

Survival Analysis Project

Luciano Costa Marius Akre Stefanny Peraza Valery Zuñiga

Introduction

For this analysis we wanted to work with a dataset different from health issues, and try to apply what we learned to other areas. In this case we took data related to animals in a shelter and their adoption¹. It should be mentioned that the data frame does not contain the date of entry of the animals to the shelter, but the date of birth, so we had to adapt to the available data, since we really wanted to apply the analysis in another area, and therefore the results will be more a function of the age that an animal has before it is adopted, given that it is in the shelter.

In terms of survival analysis, the objective of this project is to determine the “risk” that pets in an animal shelter have of being adopted , based on different characteristics that are available in the chosen data set. It is worth mentioning that the data contains different outcomes for the animals: adoption, transfer, or no outcome. However, in our case we will only use a dichotomous output indicating whether it was adopted or not. The data ends on February 1st, 2018, after which date it is not known what happens to the animals.

We will also analyze how the following variables, when possible to include them, may influence the adoption or non-adoption of the animals.

Data dictionary:

- id: unique id for each animal
- age_upon_outcome: age of the animal when the outcome was determined
- animal_type: cat, dog, or ... something else
- breed: breed of the animal
- color: color of the animal
- date_of_birth: date of birth of the animal
- datetime: date and time when the outcome was determined
- name: name of the animal
- outcome_type: there are three possible outcomes: adoption, transfer, no outcome (euthanized, died)

¹Data taken from [Kaggle](#). We only use the `train.csv` data.

- sex: sex of the animal
- spay_neuter: whether the animal was spayed or neutered: intact or fixed

Data preparation

EDA

At a quick glance at the data, we observe that in the case of categorical variables we will have to make modifications in order to be able to work with them, for example in the case of breed, color and name we have too many different types or levels, which would make it impossible to use them all. The variable name, on the other hand, has a significant number of null values.

Table 1: Data summary

Name	raw_data
Number of rows	54408
Number of columns	11
Column type frequency:	
character	8
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
age_upon_outcome	0	1.0	4	9	0	46	0
animal_type	0	1.0	3	9	0	5	0
breed	0	1.0	3	54	0	1812	0
color	0	1.0	3	27	0	475	0
name	16433	0.7	1	12	0	11826	0
outcome_type	0	1.0	8	10	0	3	0
sex	0	1.0	4	7	0	3	0
spay_neuter	0	1.0	5	7	0	3	0

In order to be able to work with this data, these will be the first modifications we will make:

- Since the variables `breed` and `color` have too many different combinations, we will remove breed from our data, and work a bit in a color categorization that allows us to use it.

- We have names for 69.8% of the animals, so in order to use it, we will create a dummy variable `has_name`, a variable that indicates that if there is a name or not.
- Also, we decided to treat the `animal_type` and `sex` variables as factors, so they can enter the model like that.
- For the duration data, we have the `age_upon_outcome` which is the difference between `date_of_birth` and `datetime` but this is not numeric, so we create our own variable `time_to_outcome`.
- We will work with `spay_neuter` as our grouping variable. We would like to verify if there are differences in adoption times if the animal is spay neutered or not. If we have an `Unknown` in the variable, we will remove the corresponding records as we do not know the information. Furthermore we do not have the sex of those records neither and most of them have early no outcome (i.e. early euthanized, died) in the range of `time_to_outcome` values. Therefore they may impact significantly our analyses while we do not have any information on their `sex` and `spay_neuter` to make reliable interpretation. Those `Unknown` records represent 8% of the dataset and we still keep almost 50 000 records after these removals.²
- We keep `animal_type` (`Unknown` `sex` and `spay_neuter` have been removed as described above). The only modification in this case will be that for `animal_type`, since there are only 5 observations in Livestock and it remains only 90 observations in Bird after the removals, we will join these categories to Other. In summary we have a majority of dogs and cats, where 48% are female and 52% male. In the case of spaying and neutering, we have 74% fixed and 26% classified intact.

<code>animal_type</code>	n	prop
Cat	18764	37.5
Dog	30669	61.4
Other	543	1.1

<code>sex</code>	n	prop
Female	23931	47.9
Male	26045	52.1

<code>spay_neuter</code>	n	prop
Fixed	37013	74.1

²The cross tables for the variables `sex`, `animal_type`, `has_name`, `color_count`, `color_shade_intens`, details on removed `Unknown` records, details on Kaplan-Meyer and Fleming-harrington estimators : see appendix 1.

Intact	12963	25.9
--------	-------	------

In the case of the output variable, where the possibilities are adopted or not, we will create a new variable `outcome` for which we take 1 for adoption and 0 for no adoption.

outcome	n	prop
0	16797	33.6
1	33179	66.4

- Since we got some negative values for our variable `time_to_outcome`, which makes no sense as the `date_of_birth` should come before the outcome (unless some very rare or demanded type of pets get adopted before they are born), we will remove these five observations (5).
- **Method to take into account the colors:** We have too many colors but we expect this feature to have a significant impact on the choice to adopt or not. So, we build some subcategories in order to reduce the number of possible values and be able to take into account the embedded information. We try two kind of grouping : by number of colors and by intensity of shade.

