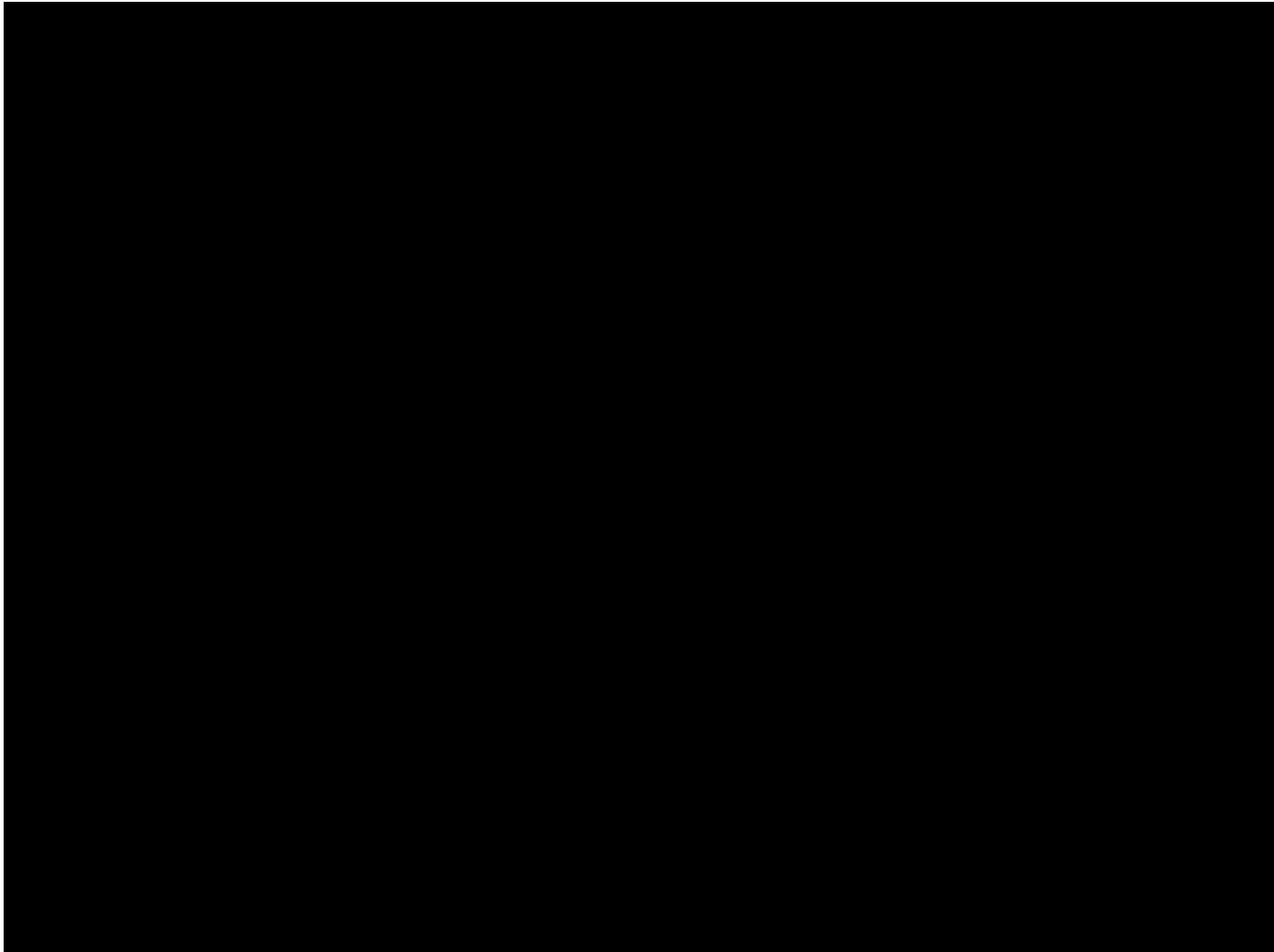


Identifying soccer formations using broadcast tracking data

Jacob Mortensen - CASSIS 2022

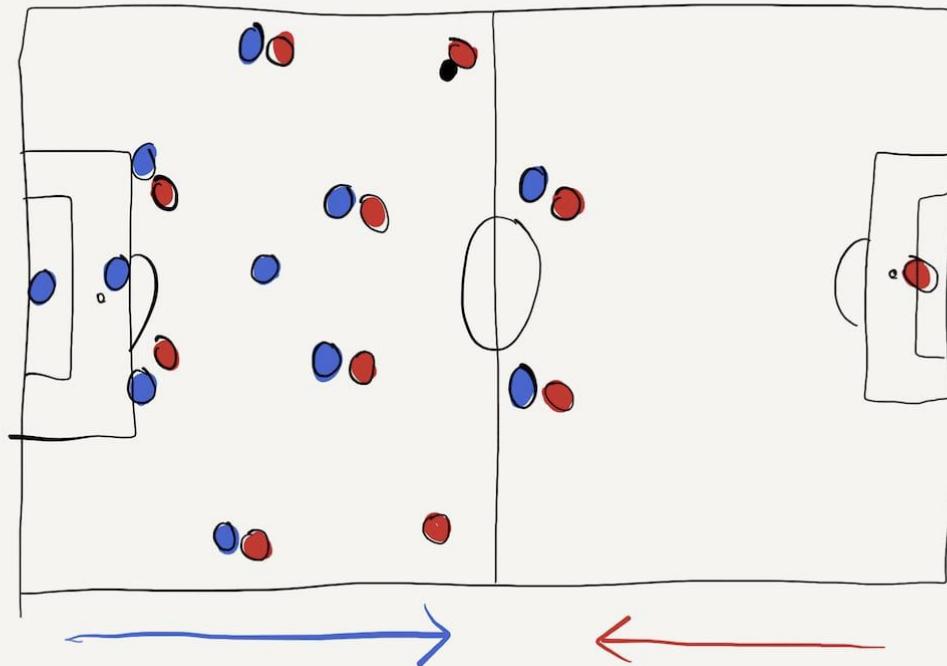


Background



Soccer Formations

● 5-3-2 GIVES NUMERICAL SUPERIORITY VS. 4-4-2



Previous Work

Bialkowski et. al. (2014) - Apply minimum entropy data partitioning (MEDP) to assign players to roles and use agglomerative hierarchical clustering to classify roles into formations

