While reading up on modern soccer analytics (I've had an itch for soccer and tracking data recently, I stumbled upon an excellent set of tutorials written by Devin Pleuler. In particular, his notebook on non-negative matrix factorization (NNMF) caught my eye. I hadn't really heard of the concept before, but it turned out to be much less daunting once I realized that it is just another type of matrix decomposition. Singular value decomposition (SVD), which I'm much more familiar with, belongs to the same family of calculations (although NNMF and SVD are quite different). In an effort to really gain a better understanding of NNMF, I set out to emulate his notebook.

In the process of converting his python code to R, I encountered three challenges with resolutions worth documenting.

1) Before the NNMF calculation, I needed to perform non-equi join with a fairly size-able data set. Unfortunately, `{dplyr}`[1] does not have built-in support for such a join 😭. I tossed aside any kind of personal implicit bias against `{data.table}`—which is certainly the go-to option in the R ecosystem for non-equi joins—and used it for this process.

2) For the NNMF calculation, the only R implementation (that I could find) comes with the {NMF} package[2], which requires the installation of the Bioconductor-exclusive {BiocManager} package. I'm relatively unfamiliar with Bioconductor, so this was not very appealing (although I did end up downloading `{NMF}` and trying it out). Instead, I ended up using `{reticulate}` to call the `skearn.decomposition.NMF()` function directly (as is done in the python code). This is a perfect example of using `{reticulate}` for a non-trivial reason (i.e. for an algorithm).

3) After the NNMF computation, I needed to perform 2-D Gaussian smoothing, which is helpful for making the output of the NNMF output more interpretable. The `{spatstat}` package had just the function for the job (`spatstat::blur()`), and it all it took for me was to write some a tidy wrapper function to integrate it nicely into my workflow.

I've always considered myself a "whatever gets the job done" kind of person, not insistent on ignoring solutions that use "base" R, `{data.table}`, python, etc. Nonetheless, replicating Devin's notebook really underscored the importance of being comfortable outside of a `{tidyverse}`-centric workflow.

Anyways, this post outlines the code and my thought process in porting Devin's code to R. I'll skip some of the details, emphasizing the things that are most interesting.

Data

We'll be working with the open-sourced StatsBomb data for the 2018 Men's World Cup, which I've called `events` below. [3]

This is a relatively large data set with lots of columns (and rows). However, we only need three columns for what we're going to do: (1) a unique identifier for each player, `player_id`, along with their (2) `x` and (3) `y` coordinates.

```
library(tidyverse)
```

A quick summary of the data shows that there are 603 unique players, and that the `x` and `y` coordinates range from 1 to 120 (yards) and 1 to 80 respectively.

```
events <-
```

```
  events %>%
  select(player_id = player.id, x = location.x, y = location.y) %>%
  drop_na() %>%
  summarize(
    n = n(),
    n_player = n_distinct(player_id),
    across(c(x, y), list(min = min, max = max, mean = mean))
  )
events

# # A tibble: 1 x 8
#       n n_player x_min x_max x_mean y_min y_max y_mean
#
# 1 224018      603     1   120  60.05     1    80  40.37
```

Non-Equi Joining with `{data.table}`

Our first challenge is to convert the following chunk of python.

```
import numpy as np

x_scale, y_scale = 30, 20

x_bins = np.linspace(0, 120, x_scale)
y_bins = np.linspace(0, 80, y_scale)

players = {}

for e in events:
    if 'player' in e.keys():
        player_id = e['player']['id']
        if player_id not in players.keys():
            players[player_id] = np.zeros((x_scale, y_scale))
        try:
            x_bin = int(np.digitize(e['location'][0], x_bins[1:],
right=True))
            y_bin = int(np.digitize(e['location'][1], y_bins[1:],
right=True))
            players[player_id][x_bin][y_bin] += 1
        except:
            pass
```

This code creates a nested `dict`, where the keys are player id’s and the values are 20×30 matrices. Each element in the matrix is an integer that represents the count of times that the player was recorded being at a certain position on the pitch. (These counts range from 0 to 94 for this data set.)

Some technical details:

1. The python `events` is actually a pretty heavily nested list[4], hence the non-rectangular operations such as `e['player']['id']`.
2. Observations with missing coordinates are ignored with the `try`–`except` block.