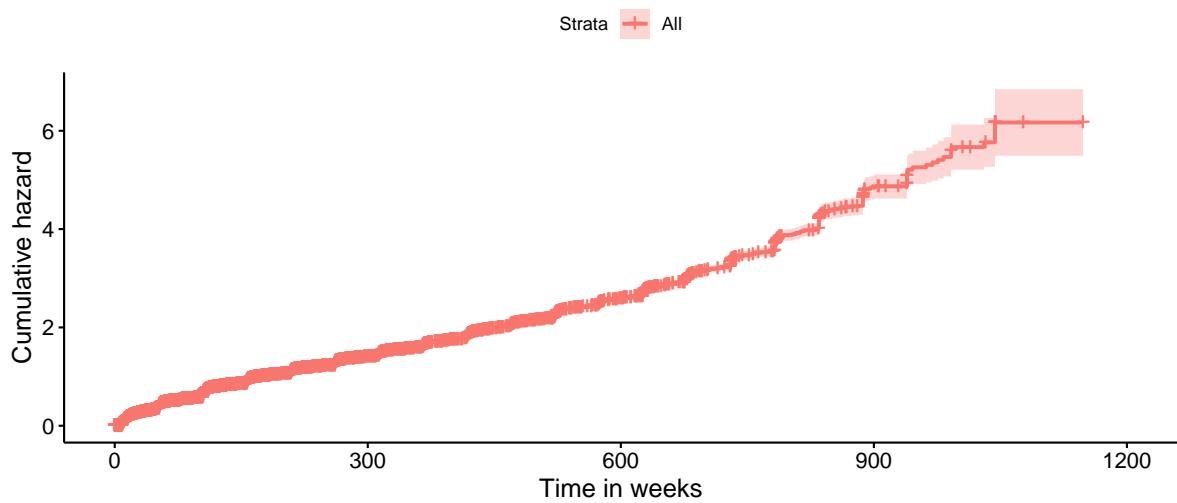
Now we chose the variable we will use as a clean data, check that they have the desired formats and do some previous analysis on the variables. The final total observation is 49,972.

Within the animals, there is not a difference that seems to be important according to sex, at least not proportionally. In the case of animals with names, more than 77% have been adopted against 34% in the case of those without names. Something similar happens with the animals that have been spayed or neutered, the proportion of adopted animals in this case exceeds 80%, while in the group of those that have not undergone surgery, the percentage of adopted animals is barely 26%. Lastly, dogs are not only the largest number of animals but also have the highest adoption rate, while among cats there is practically half and half between adopted and non-adopted, and among others type there is the lower adoption rate (36%). By looking at the distribution of the enriched dataset, it seems that having more number of colors increase the chance of adoption.³

Statistical Analysis

The next graph is the survival curve and the cumulative hazard function, for this data:

³The cross tables for the variables `sex`, `animal_type`, `has_name`, `color_count`, `color_shade_intens`, details on removed `Unknown` records, details on Kaplan-Meyer and Fleming-harrington estimators : see appendix 1.



Nonparametric methods for censored data

Using the Kaplan-Meyer estimator (KM) methodology we can see that the median survival time is 106 weeks (in this particular case the time from birth to adoption, and it's about 2 years). If we estimate the probability of not being adopted when the animal is one year old, we see that this value is 70.8% (for further information look at Appendix 2). We get similar results with Fleming–Harrington estimator. We will focus on the KM estimator in the following sections then.⁴

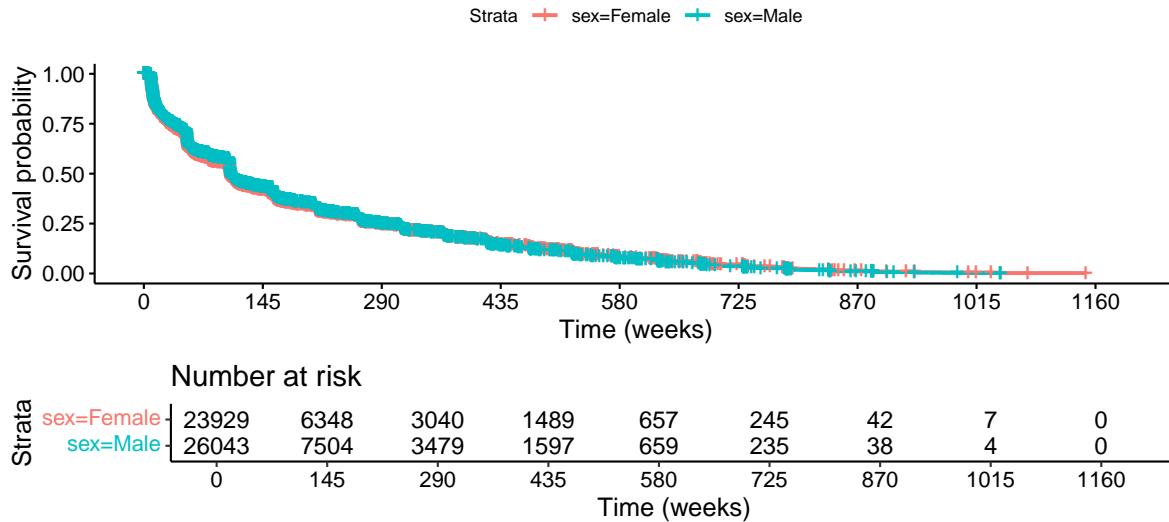
Nonparametric comparison of groups

Nonparametric comparison of 2 groups

Even if we do not have two groups in the dataset, for example with different treatments, we want to use this technique to analyze, for example, whether or not being part of the females group contributes to being adopted more quickly. So, the null hypothesis or question that we are going to try to answer is if the survival curves generated for the groups are the same, and the alternative hypothesis is that they are different. We will perform the logrank test.

⁴The cross tables for the variables `sex`, `animal_type`, `has_name`, `color_count`, `color_shade_intens`, details on removed `Unknown` records, details on Kaplan-Meyer and Fleming-harrington estimators : see appendix 1.

Kaplan–Meier estimator for Variable sex



```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ sex, data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
sex=Female	23929	15767	105	105	106
sex=Male	26043	17410	106	106	107

Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ sex, data = data)
```

	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
sex=Female	23929	15767	15617	1.44	2.73
sex=Male	26043	17410	17560	1.28	2.73

Chisq= 2.7 on 1 degrees of freedom, p= 0.1

As we can see both in the graph and in the logrank test, there is no statistical evidence to reject the null hypothesis of equality between Female and Male survival curves. This is consistent with our first basic analyses above on the cross tables. Hence, the sex does not make a statistical significant difference on the survival curves and the probabilities to be adopted.