Shaw and Glickman (2019) - Average player locations over two minute segments into observations and then perform hierarchical clustering.

Learning formations from data

General approach:

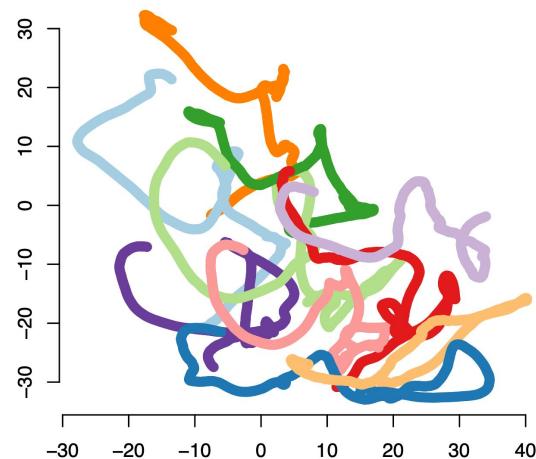
1. Aggregate frames to create “observations”
2. Perform some kind of clustering

Nuisance factors:

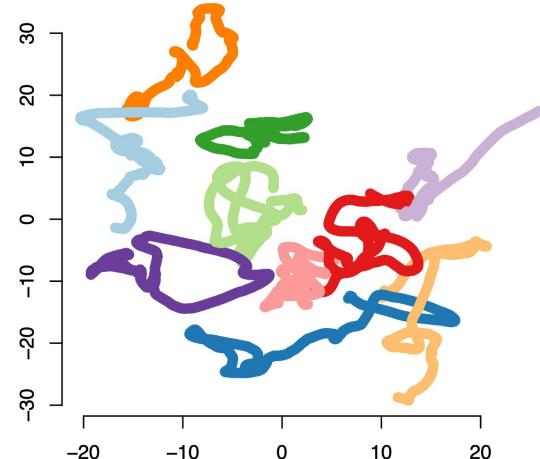
- Frame alignment
 - Broadcast data has the added complication of heavy censoring.
- Player permutation
- Contraction and expansion

