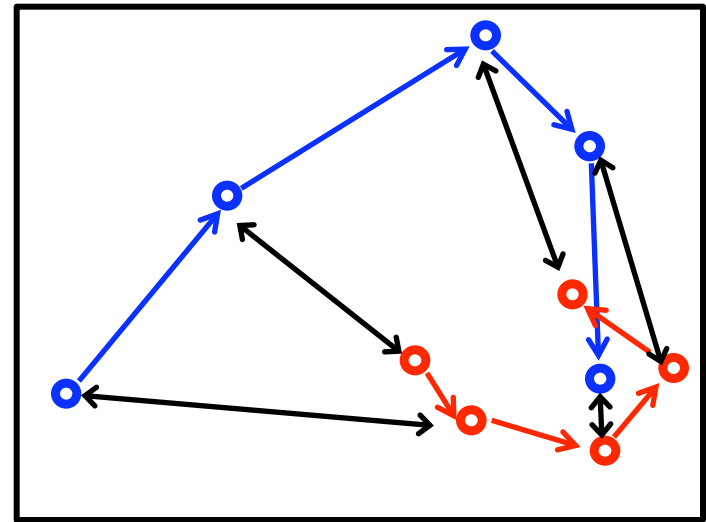
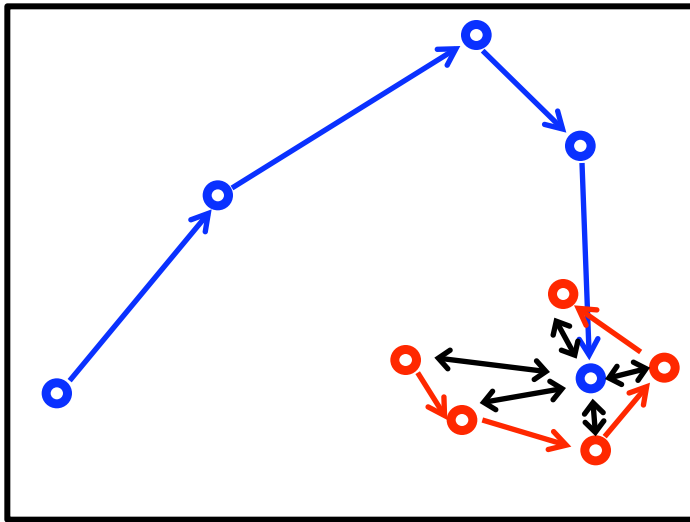


Similarity does not take into account sequential order.

“Unique assignment” correction

- Henderson et al., (2007) corrected for some of these issues by pairing fixations so that each is compared to only one in the other set
- All distances are computed, and the pairing chosen which minimizes the observed distance

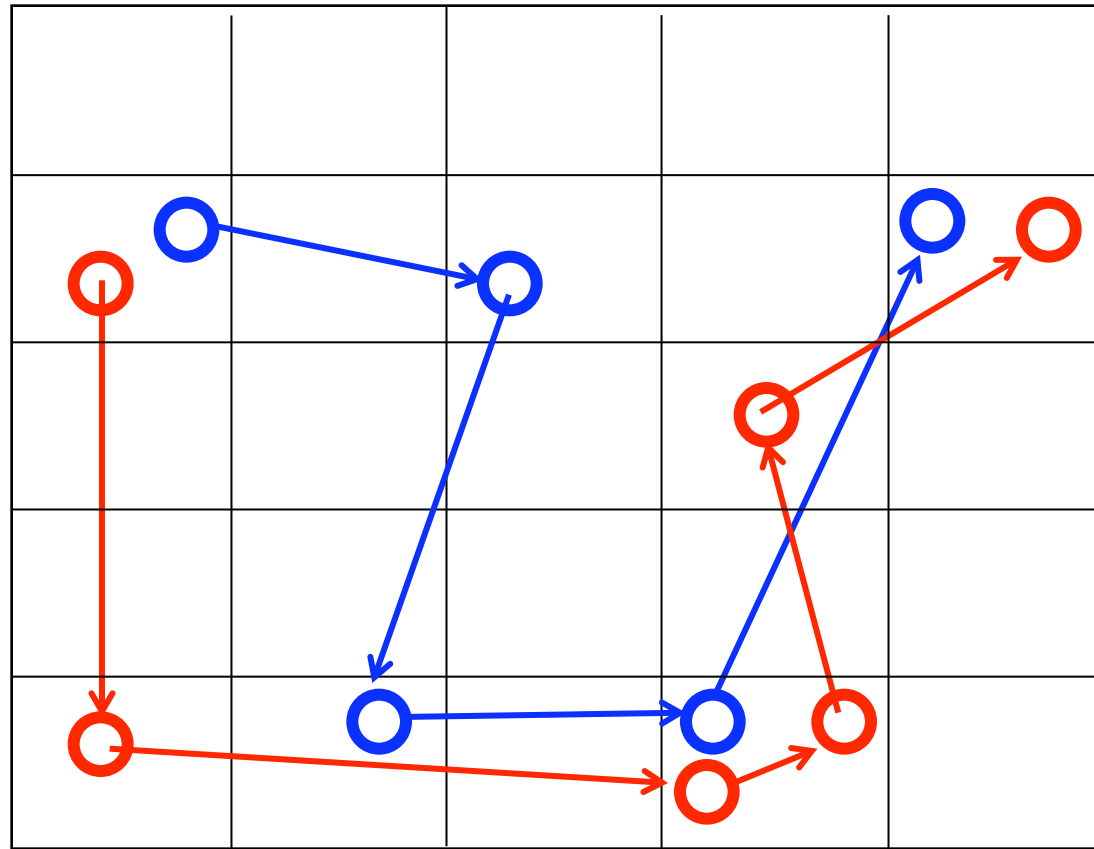
Unique assignment example



String edit distance

- Used by Brandt & Stark (1997) etc
- Sequences are converted to character strings and then aligned using the Levenshtein distance
- This quantifies *sequential* similarity by calculating the number of edits required to transform one string into the other