In the `has_name` we get a difference between the curves and it looks like the adoption goes faster for those animal that don't have a name and are aged less than 2 years old at the moment of adoption. It is the over way round for the older pets. Surprisingly, the logrank test accepts H0 ($p > 5\% \Rightarrow$ cures are STATISTICALLY similar). This remind us that sometimes, the

analysis should not be based only on the p-value (like some scientists thoughts nowadays). we can also look at other information that we have before communicating a final conclusion.

We can perform the same process with other categorical variables⁵ : - `animal_type` : at least one of the 3 (crossing) survival curves looks different and H0 is rejected : at least one is statistically different. - `spay_neuter` : the 2 survival curves look different and H0 is rejected : they are statistically different. - `color_count` : the 3 survival curves look closed BUT H0 is rejected : AT LEAST 1 is STATISTICALLY different. - `color_shade_intens` : AT LEAST one of the 4 (crossing) survival curves looks different BUT H0 is accepted : they are STATISTICALLY similar.

Nonparametric comparison of more than 2 groups

We could also compare survival between 2 groups controlling for potentially confounding. For example, we could expect that `spay_neuter` feature may have an higher impact on the probability to be adopted for a Female as she is the one who carry their young.

By using stratification on `spay_neuter`, we can indeed see that for Intact `spay_neuter` groups the medians and the survival curves are less close from each other. Furthermore, we can see that the `sex=Female, strata(spay_neuter)=Intact` group has the highest probability (i.e. the lowest chance to be adopted) while it is the other way round within the “Fixed group” : Male are the lowest chance to be adopted. However, these results should be taken with cautious as the stratified logrank test display a p value = threshold = 5% (probably due to the fact that they are more pets in the Fixed group where it looks like there are less differences between Female and Male).⁶

Semi-parametric Cox regression

So far, we have consider non parametric models, i.e. without any assumption on the distribution of the data. Let's have a look on a semi-parametric model now (Cox model), where we will additionally assume some distributions on the covariates but without any type of assumption on the component ratio of hazard.

Call:

```
coxph(formula = Surv(time_to_outcome, outcome) ~ animal_type +  
    has_name + sex + spay_neuter + color_count + color_shade_intens,  
    data = data)  
  
n= 49972, number of events= 33177
```

⁵for further information look at Appendix 2

⁶for further information look at Appendix 2

	coef	exp(coef)	se(coef)	z	Pr(> z)						
animal_typeCat	0.23545	1.26548	0.07279	3.235	0.001217 **						
animal_typeDog	-0.01486	0.98525	0.07232	-0.205	0.837231						
has_nameTRUE	-0.10005	0.90479	0.01749	-5.720	1.07e-08 ***						
sexMale	-0.01872	0.98145	0.01110	-1.688	0.091487 .						
spay_neuterIntact	-0.66741	0.51303	0.01899	-35.153	< 2e-16 ***						
color_count2	0.10392	1.10951	0.01488	6.985	2.84e-12 ***						
color_count3	0.02813	1.02853	0.03509	0.802	0.422733						
color_shade_intensDark	0.12966	1.13844	0.03378	3.839	0.000124 ***						
color_shade_intensLight	0.09097	1.09524	0.03374	2.696	0.007015 **						
color_shade_intensMedium	0.11213	1.11866	0.03271	3.428	0.000607 ***						

Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1
	exp(coef)	exp(-coef)	lower .95	upper .95							
animal_typeCat	1.2655	0.7902	1.0972	1.4595							
animal_typeDog	0.9853	1.0150	0.8550	1.1353							
has_nameTRUE	0.9048	1.1052	0.8743	0.9363							
sexMale	0.9814	1.0189	0.9603	1.0030							
spay_neuterIntact	0.5130	1.9492	0.4943	0.5325							
color_count2	1.1095	0.9013	1.0776	1.1423							
color_count3	1.0285	0.9723	0.9602	1.1018							
color_shade_intensDark	1.1384	0.8784	1.0655	1.2164							
color_shade_intensLight	1.0952	0.9130	1.0251	1.1701							
color_shade_intensMedium	1.1187	0.8939	1.0492	1.1927							
Concordance=	0.615	(se = 0.002)									
Likelihood ratio test=	1936	on 10 df,	p=<2e-16								
Wald test	= 1707	on 10 df,	p=<2e-16								
Score (logrank) test =	1752	on 10 df,	p=<2e-16								

The Cox model shows that 3 variables are not statistically significant (animal_typeDog, sexMale, color_count3), meaning those categories are not significantly different from the base category.

About the colors, known shade intensity makes statistically a significant difference to be adopted faster comparing to pets having an Unknown intensity (~ 10% more chances). Having 1 or 3 colors does not seem to make a difference but, having 2 colors comparing to 1, would increase the chances to be adopted by +10% to +12%. Having 2 colors makes statistically a significant difference comparing to having 1 color, by increasing the chance by 10% to be adopted.

Automatic model selection based on AIC

However, using all these covariates may not be the best choice to get the best model (from the AIC criteria point of view for example). By applying an automatic model selection based on AIC we get the conclusion that we should keep all the covariates in addition to an intercept, to have the best model (highest AIC).⁷

Prediction

A model can be used in two main ways : to analyze or study interactions between the covariates like we did or to predict. Let's see our predicted survival proportion for the whole data. We can see that the estimated probability of not being adopted within 1 year is slightly higher (71.4%) than the one of KM model (70.8%) but they remain close.

Now, we can also do a prediction and verify how this survival changes depending on the **spay_neuter** variable for example.

As expected, animal which were spay neutered (Fixed), have shorter survival time, that means they were adopted faster.

Model diagnostics

After getting these model, we should verify the assumptions of these model. Let's do it for the Cox model for example.

Martingale residuals

The residuals are not so well formed (not around 0). There are many outliers. Schoenfeld residuals are far from zero and not in the boundaries. Furthermore, the plot of proportionality of the hazards does not look good : H0 ($\beta = \beta(t)$) is rejected. We can try stratification or truncate to fix that. However, stratification did not make the assumption validation better⁸.