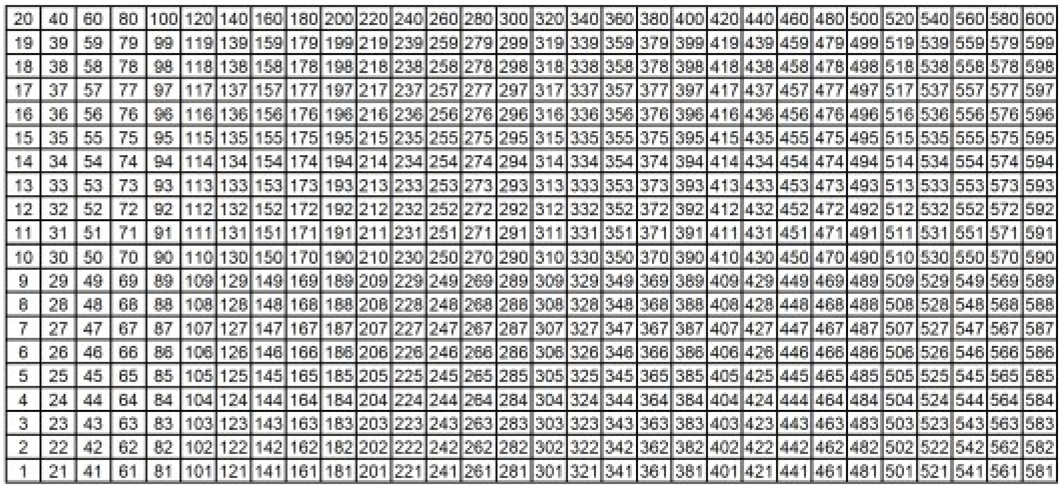
3. `x` and `y` values (elements of the `'location'` sub-list) are mapped to “bins” using `numpy`’s `digitize()` function, which is analogous to `base::cut()`.

How can we do this same data manipulation in an idiomatic R fashion? We could certainly create a named list element and use `base::cut()` to closely match the python approach. However, I prefer to stick with data frames and SQL-ish operations since I think these are much more “natural” for R users.[5]

So, going forward with data frames and joins, it’s quickly apparent that we’ll have to do some non-equi joining. `{fuzzyjoin}` and `{sqldf}` offer functionality for such an approach, but `{data.table}` is really the best option. The only minor inconvenience here is that we have to explicitly coerce our `events` data frame to a data.table.

We’ll also need a helper, grid-like data frame to assist with the binning. The 600-row `grid_xy_yards` data frame (30 `x` bins * 20 `y` bins) below is essentially a tidy definition of the cells of the grid upon which we are binning the `events` data. (One can use whatever flavor of `crossing()`, `expand.grid()`, `seq()`, etc. that you prefer to create a data frame like this.)

Visually, this grid looks like this.