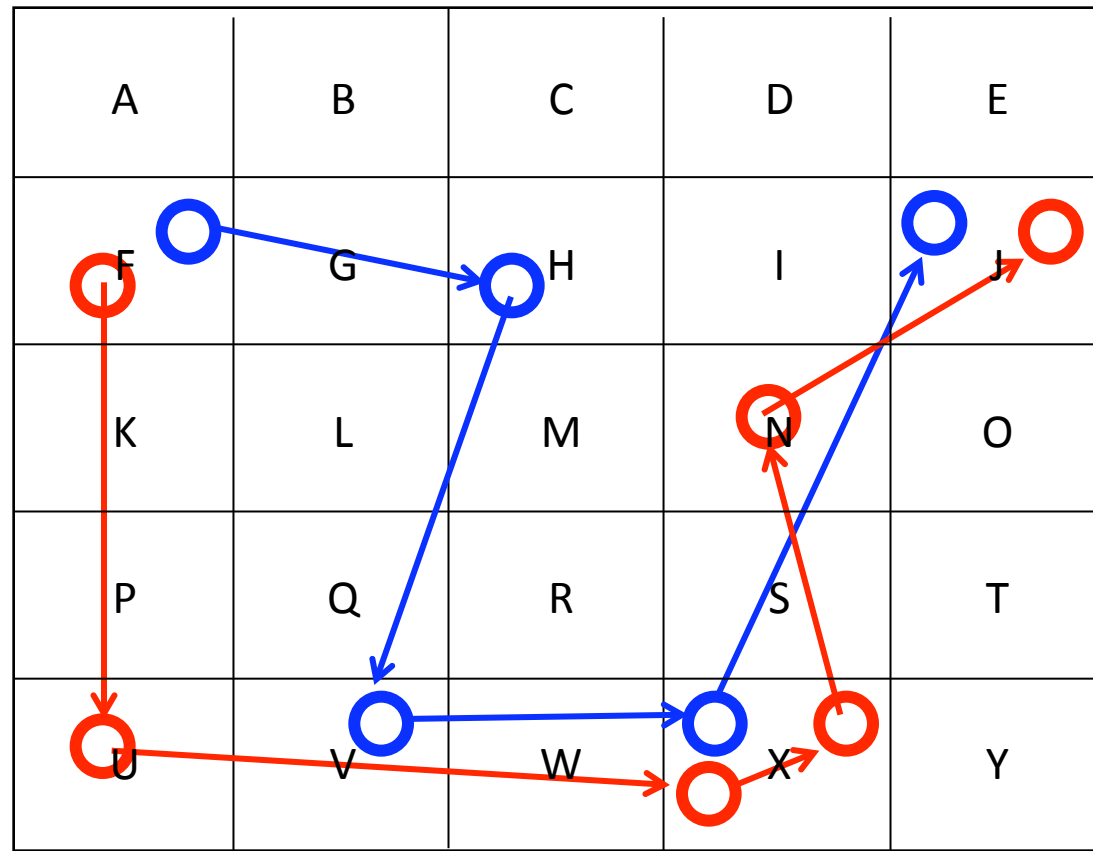
String edit distance example



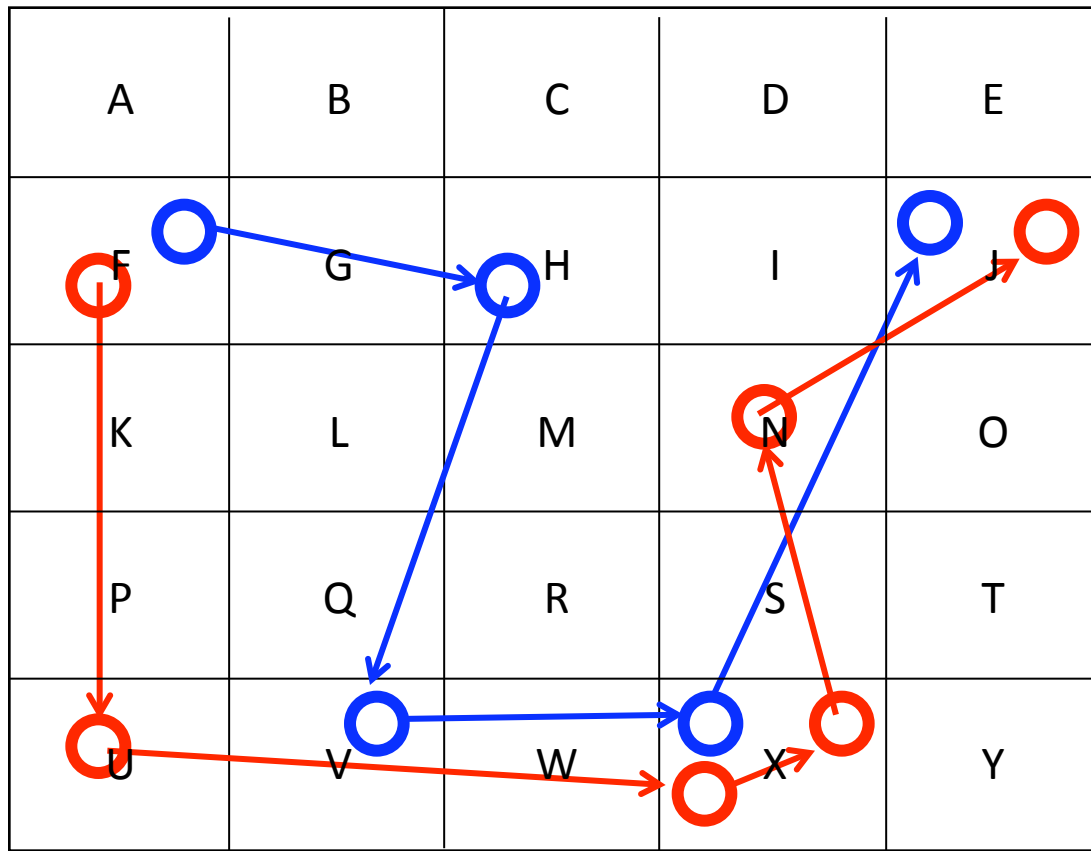
String edit distance example

A	B	C	D	E
F	G	H	I	J
K	L	M	N	O
P	Q	R	S	T
U	V	W	X	Y

String edit distance example



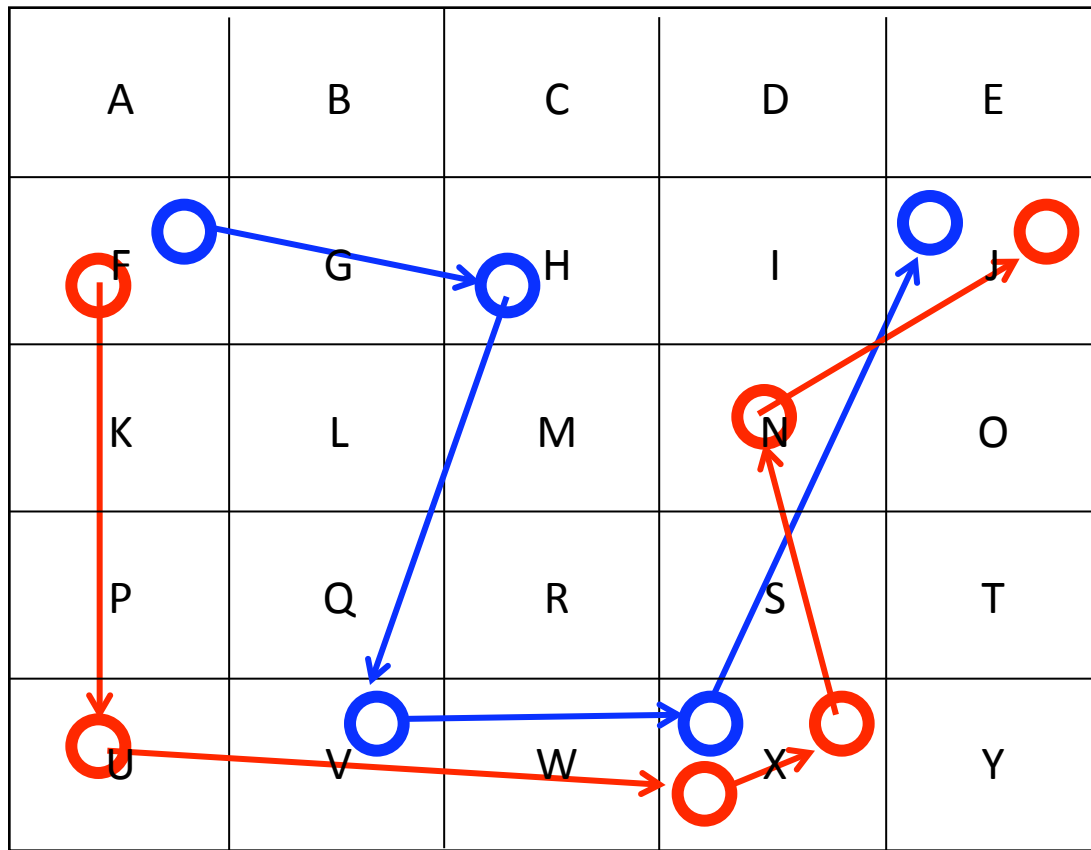
String edit distance example



F U X X N J

F H V X J

String edit distance example



~~F U X N J~~
 ↑ ↑
 H V

1. Replace U with H
2. Insert V
3. Delete J

F H V X J

= 3 edits

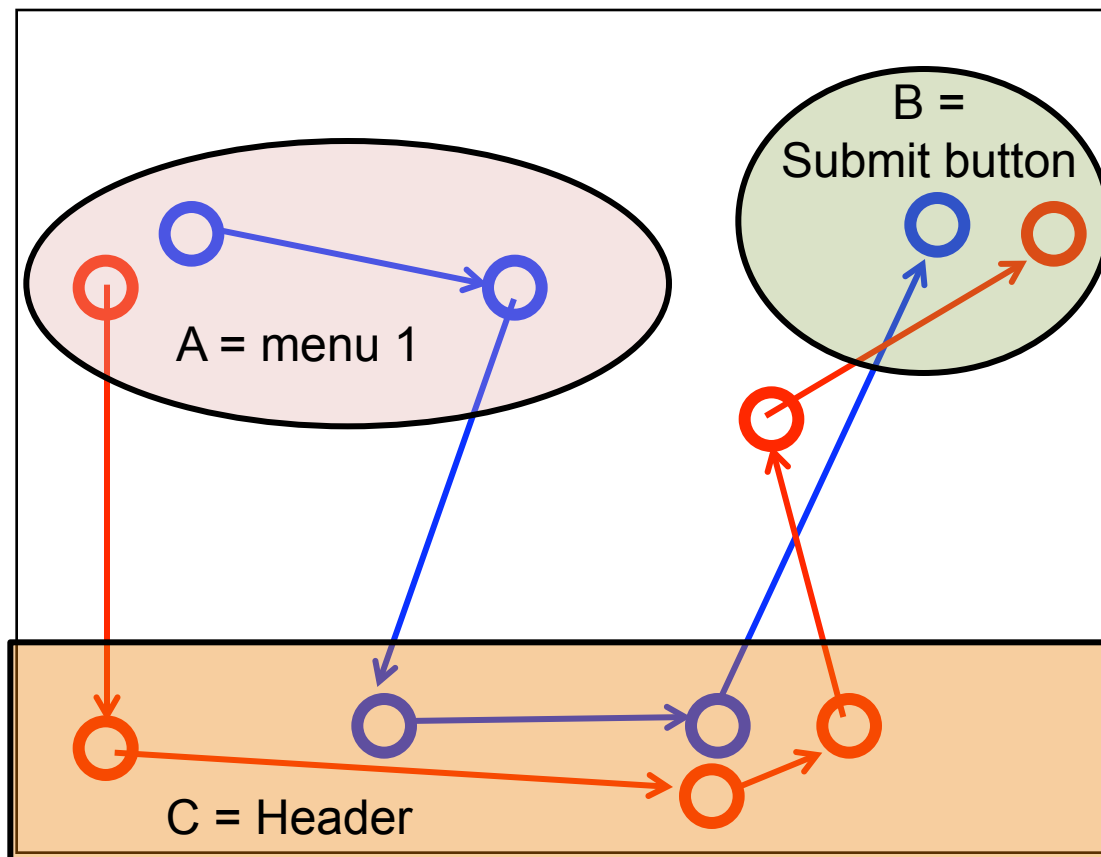
= $3 / 5 = 0.6$

Similarity = $1 - 0.6 = 0.4$

Problems with string edit distance

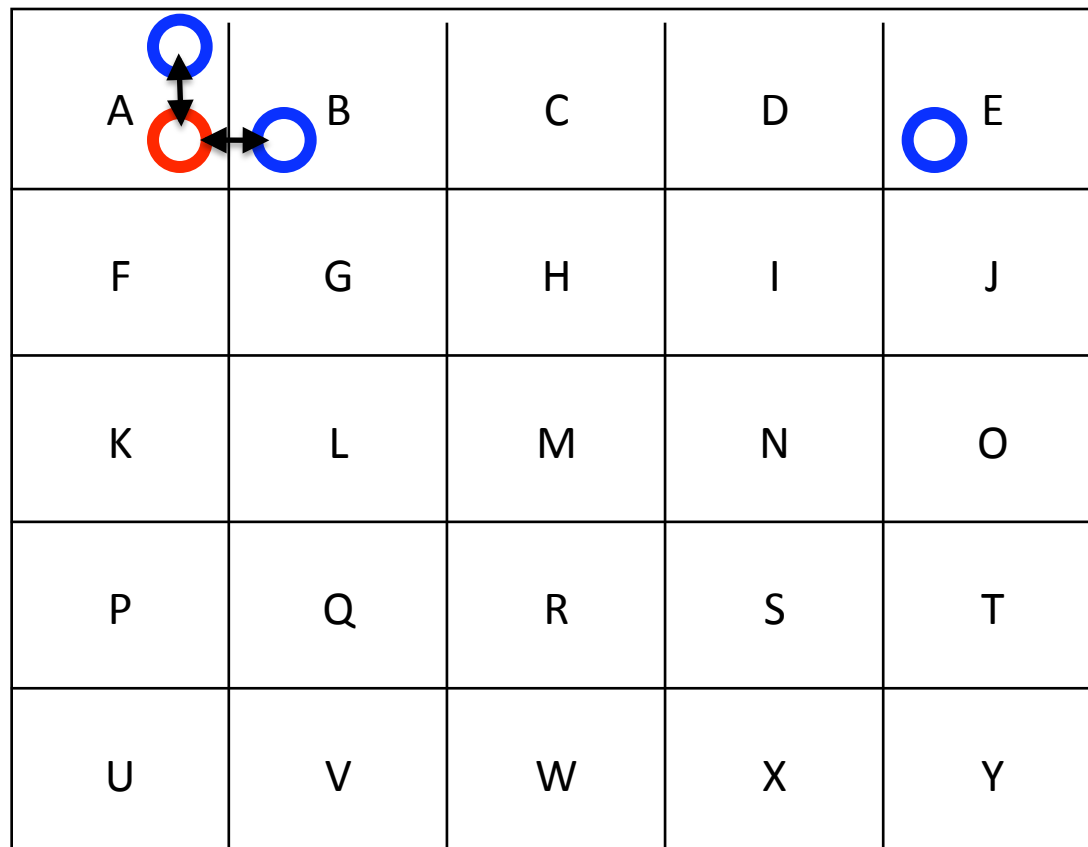
1. How to choose AOIs?

- Grid? Objects of interest?



Problems with string edit distance

2. All differences are scored equally
 - Loss of precision



Summary:

some scanpath comparison methods

Linear distance

- Simple and intuitive, preserves precision

- Skewed by outliers, differences in distributions (fixed by the unique assignment adjustment)

- Ignores sequential order

String edit distance

- Preserves sequential order

- Compensates for small changes in the overall shape

- Loses spatial precision

- Arbitrary AOIs

Demo

- Use demo.m to compare scanpaths of 5 fixations
 - Where do the methods do well/badly? Where do they produce counterintuitive results?
- Try loading scanpaths from TestScanpaths.mat or FoulshamUnderwood.mat, or try on your own data.