Frame Alignment

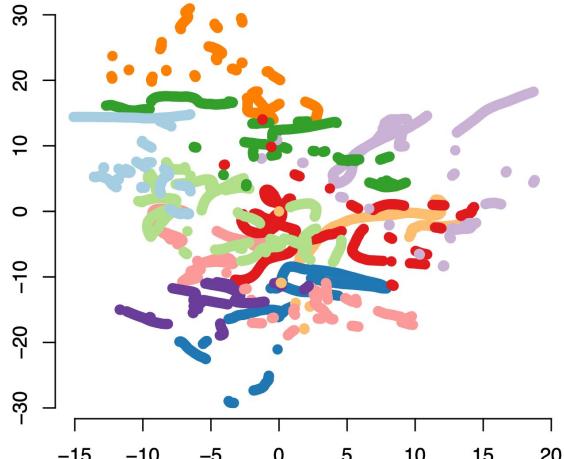
(a) Raw Multicamera Tracks



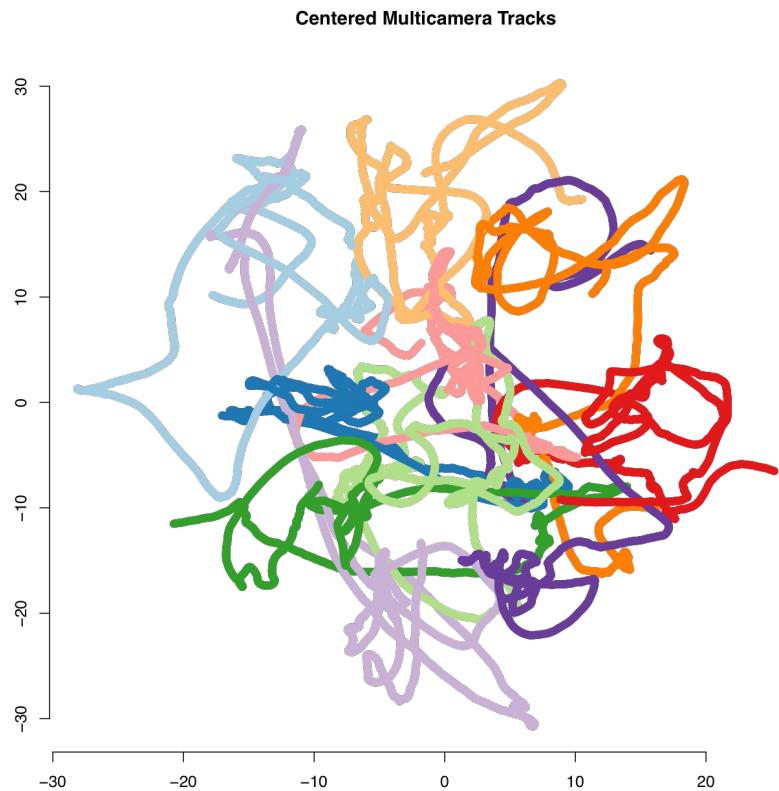
(b) Centered Multicamera Tracks



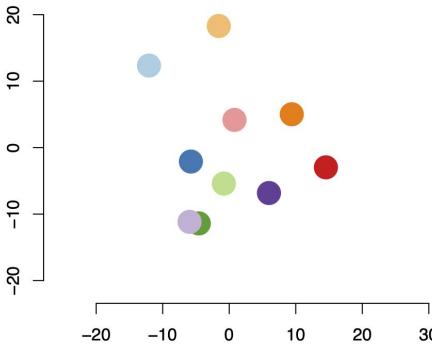
(c) Centered Broadcast Tracks



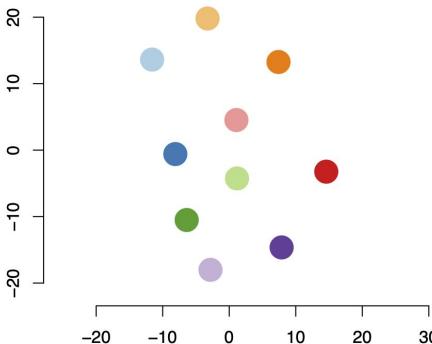
Permutation



Role estimates from average differences



Role estimates with permutation



Data

Data

- 5 games in a high level European soccer league w/ both optical tracking and broadcast tracking data
- x- and y- coordinates for 11 players on each team, at a frequency of 24 frames per second
- team IDs, player IDs, and possession indicator
- Camera window from broadcast tracking data is used to censor multicamera tracking data, creating a set of “perfect” broadcast tracking data
- **Heavily censored:** the largest percentage of frames where all 10 outfield players were observed for a given team was just 8.48 percent.

Method

Atomic Configuration Distance

ACD is a permutation invariant distance measure that calculates the distance between two collections of points by associating a density with each collection of points and calculating the L2 norm between the densities.