20	40	60	80	100	120	140	160	180	200	220	240	260	280	300	320	340	360	380	400	420	440	460	480	500	520	540	560	580	600
19	39	59	79	99	119	139	159	179	199	219	239	259	279	299	319	339	359	379	399	419	439	459	479	499	519	539	559	579	599
18	38	58	78	98	118	138	158	178	198	218	238	258	278	298	318	338	358	378	398	418	438	458	478	498	518	538	558	578	598
17	37	57	77	97	117	137	157	177	197	217	237	257	277	297	317	337	357	377	397	417	437	457	477	497	517	537	557	577	597
16	36	56	76	96	116	136	156	176	196	216	236	256	276	296	316	336	356	376	396	416	436	456	476	496	516	536	556	576	596
15	35	55	75	95	115	135	155	175	195	215	235	255	275	295	315	335	355	375	395	415	435	455	475	495	515	535	555	575	595
14	34	54	74	94	114	134	154	174	194	214	234	254	274	294	314	334	354	374	394	414	434	454	474	494	514	534	554	574	594
13	33	53	73	93	113	133	153	173	193	213	233	253	273	293	313	333	353	373	393	413	433	453	473	493	513	533	553	573	593
12	32	52	72	92	112	132	152	172	192	212	232	252	272	292	312	332	352	372	392	412	432	452	472	492	512	532	552	572	592
11	31	51	71	91	111	131	151	171	191	211	231	251	271	291	311	331	351	371	391	411	431	451	471	491	511	531	551	571	591
10	30	50	70	90	110	130	150	170	190	210	230	250	270	290	310	330	350	370	390	410	430	450	470	490	510	530	550	570	590
9	29	49	69	89	109	129	149	169	189	209	229	249	269	289	309	329	349	369	389	409	429	449	469	489	509	529	549	569	589
8	28	48	68	88	108	128	148	168	188	208	228	248	268	288	308	328	348	368	388	408	428	448	468	488	508	528	548	568	588
7	27	47	67	87	107	127	147	167	187	207	227	247	267	287	307	327	347	367	387	407	427	447	467	487	507	527	547	567	587
6	26	46	66	86	106	126	146	166	186	206	226	246	266	286	306	326	346	366	386	406	426	446	466	486	506	526	546	566	586
5	25	45	65	85	105	125	145	165	185	205	225	245	265	285	305	325	345	365	385	405	425	445	465	485	505	525	545	565	585
4	24	44	64	84	104	124	144	164	184	204	224	244	264	284	304	324	344	364	384	404	424	444	464	484	504	524	544	564	584
3	23	43	63	83	103	123	143	163	183	203	223	243	263	283	303	323	343	363	383	403	423	443	463	483	503	523	543	563	583
2	22	42	62	82	102	122	142	162	182	202	222	242	262	282	302	322	342	362	382	402	422	442	462	482	502	522	542	562	582
1	21	41	61	81	101	121	141	161	181	201	221	241	261	281	301	321	341	361	381	401	421	441	461	481	501	521	541	561	581

And if you prefer numbers instead of a chart, see the first 10 rows below.

```
grid_xy_yards

# # A tibble: 600 x 5
#     idx     x      y next_y next_x
#
# 1     1     0   0      4.211   4.138
# 2     2     0   4.211   8.421   4.138
# 3     3     0   8.421 12.63   4.138
# 4     4     0 12.63   16.84   4.138
# 5     5     0 16.84   21.05   4.138
# 6      6      0 21.05  25.26   4.138
# 7      7      0 25.26  29.47   4.138
# 8      8      0 29.47  33.68   4.138
# 9      9      0 33.68  37.89   4.138
# 10     10      0 37.89  42.11   4.138
# # ... with 590 more rows
```

Two things to note about this supplementary data frame:

1. Cells aren't evenly spaced integers, i.e. `x` cells are defined at 0, 4.138, 8.276, …, 80 instead of something like 0, 4, 8, …, 80, and `y` cells are defined at 0, 4.211, 8.421, …, 120 instead of something like 0, 4, 8, …, 120). That's simply due to using 30 and 20 instead of 31 and 21 to split up the `x` and `y` ranges respectively. I point this out because this SQL-ish approach would have been much easier if these numbers were just integers! We could have done an inner join on an integer grid instead of non-equi-joining upon a grid of floating point numbers. Unfortunately, joining on floating point numbers as keys leads to inconsistent results, simply due to the nature of floating points.[6]

2. The index `idx` is important! This will come back into play when we do the NNMF procedure, at which point we'll "flatten" out our `x`–`y` pairs into a 1-d format.

Ok, on to the actual data joining.

```
events_dt <- events %>% drop_na() %>% data.table::as.data.table()
grid_xy_yards_dt <- grid_xy_yards %>% data.table::as.data.table()

# We don't even have to load `{data.table}` for this to work!
events_binned <-
  events_dt[grid_xy_yards_dt, on=.(x > x, x <= next_x, y >= y, y <
next_y)] %>%
  as_tibble() %>%
  select(player_id, idx, x, y)
events_binned

# # A tibble: 224,038 x 4
#    player_id   idx     x      y
#
#   1       5462      1      0      0
#   2       5467      1      0      0
#   3       5488      1      0      0
#   4       3632      1      0      0
#   5       5576      1      0      0
#   6       5595      1      0      0
#   7       5263      1      0      0
#   8       4063      1      0      0
#   9       5231      1      0      0
# 10       5231      1      0      0
# # ... with 224,028 more rows
```

In retrospect, this join was pretty straightforward!