The model would not be validated from a theoretical point of view, although the results of our previous analyses of the models seem very consistent to the behaviors that we could have expected a priori. Indeed, conclusions of the analyses seem also consistent to what we may observe in reality for pet adoption. We could conclude by take all previous results with cautious and also remind this common aphorism: “All models are wrong, but some are useful”, George E. P. Box

⁷for further information look at Appendix 3

⁸for further information look at Appendix 4

Appendix

Appendix 1: cross tables

	0	1	Total
has_name			
FALSE	7,984 (66%)	4,141 (34%)	12,125 (100%)
TRUE	8,811 (23%)	29,036 (77%)	37,847 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

	0	1	Total
sex			
Female	8,162 (34%)	15,767 (66%)	23,929 (100%)
Male	8,633 (33%)	17,410 (67%)	26,043 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

	0	1	Total
spay_neuter			
Fixed	7,146 (19%)	29,865 (81%)	37,011 (100%)
Intact	9,649 (74%)	3,312 (26%)	12,961 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

	0	1	Total
animal_type			
Other	346 (64%)	197 (36%)	543 (100%)
Cat	8,799 (47%)	9,962 (53%)	18,761 (100%)
Dog	7,650 (25%)	23,018 (75%)	30,668 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

	0	1	Total
color_count			
1	8,462 (39%)	13,254 (61%)	21,716 (100%)
2	7,972 (30%)	18,894 (70%)	26,866 (100%)
3	361 (26%)	1,029 (74%)	1,390 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

	0	1	Total
	0	1	Total
color_shade_intens			
Unknown	1,018 (46%)	1,175 (54%)	2,193 (100%)
Dark	3,033 (36%)	5,441 (64%)	8,474 (100%)
Light	7,726 (31%)	17,236 (69%)	24,962 (100%)
Medium	5,018 (35%)	9,325 (65%)	14,343 (100%)
Total	16,795 (34%)	33,177 (66%)	49,972 (100%)

Cross tables details for Unknown sex (removed from the final dataset), after removing the negative values for our variable `time_to_outcome` (-5).

	Female	Male	Unknown	Total
outcome				
0	8,162 (34%)	8,633 (33%)	4,335 (98%)	21,130 (39%)
1	15,767 (66%)	17,410 (67%)	96 (2%)	33,273 (61%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

	Female	Male	Unknown	Total
animal_type				
Cat	9,476 (40%)	9,285 (36%)	1,796 (41%)	20,557 (38%)
Dog	14,227 (59%)	16,441 (63%)	161 (4%)	30,829 (57%)
Other	226 (1%)	317 (1%)	2,474 (56%)	3,017 (6%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

	Female	Male	Unknown	Total
has_name				
FALSE	5,961 (25%)	6,164 (24%)	4,306 (97%)	16,431 (30%)
TRUE	17,968 (75%)	19,879 (76%)	125 (3%)	37,972 (70%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

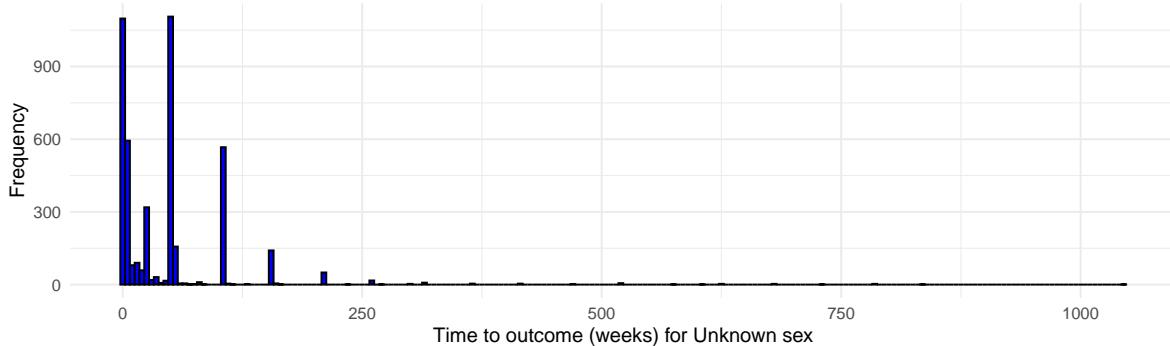
	Female	Male	Unknown	Total
spay_neuter				

	Female	Male	Unknown	Total
Fixed	17,594 (74%)	19,417 (75%)	0 (0%)	37,011 (68%)
Intact	6,335 (26%)	6,626 (25%)	0 (0%)	12,961 (24%)
Unknown	0 (0%)	0 (0%)	4,431 (100%)	4,431 (8%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

	Female	Male	Unknown	Total
color_count				
1	10,962 (46%)	10,754 (41%)	2,782 (63%)	24,498 (45%)
2	12,326 (52%)	14,540 (56%)	1,625 (37%)	28,491 (52%)
3	641 (3%)	749 (3%)	24 (1%)	1,414 (3%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

	Female	Male	Unknown	Total
color_shade_intens				
Dark	4,278 (18%)	4,196 (16%)	652 (15%)	9,126 (17%)
Light	11,449 (48%)	13,513 (52%)	1,101 (25%)	26,063 (48%)
Medium	6,375 (27%)	7,968 (31%)	2,579 (58%)	16,922 (31%)
Unknown	1,827 (8%)	366 (1%)	99 (2%)	2,292 (4%)
Total	23,929 (100%)	26,043 (100%)	4,431 (100%)	54,403 (100%)

Histogram of Values of time_to_outcome in weeks for Unknown sex



Appendix 2: Nonparametric methods

KM and FH methods

Kaplan-Meier and Fleming-harrington estimators

*** Kaplan-Meier estimator ***

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ 1, data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
[1,]	49972	33177	106	106	106