$$d^{(acd)}(X, Y) = \|\rho_X(s, \Sigma) - \rho_Y(s, \Sigma)\|_2^2$$

$$\rho_X(s, \Sigma) = \frac{1}{N_x} \sum_{i=1}^{N_x} \phi(s; x_i, \Sigma)$$

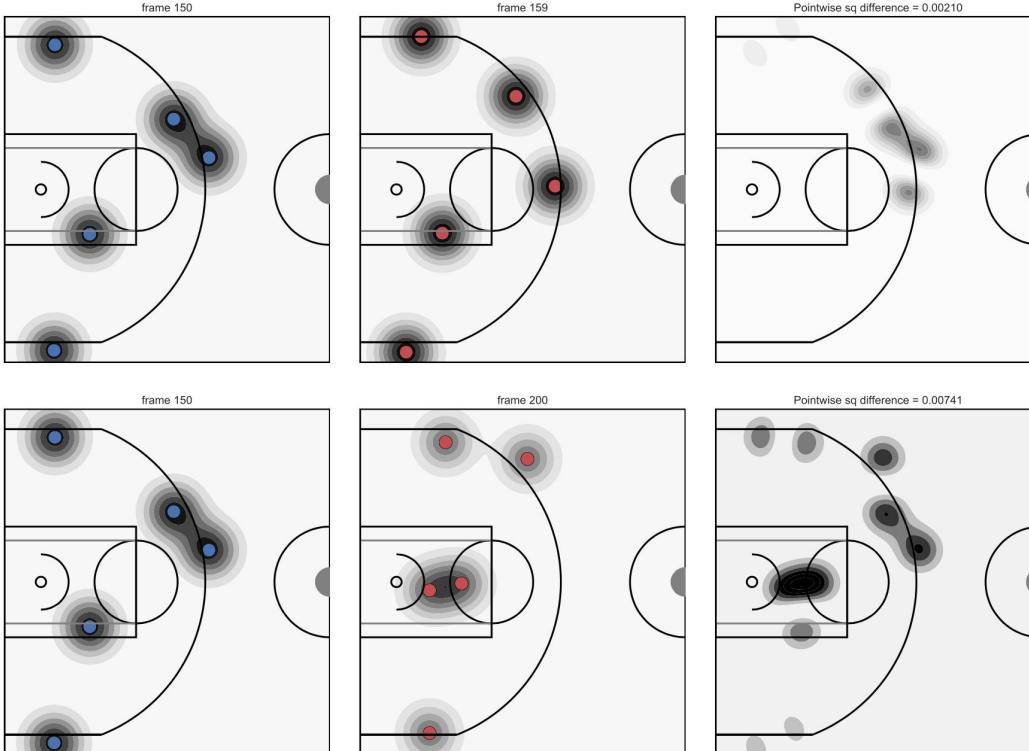
Atomic Configuration Distance

$$\begin{aligned} d^{(acd)}(X, Y) &= \|\rho_X(s, \Sigma) - \rho_Y(s, \Sigma)\|_2^2 \\ &= \int_{s \in \mathbb{R}^D} (\rho_X(s, \Sigma) - \rho_Y(s, \Sigma))^2 ds \\ &= S(\rho_X, \rho_X) + S(\rho_Y, \rho_Y) - 2S(\rho_X, \rho_Y) \end{aligned}$$

Miller and Bornn (2020) showed that

$$S(\rho_X, \rho_Y) = \left(\frac{1}{4\pi}\right)^{D/2} \frac{|\Sigma|^{-1/2}}{N_x N_y} \sum_{i=1}^{N_x} \sum_{j=1}^{N_y} \exp\left(-\frac{1}{4}(x_i - y_j)' \Sigma^{-1} (x_i - y_j)\right)$$

Atomic Configuration Distance



Solves for two nuisance factors:

- Permutation invariant
- Valid if $N_x \neq N_y$

Minimum Entropy Data Partitioning (MEDP)

Let the formation density be $P(\mathbf{x}) = \frac{1}{N} \sum_{n=1}^N P_n(\mathbf{x})$ and maximize $\sum_{i=1}^N KL(P_n||P)$