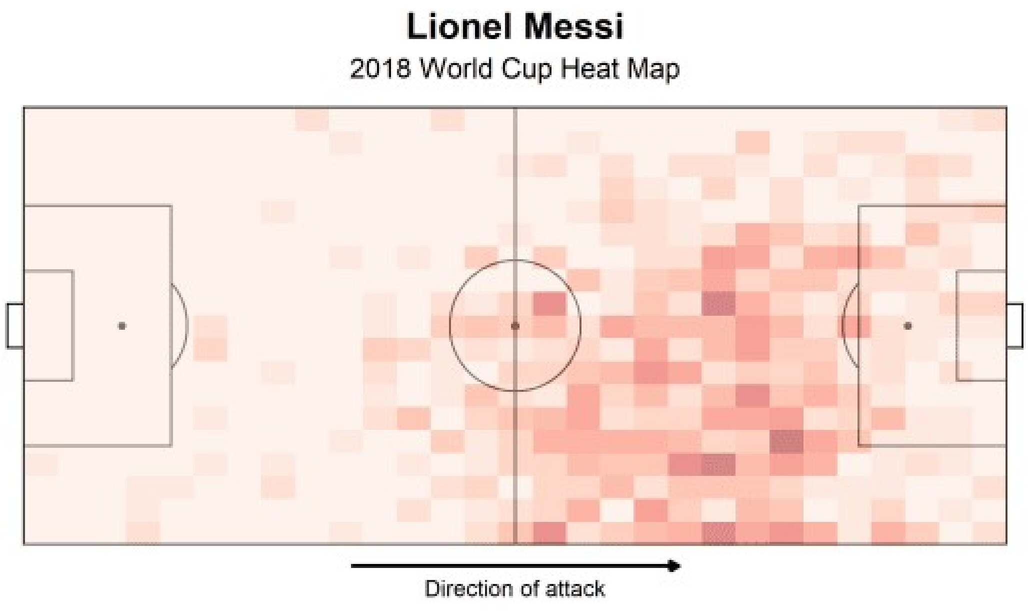
The rest of the code below is just doing the actual tallying.

1. First, we make an intermediate data set `grid_players`, which is the Cartesian product of all possible cells in the grid and all players in `events`.
2. Second, we “add back” missing cells to `events_binned` using the intermediate data set `grid_players`.

In the end, we end up with a `players` data frame with 603 `player_id`s * 30 `x` bins * 20 `y` bins = 361,800 rows.

```
# This `dummy` column approach is an easy way to do a Cartesian join
when the two data frames don't share any column names.
grid_players <-
  grid_xy_yards %>%
  mutate(dummy = 0L) %>%
  # Cartesian join of all possible cells in the grid and all players in
`events`.
  full_join(
    events %>%
      drop_na() %>%
      distinct(player_id) %>%
      mutate(dummy = 0L),
    by = 'dummy'
  )

players <-
  events_binned %>%
  group_by(player_id, x, y, idx) %>%
  summarize(n = n()) %>%
  ungroup() %>%
  # Rejoin back on the grid to 'add back' cells with empty counts (i.e.
`n = 0`).
  full_join(grid_players, by = c('player_id', 'x', 'y', 'idx')) %>%
  select(-dummy, -next_x, -next_y) %>%
  replace_na(list(n = 0L)) %>%
  arrange(player_id, x, y)
players

# # A tibble: 361,800 x 5
#    player_id     x      y   idx     n
#
#  1      2941     0  0         1     0
#  2      2941     0  4.211     2     0
#  3      2941     0  8.421     3     0
#  4      2941     0 12.63      4     0
#  5      2941     0 16.84      5     0
#  6      2941     0 21.05      6     0
#  7      2941     0 25.26      7     0
#  8      2941     0 29.47      8     0
#  9      2941     0 33.68      9     0
# 10      2941     0 37.89     10     0
# # ... with 361,790 more rows
```

To make this a little bit more tangible, let’s plot Messi’s heatmap. (Is this really a blog post about soccer if it doesn’t mention Messi 😆?)