*** Fleming-harrington estimator ***

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ 1, data = data[, -1], type = "fleming-harrington")
```

	n	events	median	0.95LCL	0.95UCL
[1,]	49972	33177	106	106	106

*** stimated probability of not being adopted within 1 year old ***

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ 1, data = data[, -1])
```

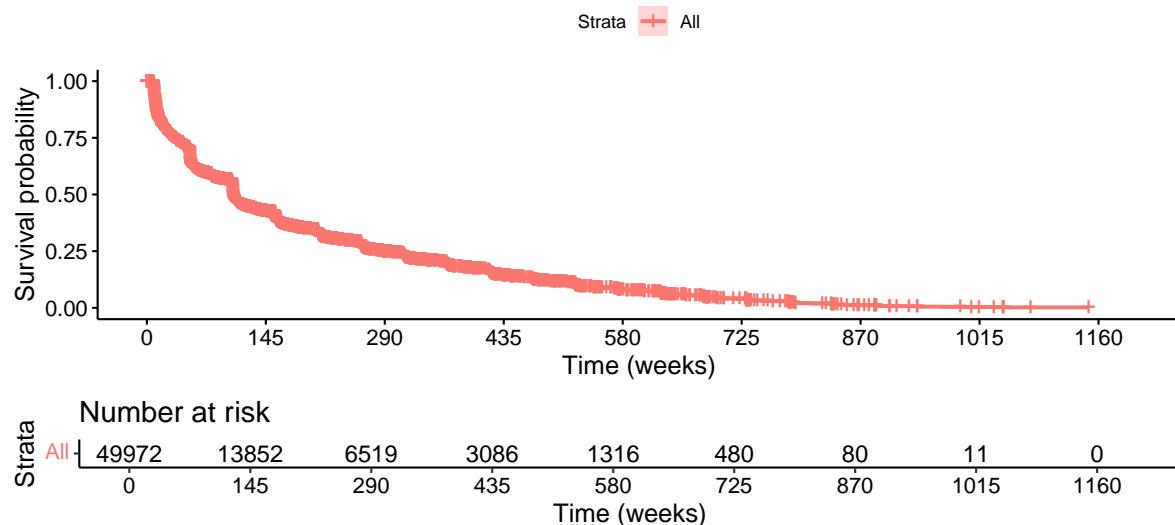
time	n.risk	n.event	survival	std.err	lower	95% CI	upper	95% CI
52	29309	12989	0.708	0.00217	0.703		0.712	

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ 1, data = data[, -1], type = "fleming-harrington")
```

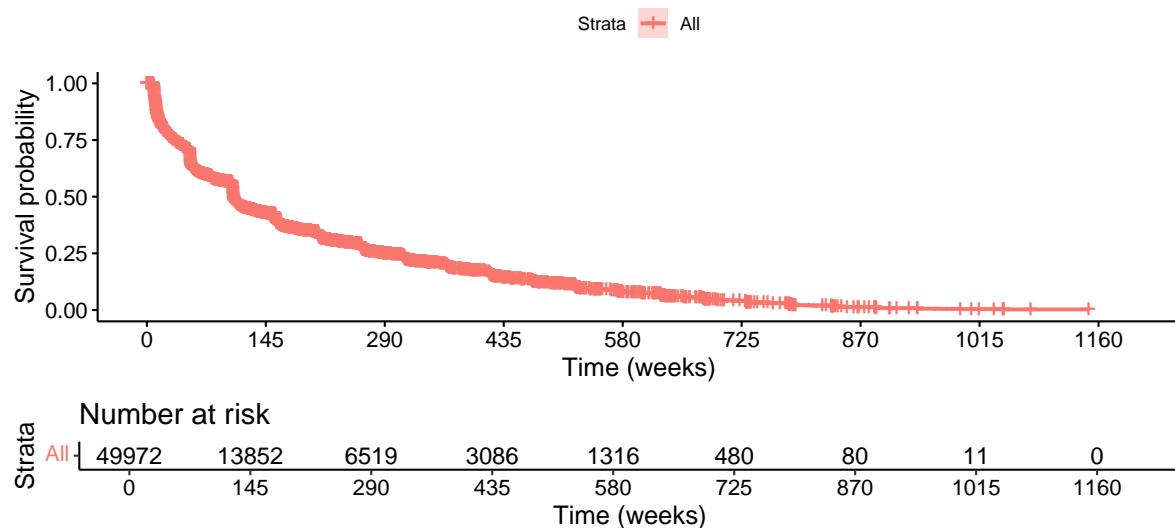
time	n.risk	n.event	survival	std.err	lower	95% CI	upper	95% CI
52	29309	12989	0.708	0.00217	0.704		0.712	

*** Kaplan-Meier and Fleming-Harrington estimators ***

Kaplan–Meier estimator



Fleming–harrington estimator

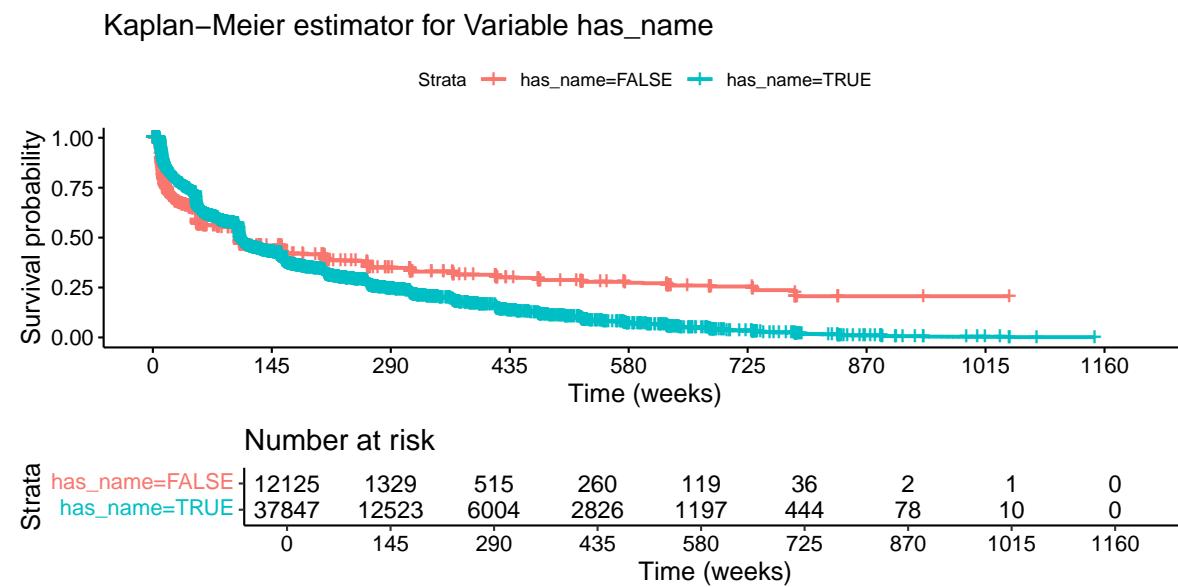


comparison of groups

Variable has_name

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ has_name,
  data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
has_name=FALSE	12125	4141	105	105	105
has_name=TRUE	37847	29036	106	106	107



Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ has_name,
          data = data[, -1])
```