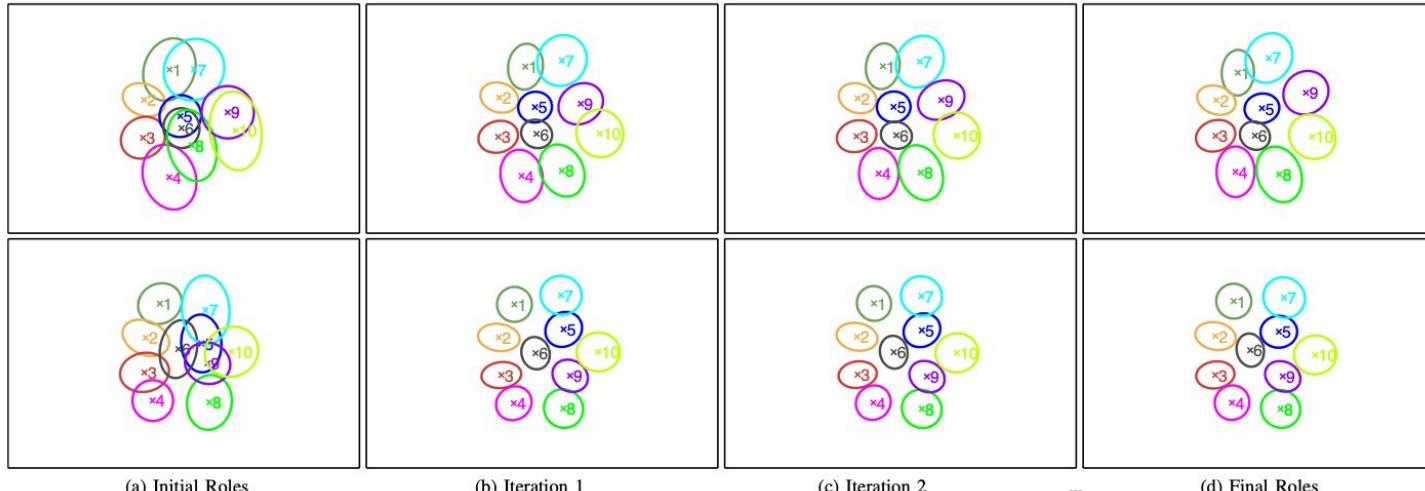


Image taken from Bialkowski et. al. 2014

Minimum Entropy Data Partitioning (MEDP)

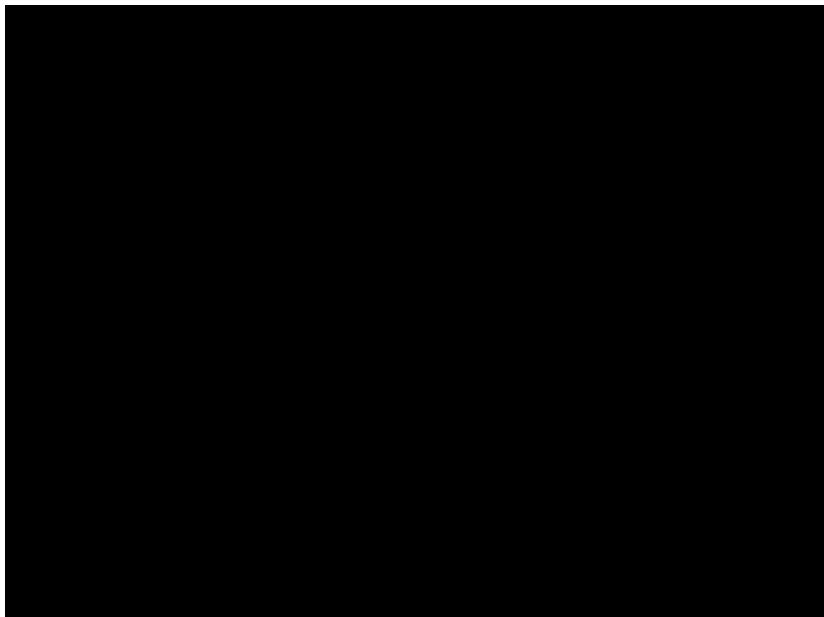
In practice, KL cannot be maximized efficiently, so we follow Bialkowski et. al. (2014) and take an EM-like approach.

1. Initialize algorithm by assuming that players maintain the same role throughout the segment
2. Estimate 2d Gaussian for each role based on centered player locations
3. Calculate cost matrix by evaluating the role densities at each player location and use Hungarian algorithm to permute players with roles to minimize cost
4. Repeat 2-3 until no further reassessments occur

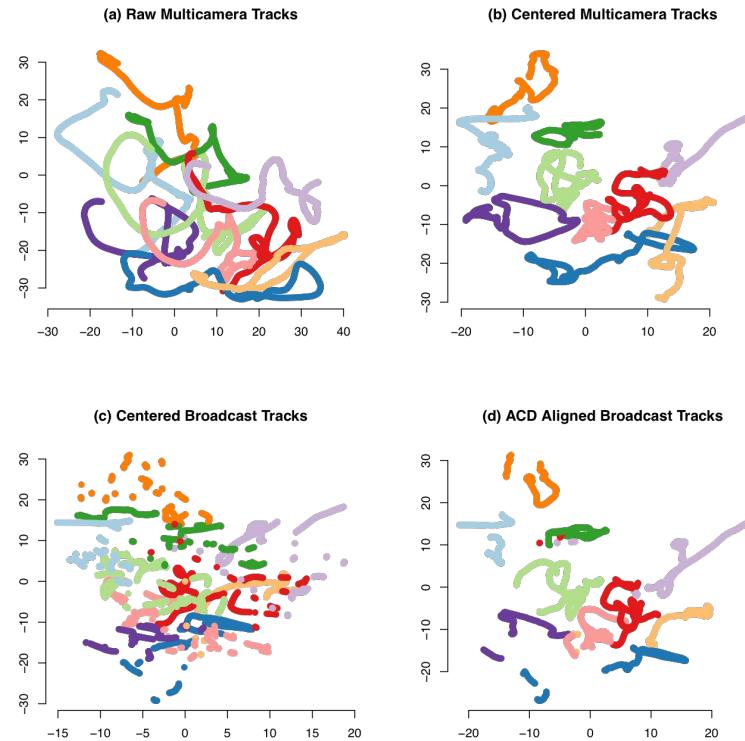
NOTE: We adapt the Hungarian algorithm for use with censored data by setting cost to infinity for missing players. This ensures that observed player locations get assigned to the “cheapest” role density.