Non-Negative Matrix Factorization (NNMF) with `{reticulate}` and `sklearn`

Next up is the actual NNMF calculation. I don’t care if you’re the biggest R stan in the world—you have to admit that the python code to perform the NNMF is quite simple and (dare I say) elegant. The `comps=30` here means

```
from sklearn.decomposition import NMF

# Flatten individual player matrices into shape=(600,) which is the
product of the original shape components (30 by 20)
unraveled = [np.matrix.flatten(v) for k, v in players.items()]
comps = 30
model = NMF(n_components=comps, init='random', random_state=0)
W = model.fit_transform(unraveled)
```

My understanding is that `comps=30` is telling the algorithm to reduce our original data (with 603 players) to a lower dimensional space with 30 player “archetypes” that best represent the commonalities among the 603 players.[7] Per Devin, the choice of 30 here is somewhat arbitrary. In practice, one might perform some cross validation to identify what number minimizes some loss function, but that’s beyond the scope of what we’re doing here.

After re-formatting our `players` data into a wide format—equivalent to the `numpy.matrix.flatten()` call in the python code—we could use the `{NMF}` package for an R replication.

```
# Convert from tidy format to wide format (603 rows x 600 columns)
players_mat <-
  players %>%
  select(player_id, idx, n) %>%
  pivot_wider(names_from = idx, values_from = n) %>%
  select(-player_id) %>%
  as.matrix()

comps <- 30L
W <- NMF::nmf(NMF::rmatrix(players_mat), rank = comps, seed = 0, method
= 'Frobenius')
```

However, I found that the results weren't all that comparable to the python results. (Perhaps I needed to define the arguments in a different manner.) So why not use `{reticulate}` and call the `sklearn.decomposition.NMF()` function to make sure that we exactly emulate the python decomposition?

```
sklearn <- reticulate::import('sklearn')
# Won't work if `n_components` aren't explicitly defined as integers!
model <- sklearn$decomposition$NMF(n_components = comps, init =
'random', random_state = 0L)
W <- model$fit_transform(players_mat)
```

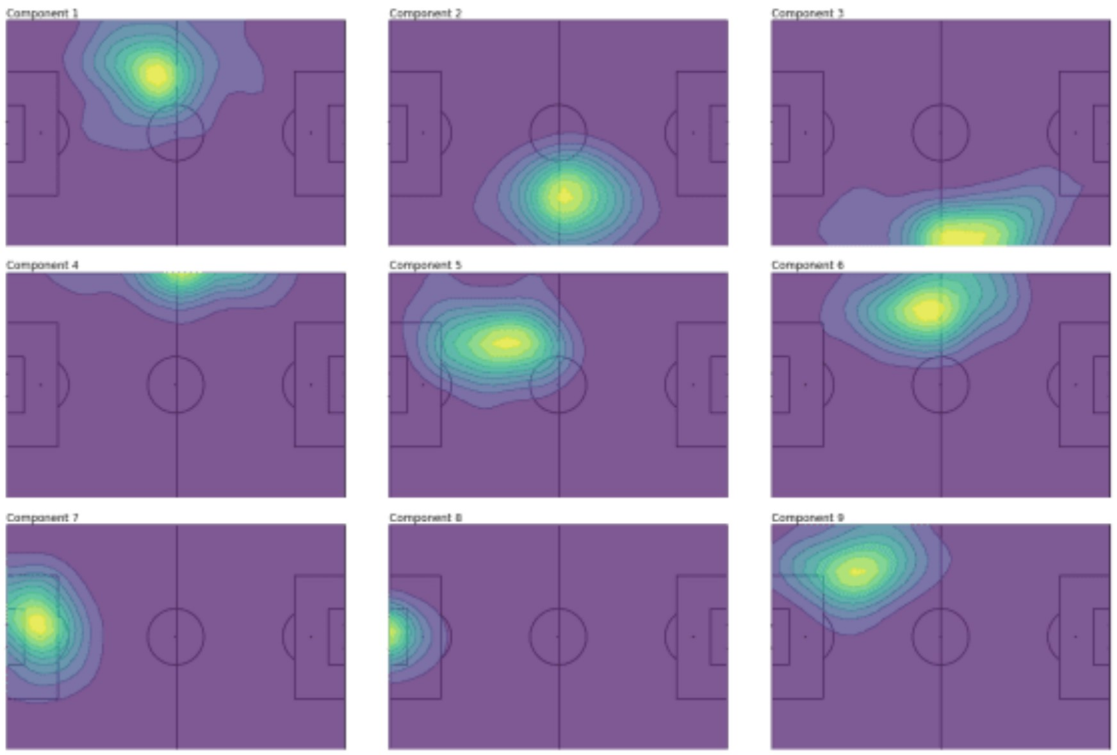
The result includes 30 20x30 matrices—one 30x20 `x`-`y` matrix for each of the 30 components (`comps`). We have some wrangling left to do to gain anything meaningful from this NNMF procedure, but we have something to work with!