	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
has_name=FALSE	12125	4141	4172	0.2329	0.272
has_name=TRUE	37847	29036	29005	0.0335	0.272

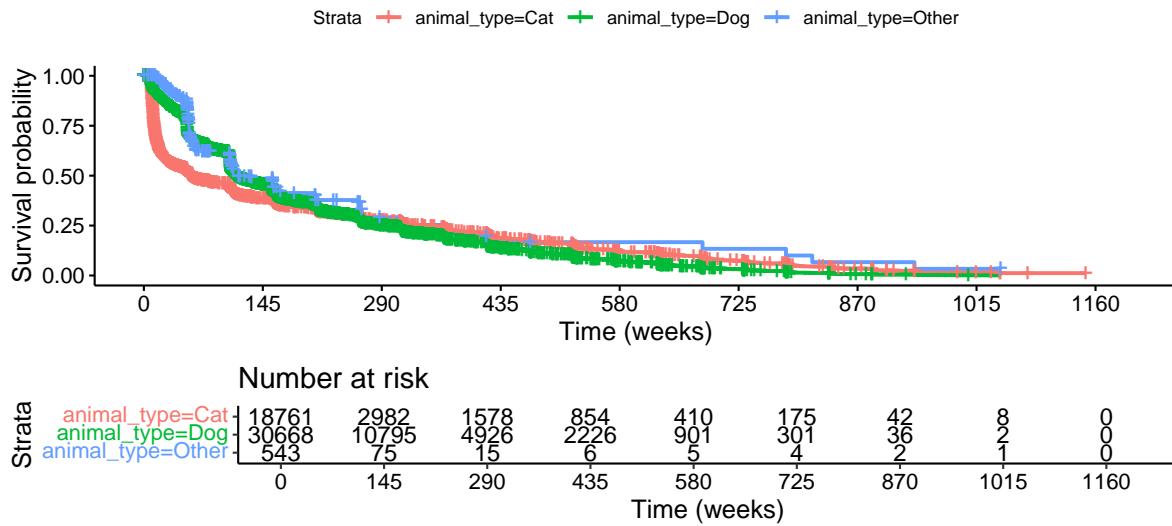
Chisq= 0.3 on 1 degrees of freedom, p= 0.6

Variable animal_type

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ animal_type,
              data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
animal_type=Other	543	197	112.6	107.1	163.0
animal_type=Cat	18761	9962	56.9	54.7	60.3
animal_type=Dog	30668	23018	111.6	110.0	113.9

Kaplan–Meier estimator for Variable animal_type



Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ animal_type,
          data = data)
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
animal_type=Other	543	197	295	32.6	33.2
animal_type=Cat	18761	9962	8437	275.7	375.8
animal_type=Dog	30668	23018	24445	83.3	322.0

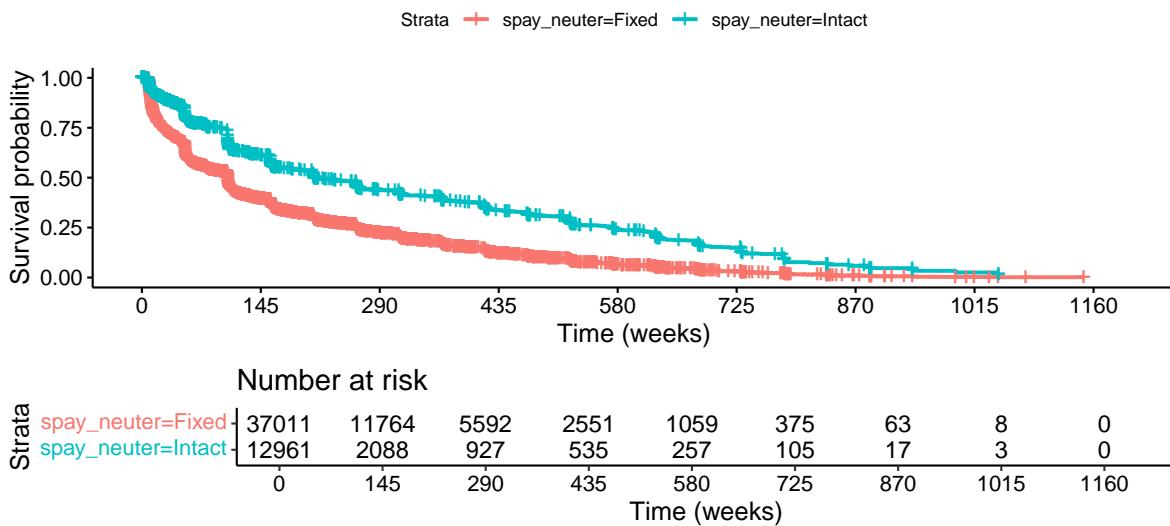
Chisq= 398 on 2 degrees of freedom, p= <2e-16