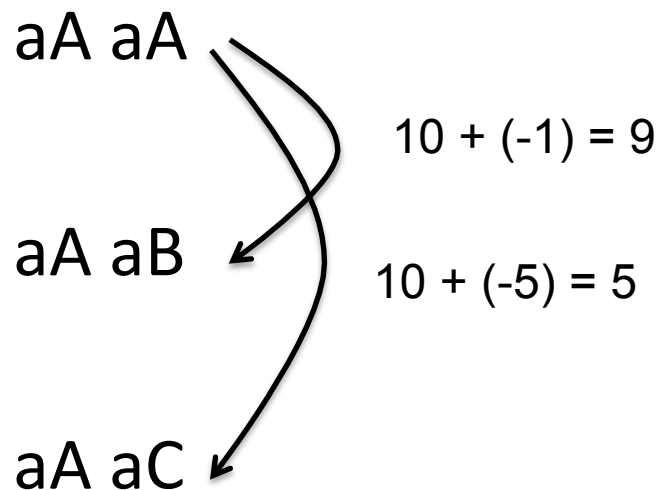
Recent advances in scanpath comparison

ScanMatch

- Cristino et al., (2011)
- As with the string edit distance, scanpaths are transformed to characters via AOIs
- Duration can be represented through temporal binning
- Users can specify relationships between AOIs using a “substitution matrix”
- Strings are aligned using Needleman-Wunsch algorithm

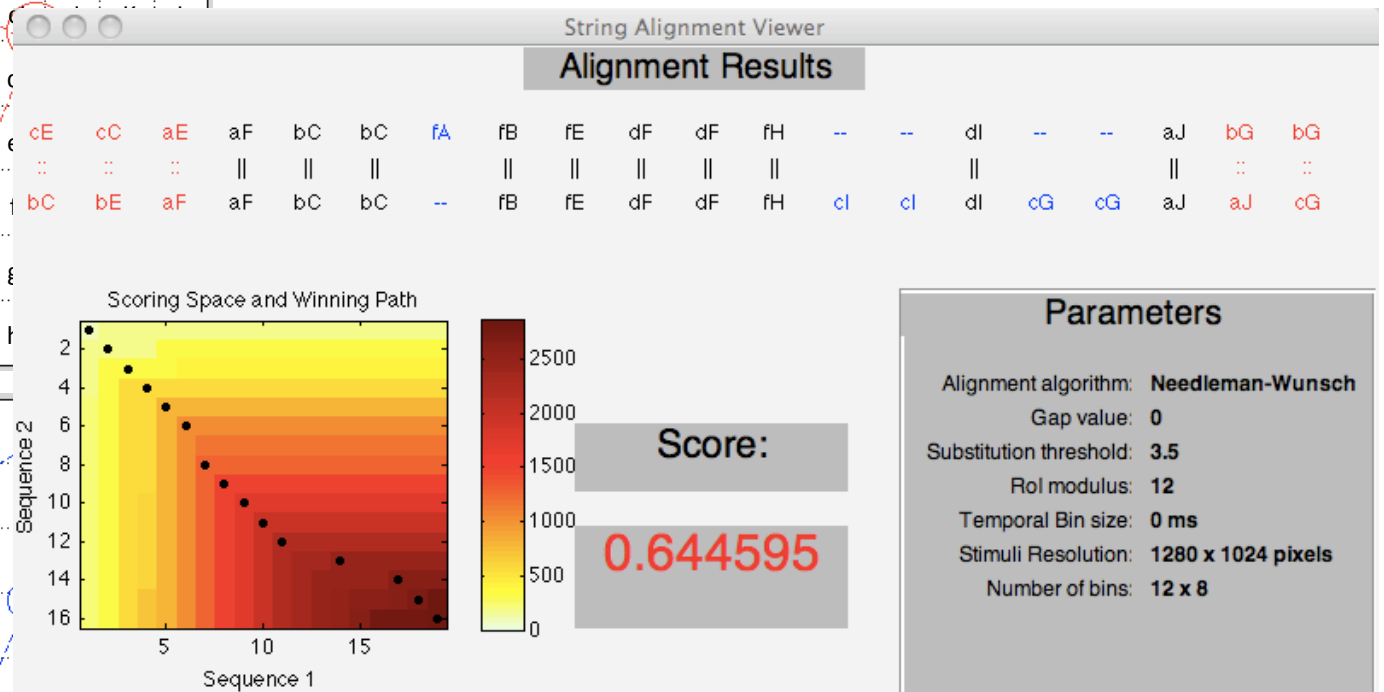
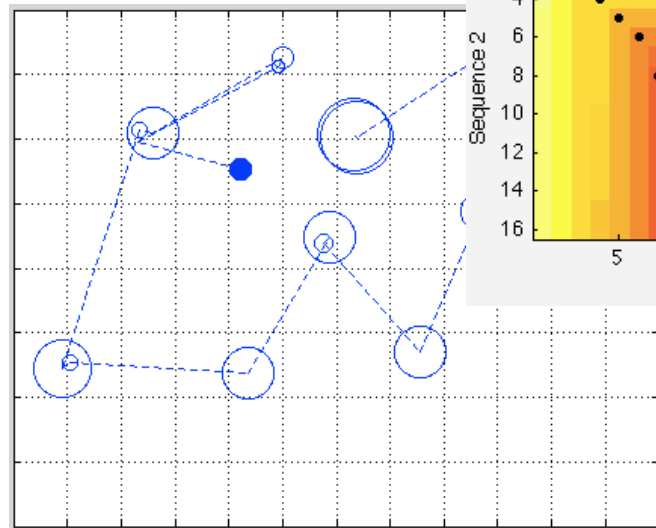
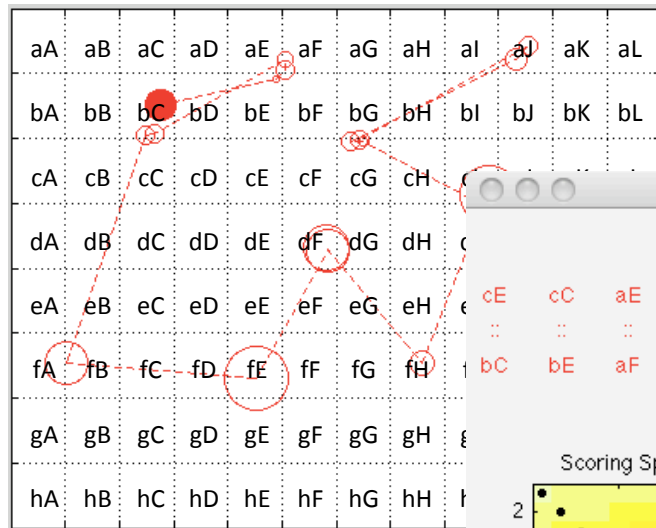
ScanMatch: defining ROI relationships

- Algorithm aligns character strings according to a score



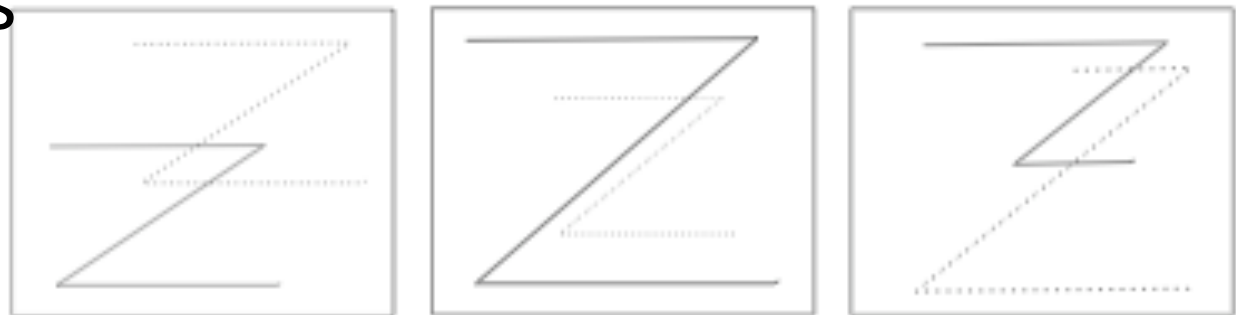
	aA	aB	aC
aA	10	-1	-5
aB	-1	10	-1
aC	-5	-1	10