Gaussian Smoothing with `{spatstat}`

The last thing to do is to post-process the NNMF results and, of course, make pretty plots. The python plotting is pretty standard `matplotlib`, with the exception of the Gaussian smoothing performed on each component's matrix `model.component_` in the loop to make sub-plots.

```
from scipy.ndimage import gaussian_filter

for i in range(9):
    # ... Excerpted
    z = np.rot90(gaussian_filter(model.components_[i].reshape(x_scale,
y_scale), sigma=1.5), 1)
    # ... Excerpted
```

The first 9 smoothed component matrices come out looking like this. [8]



There's a couple of steps involved to do the same thing in R.

1. First, we'll convert the components matrices to a tidy format, `decomp_tidy`

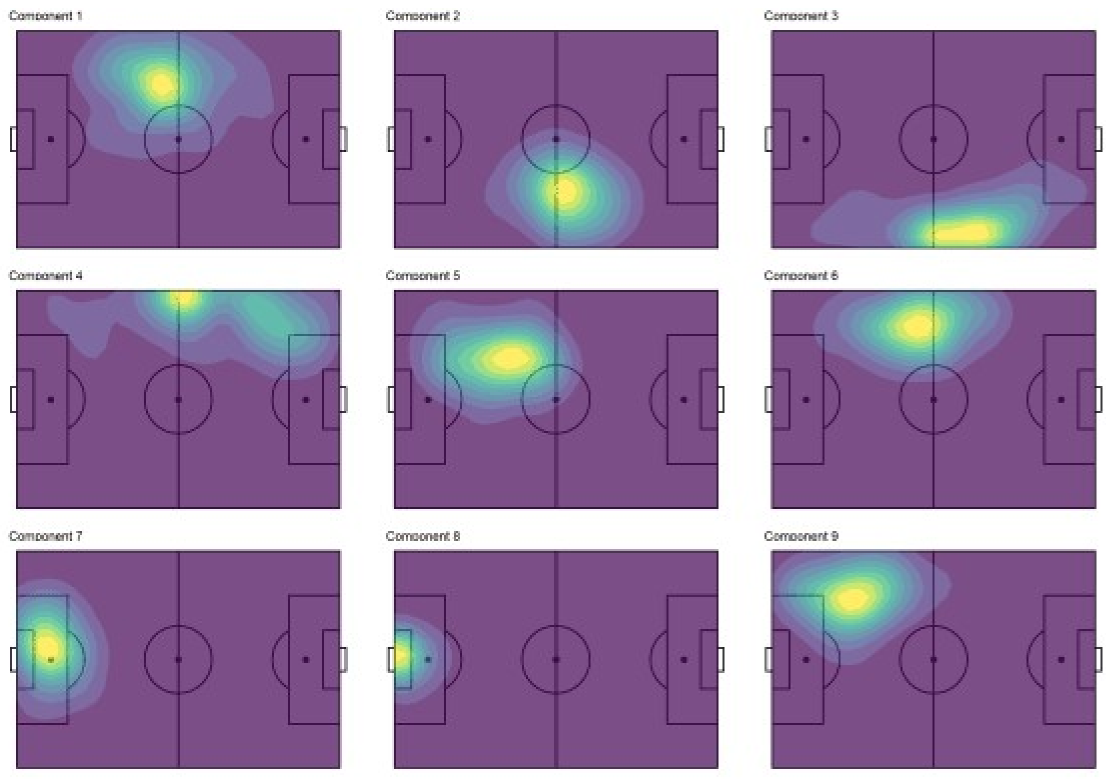
2. Second, we'll join our tidied components matrices with our tidy grid of cells, `grid_xy_yards`, and convert our `x` and `y` bins to integers in preparation of the matrix operation performed in the subsequent step.