Frame Alignment Algorithm

1. Take a sequence S_1, \dots, S_T where at least 1 player is observed in every frame
2. Find the δ_t that minimizes the ACD between $S_t + \delta_t$ and S_{t+1} for all $t=1, \dots, T-1$, where δ_t is a matrix with all rows equal to $(\delta_{tx}, \delta_{ty})$
3. Calculate translated frames $S_{\Delta t} = S_t + \sum_{j=t}^{T-1} \delta_j$
4. Use MEDP to calculate role distribution for sequence, and use centroid of role distribution to translate sequence to origin



Frame Alignment Algorithm



Aggregate and Scale

- Take similar approach to Shaw and Glickman and aggregate frames over 120 second windows, but we use MEDP rather than average difference approach
 - Average offense and defense separately
 - Exclude possessions < 5 seconds in length
 - Do not average across periods or player substitutions
- Scale data by empirical standard deviation of x- and y-coordinates

Cluster using Gaussian Mixture Model

We fit a standard GMM using expectation maximization with some small adaptations:

- Hungarian algorithm is used to account for the effects of player permutation
- EM has to be adapted for incomplete observations following Gharamani and Jordan (1994):

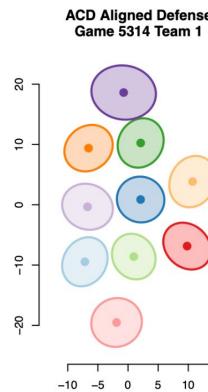
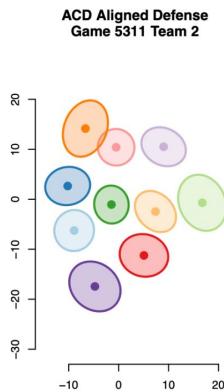
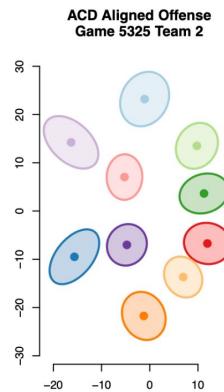
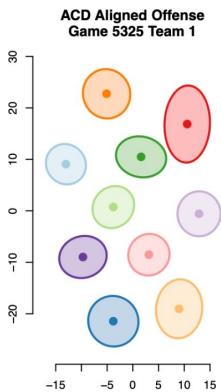
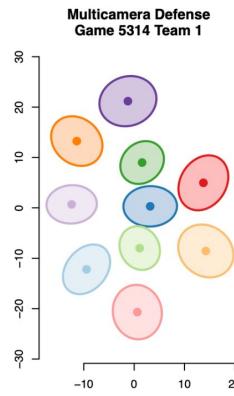
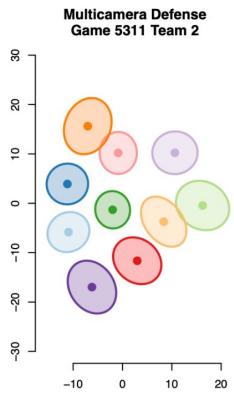
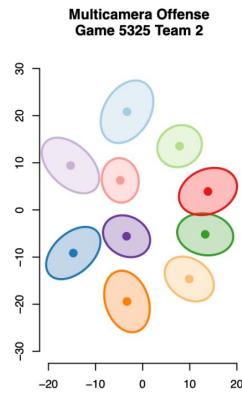
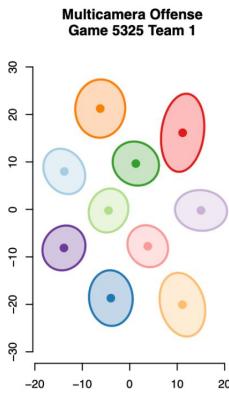
$$\hat{z}_{ik} = P(z_i = k) = \frac{\prod_{p=1}^{2P} (\mathcal{N}(x_{ip} | \mu_{kp}, \sigma_{kp}^2))^{I(o_{ip}=1)}}{\sum_{\ell=1}^K \prod_{p=1}^{2P} (\mathcal{N}(x_{ip} | \mu_{\ell p}, \sigma_{\ell p}^2))^{I(o_{ip}=1)}}$$