ScanMatch examples

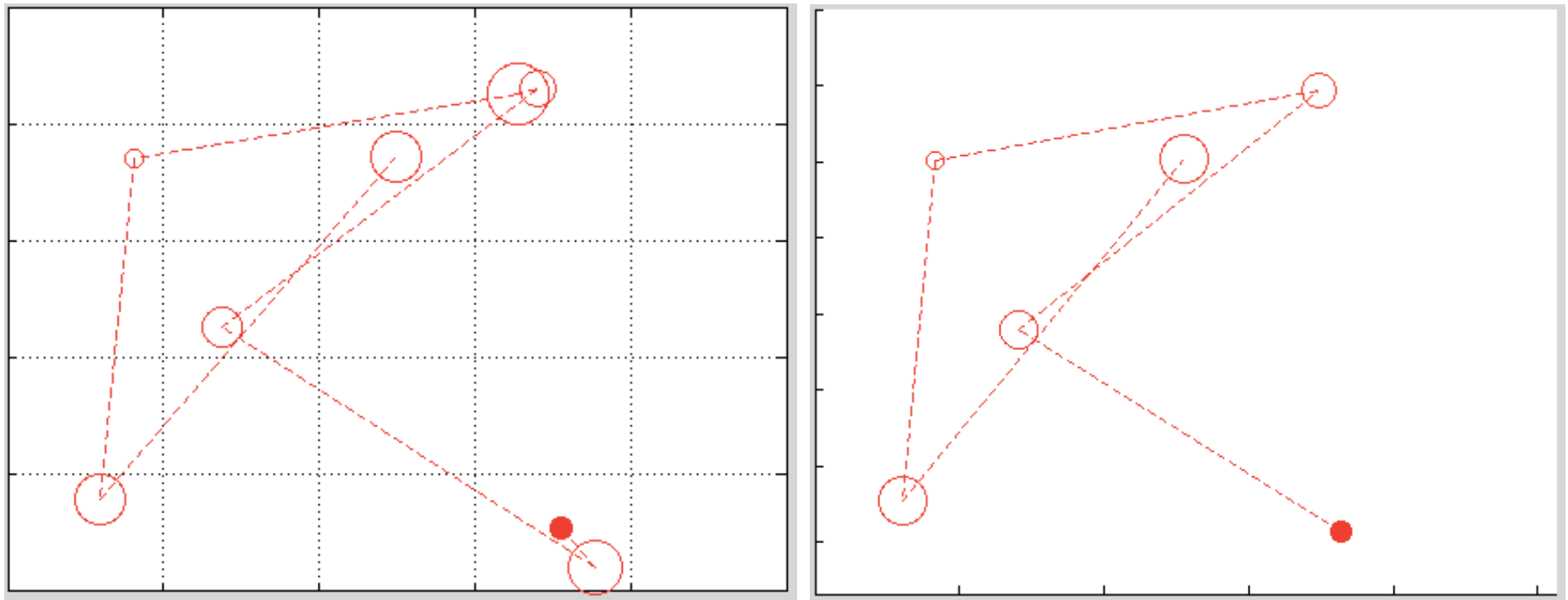


MultiMatch

- Jarodzka et al., (2010) and Dewhurst et al., (2012) aim to remove the need for AOIs by comparing idealised saccade vectors
- Scanpaths are simplified according to user-specified thresholds...
- ...then aligned and compared along different dimensions



MultiMatch: scanpath simplification



MultiMatch: vector alignment

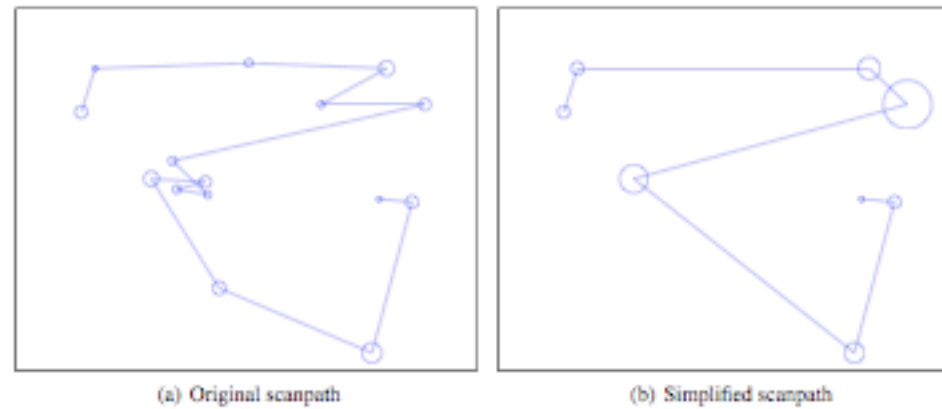
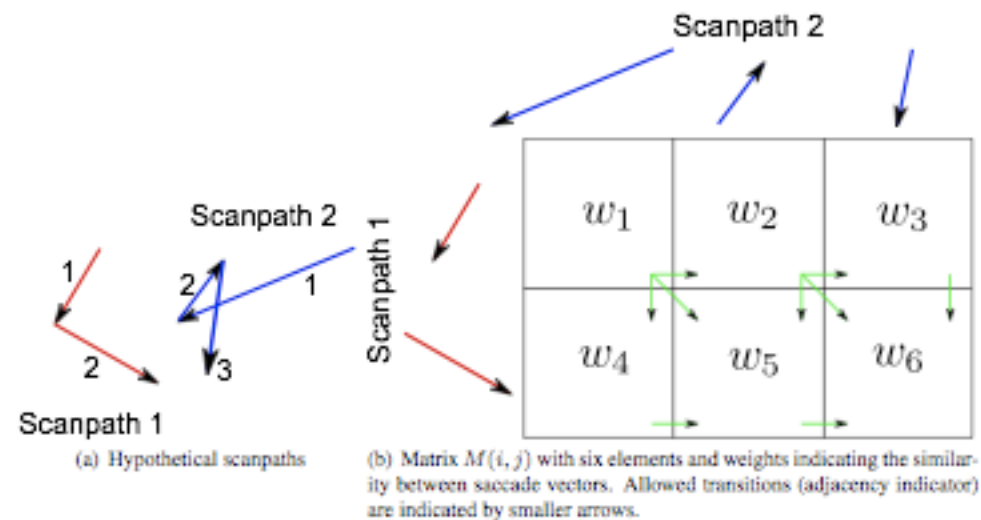


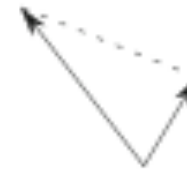
Figure 3: Example of scanpath simplification. Notice how saccade vectors with similar direction and/or short saccade vectors at similar positions are merged. Fixation durations associated with small, merged vectors are added to the beginning of a new, larger vector.



MultiMatch: vector comparison

Table 1 Dimension subtraction

Shape: This is the vector difference between aligned saccade pairs, $(u_i - v_j)$ —a measure of similarity in scanpath shape. The resulting similarity value is normalised by $2 \times$ the screen diagonal (the maximum theoretical value).



Length: This is the difference in length between the endpoints of saccade vectors—a measure of similarity in saccadic amplitude. The resulting similarity value is normalized by the screen diagonal.



Direction: This is the angular distance between saccade vectors—a measure of similarity in shape when saccadic amplitudes are different. The resulting similarity value is normalized by π .