3. Lastly, we'll perform the Gaussian smoothing on nested data frames with a custom function, `smoothen_dimension`, that wraps `spatstat::blur()`. This function also maps `idx` back to field positions (in meters instead of yards) using the supplementary `grid_xy_rev_m`[9] data frame (which is a lot like `grid_xy_yards`)

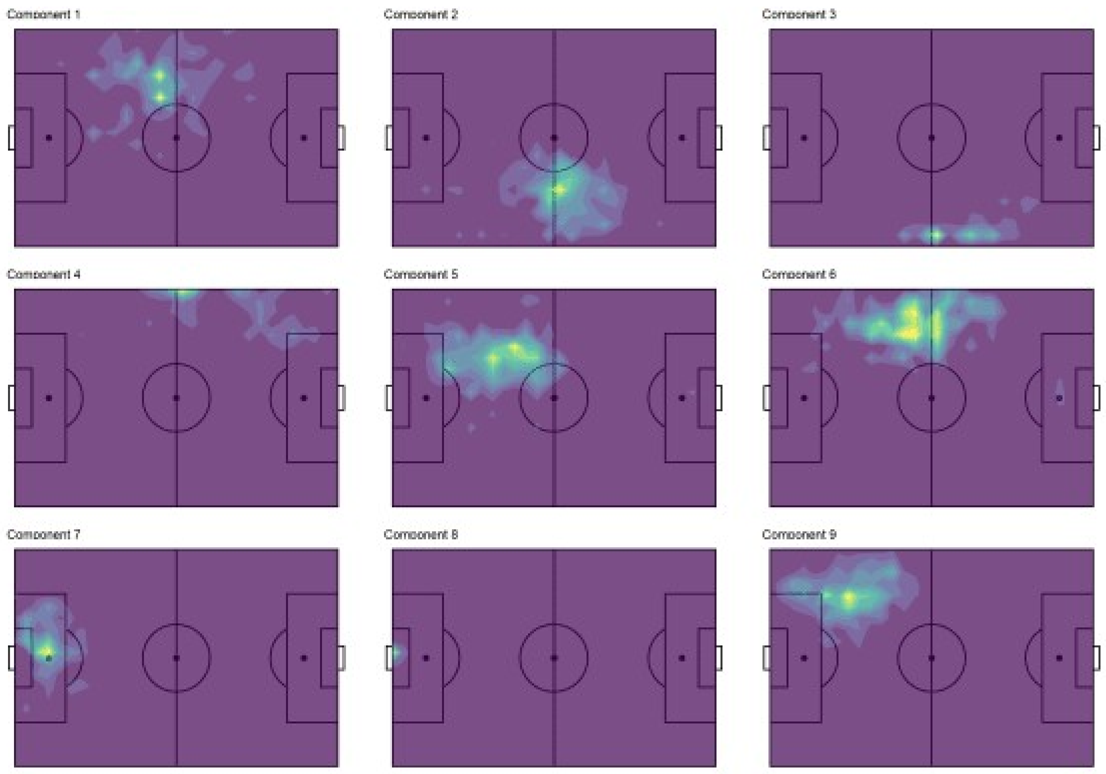
```
# 1
decomp_tidy <-
  model$components_ %>%
  as_tibble() %>%
  # "Un-tidy" tibble with 30 rows (one for each dimension) and 600
columns (one for every `idx`)
  mutate(dimension = row_number()) %>%
  # Convert to a tidy tibble with dimensions * x * y rows (30 * 30 * 20
= 18,000)
  pivot_longer(-dimension, names_to = 'idx', values_to = 'value') %>%
  # The columns from the matrix are named `V1`, `V2`, ... `V600` by
default, so convert them to an integer that can be joined on.
  mutate(across(idx, ~str_remove(.x, '^V') %>% as.integer()))

# 2
decomp <-
  decomp_tidy %>%
  # Join on our grid of x-y pairs.
  inner_join(
    # Using `dense_rank` because we need indexes here (i.e. 1, 2, ...,
30 instead of 0, 4.1, 8.2, ..., 120 for `x`).
    grid_xy_yards %>%
      select(idx, x, y) %>%
      mutate(across(c(x, y), dense_rank))
  )

# 3
smoothen_component <- function(.data, ...) {
  mat <-
    .data %>%
    select(x, y, value) %>%
    pivot_wider(names_from = x, values_from = value) %>%
    select(-y) %>%
    as.matrix()

  mat_smoothed <-
    mat %>%
    spatstat::as.im() %>%
    # Pass `sigma` in here.
    spatstat::blur(...) %>%
    # Could use `spatstat::as.data.frame.im()`, but it converts directly
to x,y,value triplet of columns, which is not the format I want.
    pluck('v')

  res <-
    mat_smoothed %>%
    # Convert 20x30 y-x matrix to tidy format with 20*30 rows.
    as_tibble() %>%
    mutate(y = row_number()) %>%
    pivot_longer(-y, names_to = 'x', values_to = 'value') %>%
      # The columns from the matrix are named `V1`, `V2`, ... `V30` by
default, so convert them to an integer that can be joined on.
    mutate(across(x, ~str_remove(.x, '^V') %>% as.integer())) %>%
    arrange(x, y) %>%
    # "Re-index" rows with `idx`, ranging from 1 to 600.
    mutate(idx = row_number()) %>%
    select(-x, -y) %>%
    # Convert `x` and `y` indexes (i.e. 1, 2, 3, ..., to meters and
flip the y-axis).
    inner_join(grid_xy_rev_m) %>%
    # Re-scale smoothed values to 0-1 range.
    mutate(frac = (value - min(value)) / (max(value) - min(value))) %>%
