Football data analysis
An example with the Countr package.

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Abstract

The main motivation to develop the Countr by the authors was to create an alternative to the Poisson model to fit the number of goals scored by a team in a football match. Despite its clear limitations, the Poisson model was systematically used in the literature perhaps due to its simplicity. We briefly explain in this document why the renewal-count models should be preferred for football data. We hope that the development of the Countr package will encourage more data analyst to use renewal-count models, especially when investigating sports data.

This vignette is part of package Countr (see Kharrat et al., 2019).

Before starting our analysis, we need to load the useful packages. On top of Countr, the dplyr package (Wickham and Francois, 2016) will be used:

\begin{verbatim}
library(Countr)
library(dplyr)
\end{verbatim}

1 Motivation

As discussed in length in Kharrat (2016, Chapter 4) or more briefly in Boshnakov et al. (2017), the main issue with the Poisson model when modelling the goals scored by a team in football is that the hazard function (the instant probability of scoring) remains constant for every time unit (minutes say in football). However, empirical studies showed that this is rather questionable as goals are more likely to be scored at the end of each half because of players tiredness, ... see for example Dixon and Robinson (1998, Figure 1).

This flexibility is allowed by renewal-count model when selecting the appropriate interval-arrival times density. One strategy to select this density is discussed in Kharrat (2016, Chapter 4) and is beyond the scope of this document. Here we simply say that the weibull density seemed to provide the best fit and will be used in the rest of this study.

2 Comparing the Poisson and weibull models

Our aim here is not to conduct an extensive analysis of the data but simply to highlight the improvement introduced by the weibull-count model compared to Poisson. For an example with extensive analysis, see the fertility data example.
2.1 Data

The football dataset is shipped with the Countr package and can be loaded in the usual way by a call to the data() function:

```r
data(football)
table(football$awayTeamGoals)
```

The data contains the final scores of the 1104 matches (380 matches per season) played in English Premier League from seasons 2009/2010 to season 2016/2017. The game data and home and away team names are also provided. We focus in this study on the goals scored by the away team.

The Poisson model can be fitted in a standard way by a call to glm() with the family argument set to poisson. The weibull-count-model is fitted by a call to renewalCount() with dist = "weibull". The model considered here is intercept only (no covariates specified).

```r
away_poiss <- glm(formula = awayTeamGoals ~ 1, family = poisson, data = football)
away_wei <- renewalCount(formula = awayTeamGoals ~ 1, data = football,
dist = "weibull", weiMethod = "conv_dePril",
computeHessian = FALSE,
control = renewal.control(trace = 0,
method = "nlminb")
)
```

2.2 Visual inspection

We start by investigating the distribution of goals and the associated fitted probabilities induced by both models. The away team rarely scores more than 4 goals and hence we decided to aggregate counts of 5 and larger. This can be done in the usual way by specifying the break argument.

```r
breaks_ <- 0:5
pears <- compareToGLM(poisson_model = away_poiss,
breaks = breaks_, weibull = away_wei)
```

```r
frequency_plot(pears$Counts, pears$Actual,
dplyr::select(pears, contains("_predicted")),
colours = c("grey", "blue", "green", "black")
)
As expected, the most likely outcome for away goals is 0, 1 and to some extent 2. Eyeballing, the weibull-count model is a clear improvement over the Poisson model. Even of the other count values, it seems that the weibull-count model still slightly outperforms the Poisson alternative. These findings will be confirmed formally in the next sections by running formal statistical tests.

2.3 Likelihood ratio test

The Poisson model is a special case of the weibull-count with shape parameter set to 1. Therefore, the two models are nested and the likelihood ratio can be used to discriminate between them as explained in Cameron and Trivedi (2013, Chapter 6):

```r
library(lmtest)
lr <- lrtest(away_poiss, away_wei)

lr
```

Likelihood ratio test

Model 1: awayTeamGoals ~ 1
Model 2: awayTeamGoals ~ 1

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>LogLik</th>
<th>Chisq</th>
<th>Pr(&gt;Chisq)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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<td>-4364.3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>-4350.1</td>
<td>28.484</td>
<td>9.448e-08 ***</td>
</tr>
</tbody>
</table>

---

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The likelihood ratio test null hypothesis (both model present equal fits) is rejected at any convenience level and confirms that the Weibull addition induced by the shape parameter does improve the fitting.

### 2.4 Chi-square goodness-of-fit test

Finally, a formal chi-square goodness-of-fit test has been described in in Cameron and Trivedi (2013, Section 5.3.4) and implemented in Countr::chiSq_gof(). It can be used to judge how well the weibull model describes the data:

```r
gof_wei <- chiSq_gof(away_wei, breaks = breaks_)
gof_pois <- chiSq_gof(away_poiss, breaks = breaks_)
print(gof_wei)
```

chi-square goodness-of-fit test

<table>
<thead>
<tr>
<th>Cells considered</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>&gt;= 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF</td>
<td>Chisq</td>
<td>Pr(&gt;Chisq)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>5</td>
<td>7.1479</td>
<td>0.2099</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The test concludes that the null hypothesis cannot be rejected (and hence that the weibull-count model describes the data well). Note that the same statistic computed for the Poisson model yields a value `formatC(gof_pois[, 2])` compared to $\chi^2(5)$ critical value of 9.24 at 5%. The Poisson model is hence strongly rejected.

We conclude this analysis by saving the work space to avoid re-running the computation in future exportation of the document:

```r
save.image()
```

### References