Position: This is the difference in position between aligned fixations—a common measure of scanpath similarity in terms of Euclidean distance. The resulting similarity value is normalised by the screen diagonal.

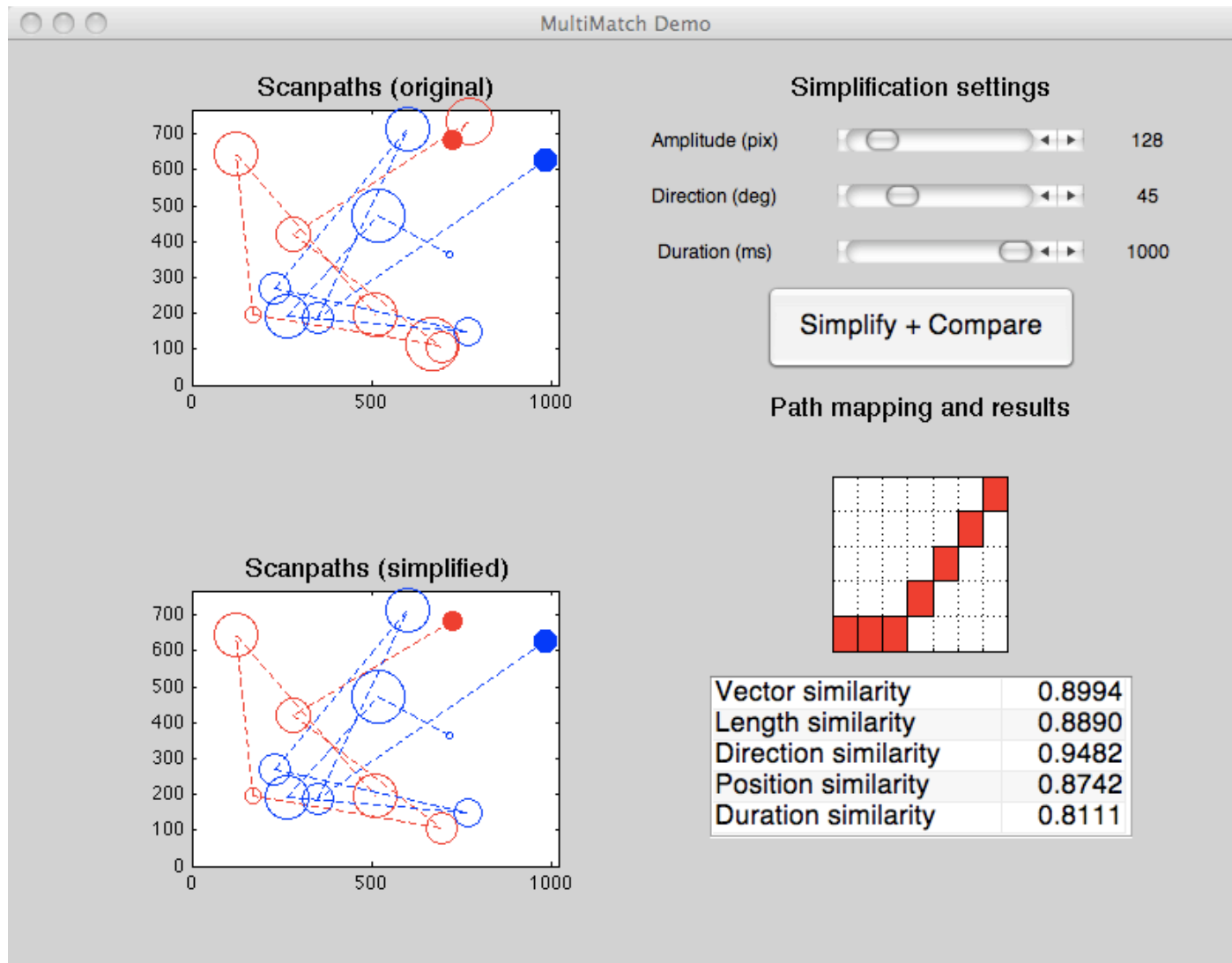


Duration: This is the difference in fixation durations between aligned fixations—a measure of similarity in processing time. The resulting similarity value is normalized against the maximum duration of the two being compared.



For each of the five dimensions—shape (vector difference), length, direction, position, and fixation duration—a difference can be calculated. Arrows denote vector–saccade pairs. The sizes of the circles in the duration case indicate one fixation that is longer than the other.

MultiMatch example

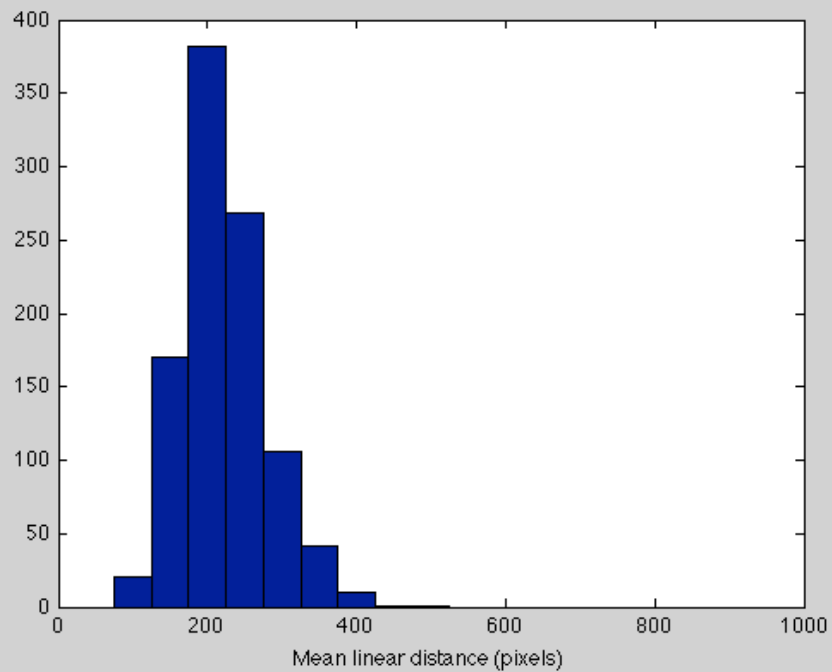


Where is the baseline?

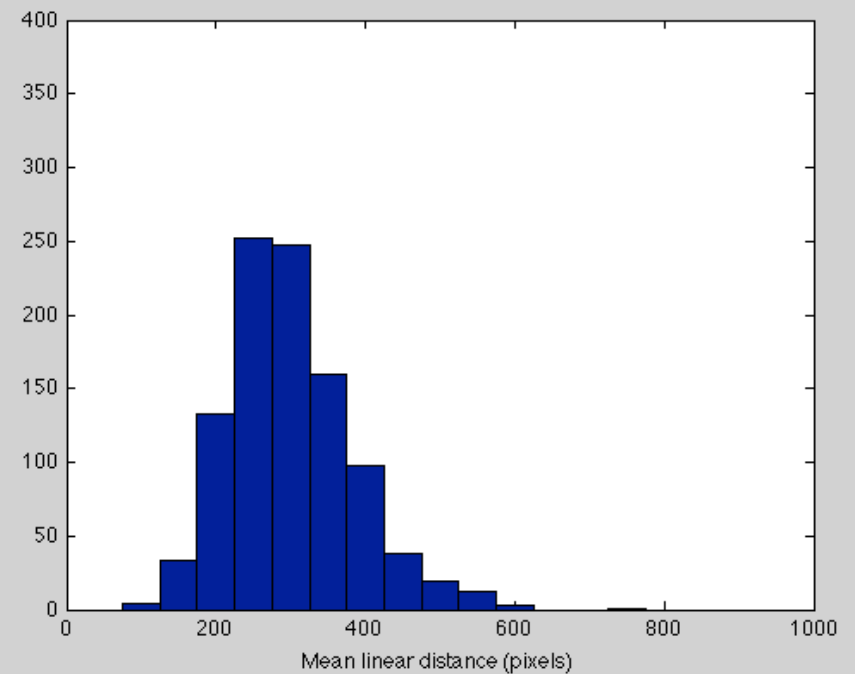
- Often, we want to conclude that scanpaths are more (or less) similar than chance. But what is *chance*?