    ungroup()
  res
}

decomp_smooth <-
  decomp %>%
  nest(data = -c(dimension)) %>%
  # `sigma` passed into `...` of `smoothen_component()`. (`data` passed
as first argument.)
```

```
  mutate(data = map(data, smoothen_component, sigma = 1.5)) %>%
  unnest(data)
decomp_smooth

# # A tibble: 18,000 x 8
#    dimension    value   idx      x      y next_y next_x     frac
#
#  1         1 0.002191     1      0 68      4.211  4.138 0.004569
#  2         1 0.004843     2      0 64.42  8.421  4.138 0.01064
#  3         1 0.008334     3      0 60.84 12.63   4.138 0.01863
#  4         1 0.01130      4      0 57.26 16.84   4.138 0.02541
#  5         1 0.01258      5      0 53.68 21.05   4.138 0.02834
#  6         1 0.01208      6      0 50.11 25.26   4.138 0.02719
#  7         1 0.01033      7      0 46.53 29.47   4.138 0.02319
#  8         1 0.008165     8      0 42.95 33.68   4.138 0.01824
#  9         1 0.006156     9      0 39.37 37.89   4.138 0.01364
# 10         1 0.004425    10      0 35.79 42.11   4.138 0.009680
# # ... with 17,990 more rows
```

With the data in the proper format, the plotting is pretty straightforward `{ggplot2}` code (so it’s excerpted).



Viola! I would say that our R version of the python plot is very comparable (just by visual inspection). Note that we could achieve a similar visual profile without the smoothing—see below—but the smoothing undoubtedly makes pattern detection a little less ambiguous.



From the smoothed contours, we can discern several different player profiles (in terms of positioning).

- Components 1, 5, 9: left back
- Components 2: right midfielder
- Component 3: attacking right midfielder
- Component 4: wide left midfielder
- Component 6: central left midfielder
- Components 7, 8: goalkeeper

The redundancy with left back and goalkeeper is not ideal. That's certainly something we could fine tune with more experimentation with components. Anyways, the point of this post wasn't so much about the insights that could be gained (although that's ultimately what stakeholders would be interested in if this were a "real" analysis).

Conclusion

Translating python code can be challenging, throwing us off from our typical workflow (for me, being `{tidyverse}`-centric). But hopefully one can see the value in "doing whatever it takes", even if it means using "non-tidy" R functions (e.g. `{data.table}`, matrices, etc.) or a different language altogether.