We replace $I(o_{ip} = 1)$ with the weight $w_{ip} = \sum_{n=1}^{N_i} o_{np}$

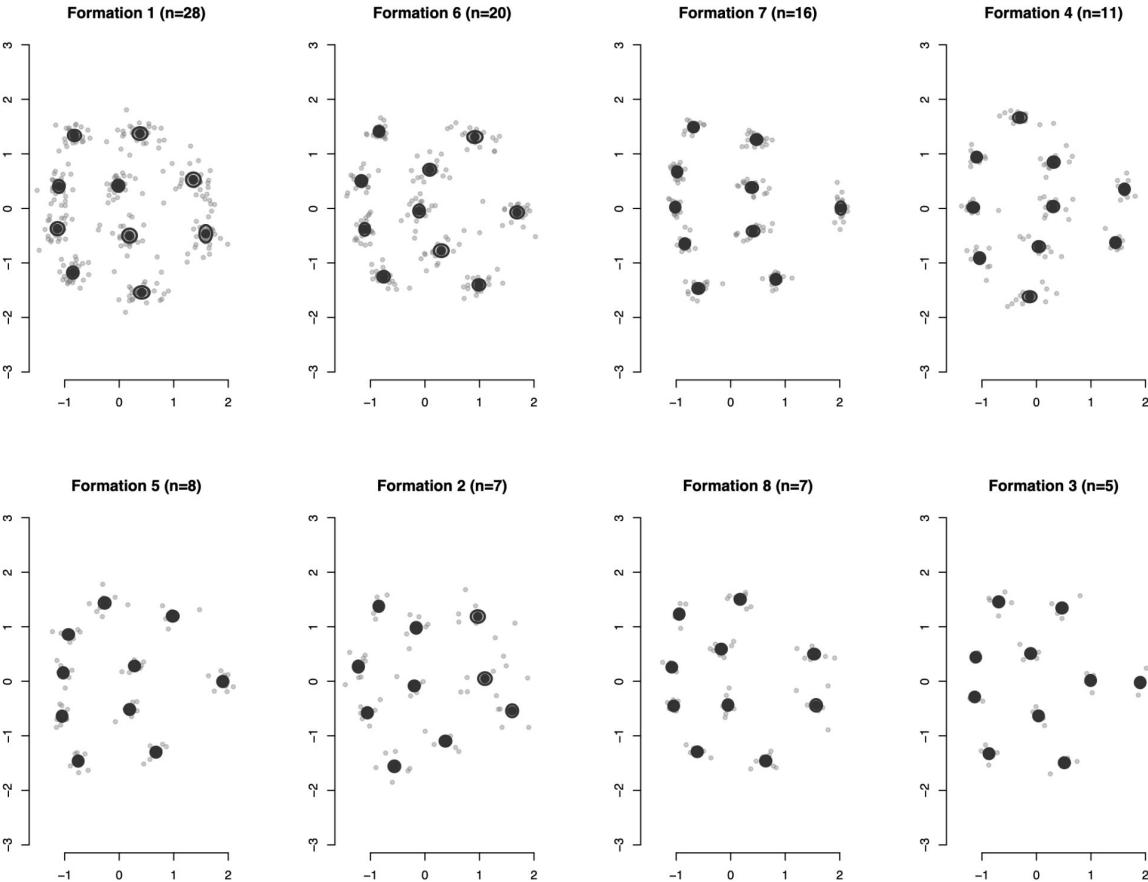
Number of clusters is selected using BIC. Determined to be 8 clusters for defense and 6 clusters for offense.