Random simulations

Linear distance

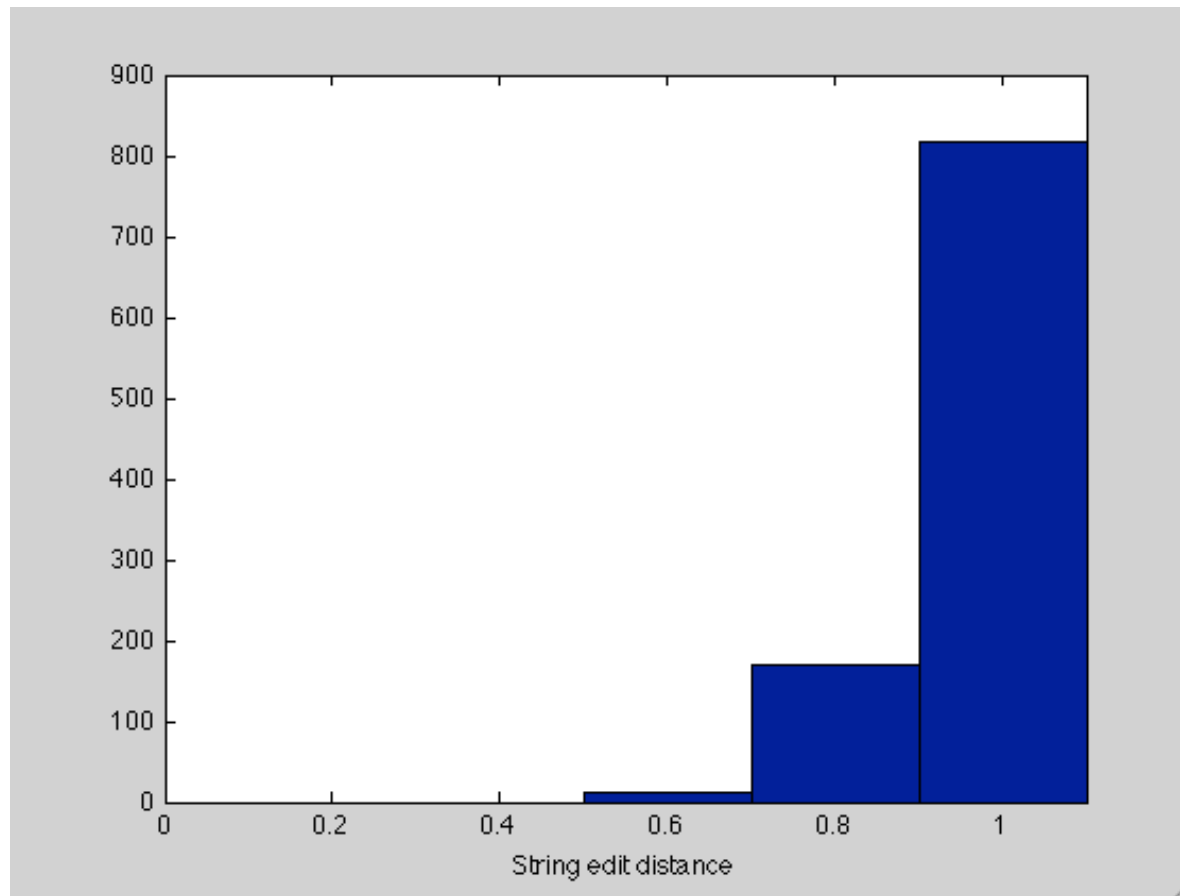


Unique assignment distance



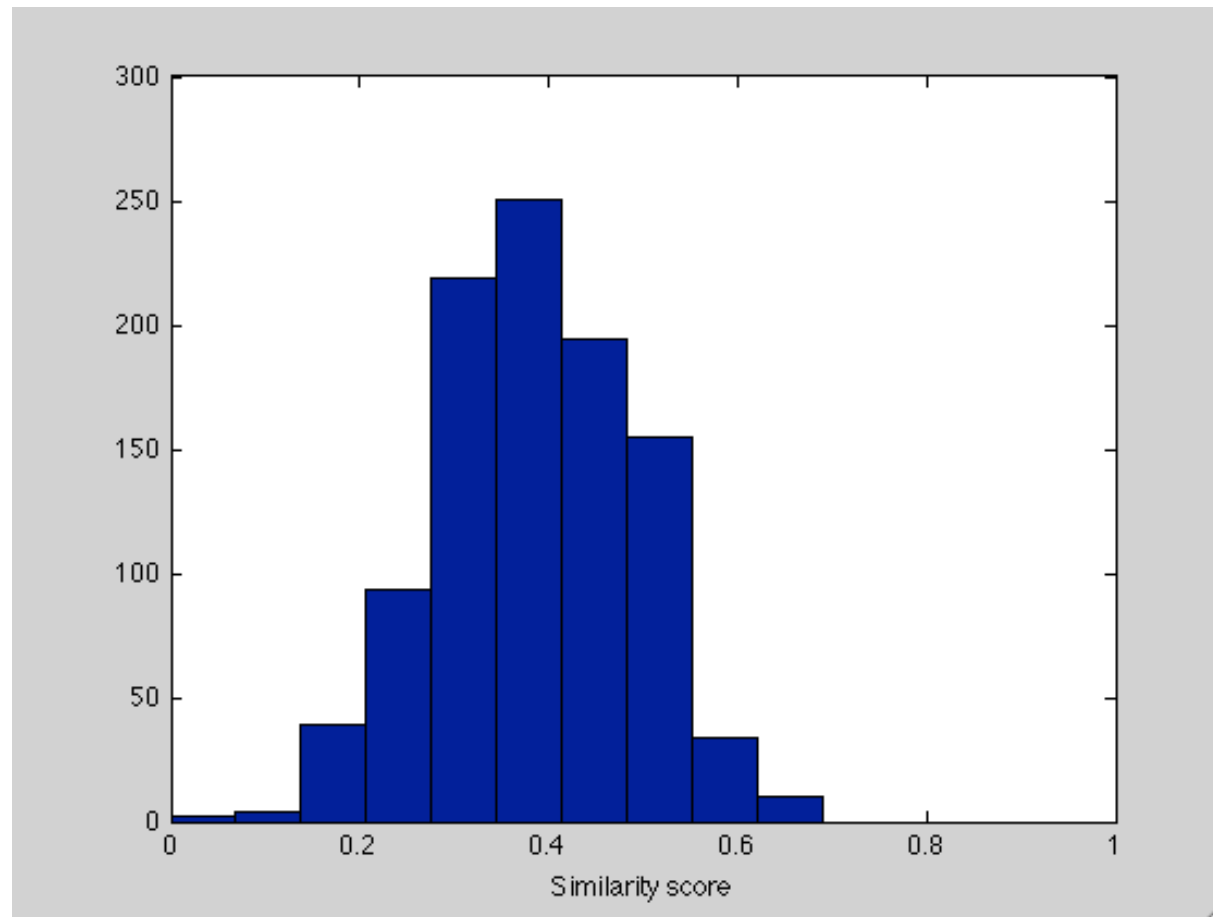
Random simulations

Linear distance
(with 5 x 5 grid = 25 AOIs)