Variable spay_neuter

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ spay_neuter,
              data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
spay_neuter=Fixed	37011	29865	105	105	105
spay_neuter=Intact	12961	3312	210	209	243

Kaplan–Meier estimator for Variable spay_neuter



Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ spay_neuter,
          data = data[, -1])
```

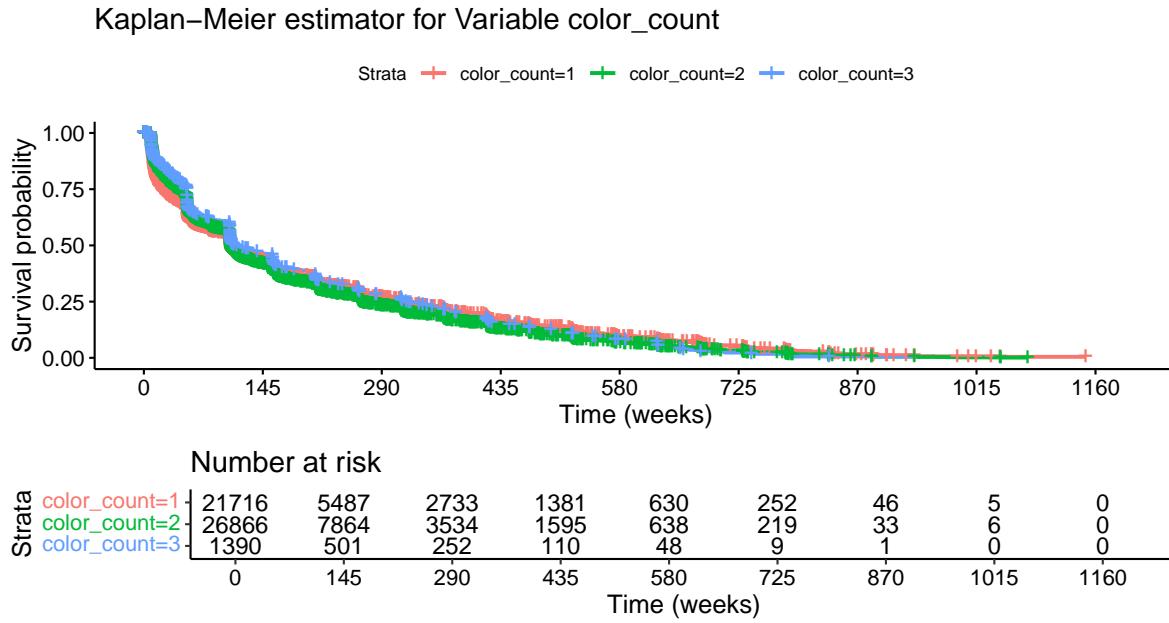
	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
spay_neuter=Fixed	37011	29865	27385	225	1297
spay_neuter=Intact	12961	3312	5792	1062	1297

Chisq= 1297 on 1 degrees of freedom, p= <2e-16

Variable color_count

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ color_count,
              data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
color_count=1	21716	13254	106	105	106
color_count=2	26866	18894	106	106	106
color_count=3	1390	1029	112	106	139



Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ color_count,
          data = data[, -1])
```

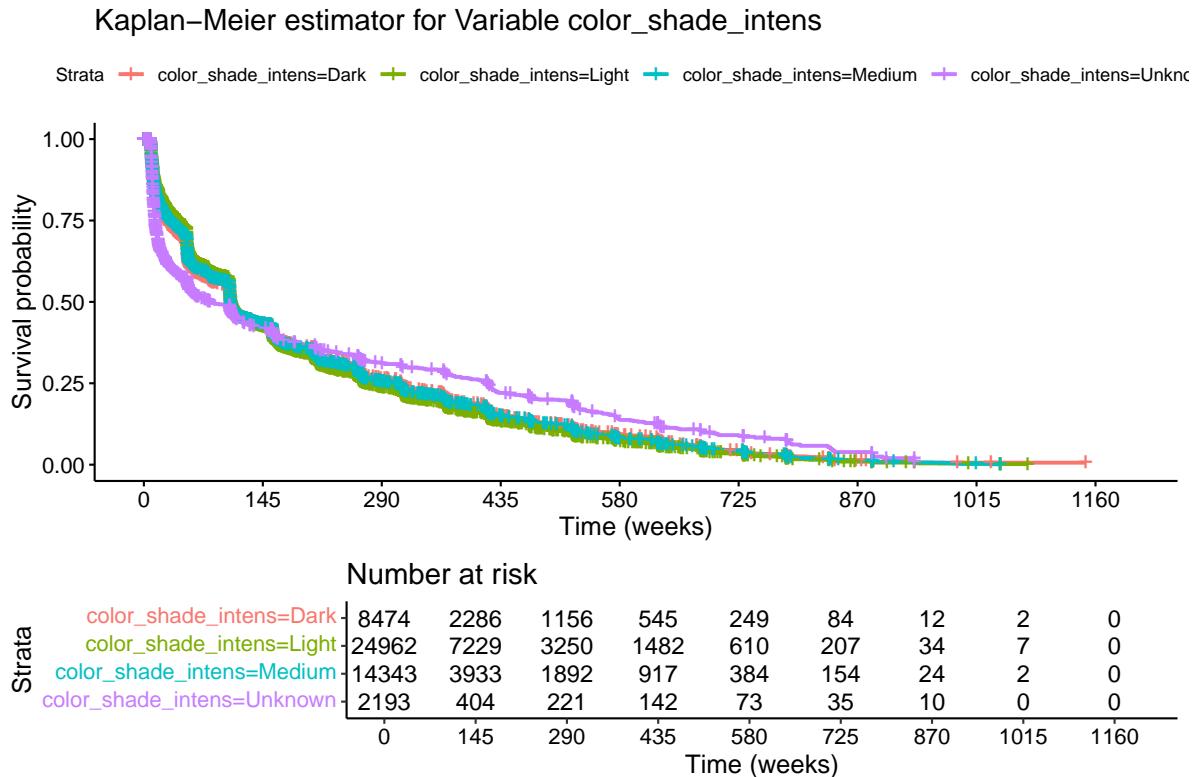
	N	Observed	Expected	$(O-E)^2/E$	$(O-E)^2/V$
color_count=1	21716	13254	13501	4.52	7.69
color_count=2	26866	18894	18579	5.33	12.21
color_count=3	1390	1029	1097	4.17	4.34