Results

Results



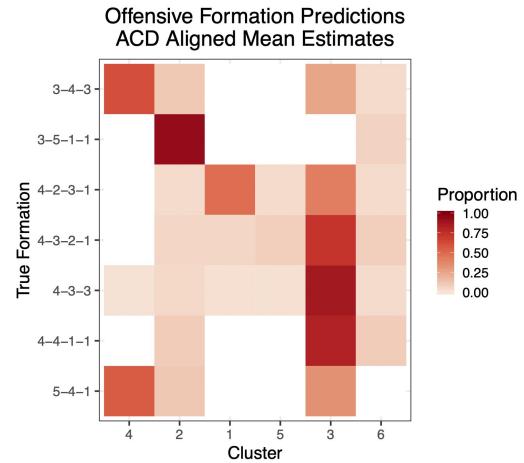
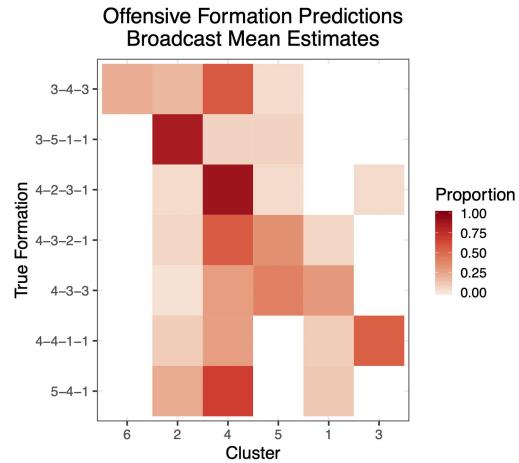
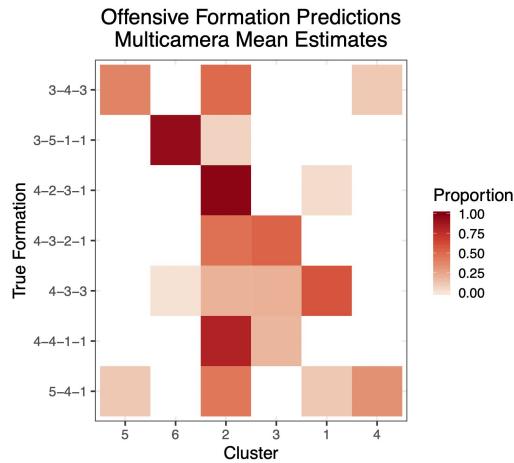
Results



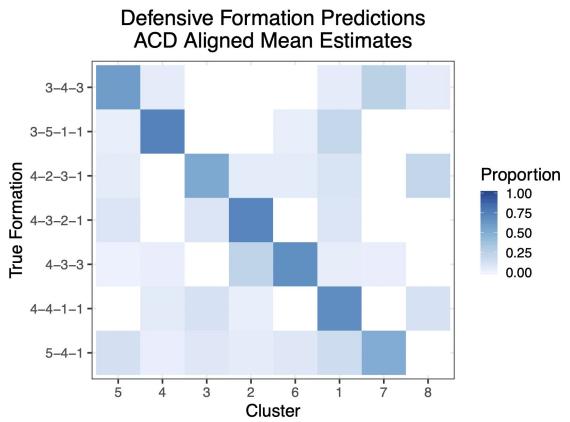
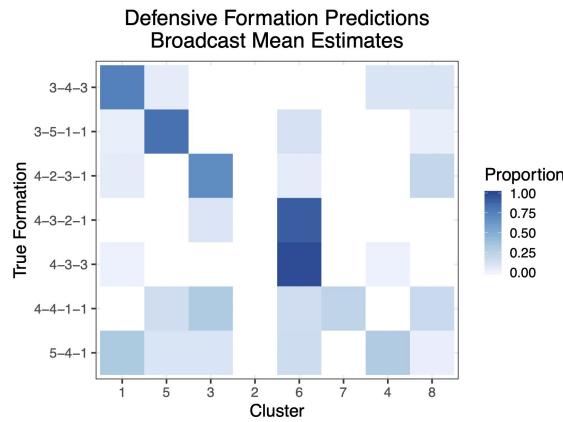
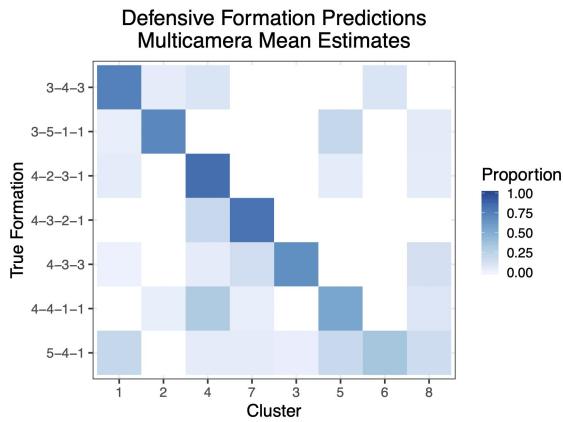
Results

- Fit mixture models to full multicamera data, broadcast mean calculated using average differences, and ACD aligned data.
- Compare clustered observations with expert-provided formation labels.

Results



Results



Summary

- Minimize atomic configuration distance to align frames
- Use MEDP to align possessions and create pseudo observations
- Use Gaussian mixture model to cluster and identify canonical formations

Acknowledgements

Acknowledgements



Natural Sciences and Engineering
Research Council of Canada

Conseil de recherches en sciences
naturelles et en génie du Canada

Canada



SIMON FRASER
UNIVERSITY

STATS

SPORT
LOGiQ

Thank you!