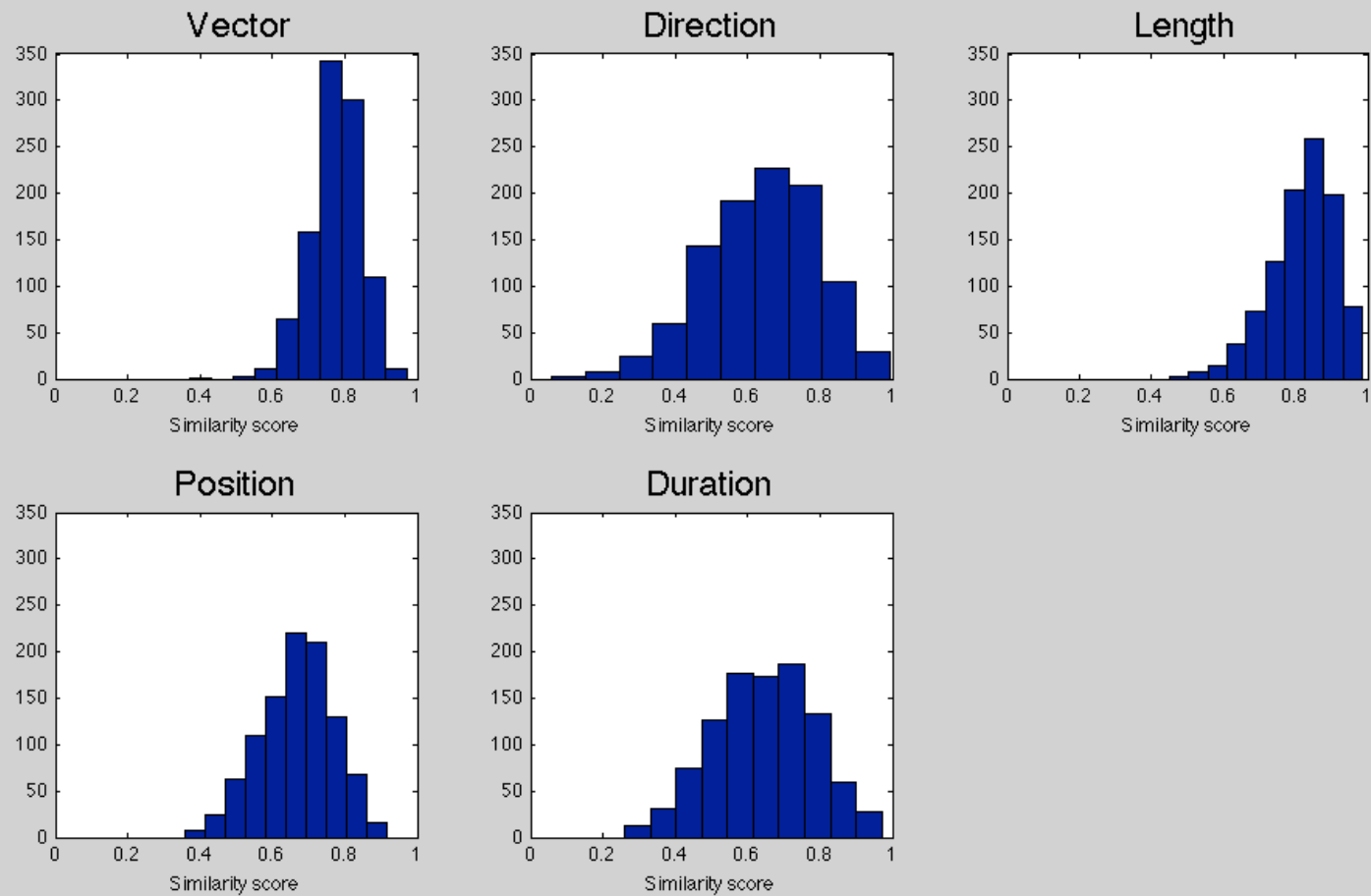
Random simulations

ScanMatch
(with 5 x 5 grid = 25 AOIs)



Random simulations

MultiMatch
(with 5 x 5 grid = 25 AOIs)



Random simulations

Between-method correlations

					MultiMatch				
	Linear distance	Unique assignment	String edit distance	ScanMatch	Vector	Direction	Length	Position	Duration
Linear distance	<i>1.00</i>	0.84	0.22	-0.26	-0.13	-0.07	-0.09	-0.40	-0.01
Unique assignment	0.84	<i>1.00</i>	0.15	-0.21	-0.10	-0.06	-0.10	-0.42	-0.01
String edit distance	0.22	0.15	<i>1.00</i>	-0.37	-0.12	-0.12	0.00	-0.19	0.04
ScanMatch	-0.26	-0.21	-0.37	<i>1.00</i>	0.12	0.08	0.08	0.16	0.08
Vector	-0.13	-0.10	-0.12	0.12	<i>1.00</i>	0.62	0.31	0.41	-0.01
Direction	-0.07	-0.06	-0.12	0.08	0.62	<i>1.00</i>	-0.05	0.36	0.00
Length	-0.09	-0.10	0.00	0.08	0.31	-0.05	<i>1.00</i>	0.17	-0.04
Position	-0.40	-0.42	-0.19	0.16	0.41	0.36	0.17	<i>1.00</i>	-0.01
Duration	-0.01	-0.01	0.04	0.08	-0.01	0.00	-0.04	-0.01	<i>1.00</i>

Other recent methods

- ScaSim (von der Malsburg et al., 2011)
 - Uses continuous representation of fixation locations and durations and weighted edit-distance
 - Designed for reading studies
- Mathot et al., (2012)
 - Geometric distance between fixation locations and durations

Demos

- Use `demoScanMatch.m` and `demoMultiMatch.m` to try out `ScanMatch` and `MultiMatch`.
- Try changing some parameters or run on example data or your own!

Some references

- Cristino, F., Mathôt, S., Theeuwes, J., & Gilchrist, I. D. (2010). ScanMatch: A novel method for comparing fixation sequences. *Behavior Research Methods*, 42(3), 692-700.
- Dewhurst, R., Nyström, M., Jarodzka, H., Foulsham, T., Johansson, R., & Holmqvist, K. (2012). It depends on how you look at it: Scanpath comparison in multiple dimensions with MultiMatch, a vector-based approach. *Behavior research methods*, 44(4), 1079-1100.
- Foulsham, T., & Underwood, G. (2008). What can saliency models predict about eye movements? Spatial and sequential aspects of fixations during encoding and recognition. *Journal of Vision*, 8(2).
- Henderson, J. M., Brockmole, J. R., Castelano, M. S. & Mack, M. (2007). In Fischer, M., Murray, W., & Hill, R. (Eds). Visual saliency does not account for eye movements during visual search in real-world scenes. *Eye movements: A window on mind and brain*, 537-562.
- Jarodzka, H., Holmqvist, K., & Nyström, M. (2010). A vector-based, multidimensional scanpath similarity measure. In Proceedings of the 2010 symposium on eye-tracking research & applications (pp. 211–218).
- Mathôt, S., Cristino, F., Gilchrist, I. D., & Theeuwes, J. (2012). A simple way to estimate similarity between pairs of eye movement sequences. *Journal of Eye Movement Research*, 5(1), 1-15.
- von der Malsburg, T., & Vasishth, S. (2011). What is the scanpath signature of syntactic reanalysis?. *Journal of Memory and Language*, 65(2), 109-127.