Chisq= 14.1 on 2 degrees of freedom, p= 9e-04

Variable color_shade_intens

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ color_shade_intens,
              data = data[, -1])
```

	n	events	median	0.95LCL	0.95UCL
color_shade_intens=Unknown	2193	1175	79.9	62	106
color_shade_intens=Dark	8474	5441	105.4	105	106
color_shade_intens=Light	24962	17236	106.1	106	107
color_shade_intens=Medium	14343	9325	105.6	105	106



Call:

```
survdiff(formula = Surv(time_to_outcome, outcome) ~ color_shade_intens,
          data = data[, -1])
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
color_shade_intens=Unknown	2193	1175	1141	0.991	1.034
color_shade_intens=Dark	8474	5441	5486	0.373	0.450
color_shade_intens=Light	24962	17236	17153	0.405	0.843
color_shade_intens=Medium	14343	9325	9397	0.547	0.767

Chisq= 2.3 on 3 degrees of freedom, p= 0.5

Stratification and comparison of more than 2 groups

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ sex + strata(spay_neuter),
              data = data)
```

	n	events	median	0.95LCL	0.95UCL
sex=Female, strata(spay_neuter)=Fixed	17594	14348	104	104	105

sex=Female, strata(spay_neuter)=Intact	6335	1419	264	261	314
sex=Male, strata(spay_neuter)=Fixed	19417	15517	105	105	105
sex=Male, strata(spay_neuter)=Intact	6626	1893	203	170	209

Call:

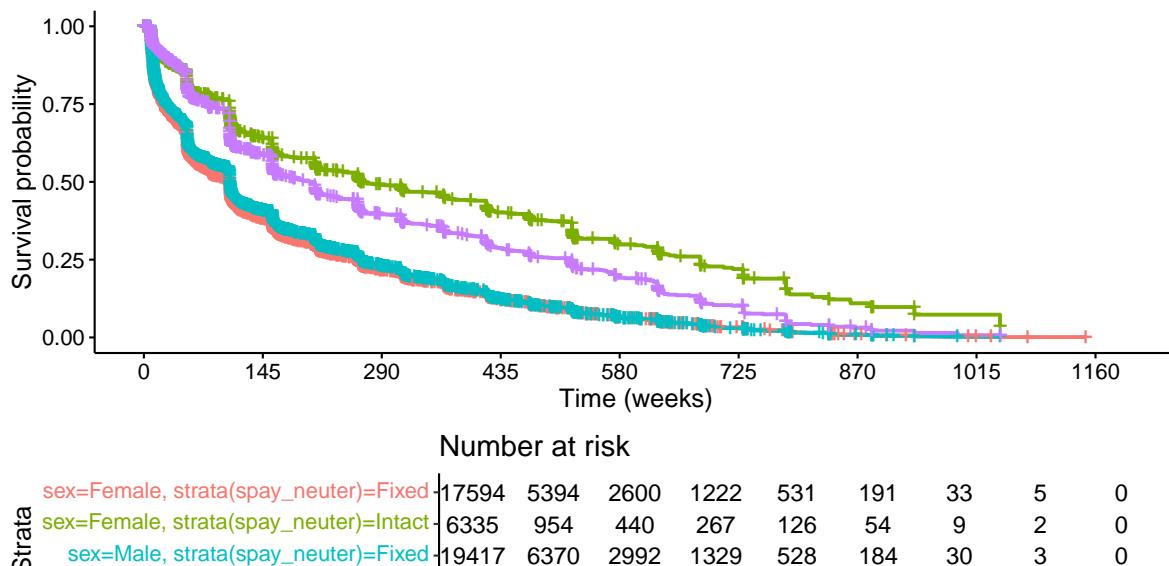
```
survdiff(formula = Surv(time_to_outcome, outcome) ~ sex + strata(spay_neuter),
          data = data)
```

	N	Observed	Expected	$(0-E)^2/E$	$(0-E)^2/V$
sex=Female	23929	15767	15587	2.07	3.93
sex=Male	26043	17410	17590	1.84	3.93

Chisq= 3.9 on 1 degrees of freedom, p= 0.05

Kaplan–Meier estimator for compounding groups sex + spay_neuter

<=Female, strata(spay_neuter)=Fixed sex=Female, strata(spay_neuter)=Intact sex=Male, strata(spay_neuter)=Fixed sex=Male, strata(spay_neuter)=Intact



Appendix 3: Semi-parametric multivariate Cox regression

Start: AIC=645865.6

Surv(time_to_outcome, outcome) ~ animal_type + has_name + sex +

```
spay_neuter + color_count + color_shade_intens
```

	Df	AIC
<none>		645866
- sex	1	645866
- color_shade_intens	3	645877
- has_name	1	645896
- color_count	2	645911
- animal_type	2	646210
- spay_neuter	1	647312

Result of the automatic model selection.

Call:

```
coxph(formula = Surv(time_to_outcome, outcome) ~ animal_type +
  has_name + sex + spay_neuter + color_count + color_shade_intens,
  data = data)
```

n= 49972, number of events= 33177

	coef	exp(coef)	se(coef)	z	Pr(> z)	
animal_typeCat	0.23545	1.26548	0.07279	3.235	0.001217	**
animal_typeDog	-0.01486	0.98525	0.07232	-0.205	0.837231	
has_nameTRUE	-0.10005	0.90479	0.01749	-5.720	1.07e-08	***
sexMale	-0.01872	0.98145	0.01110	-1.688	0.091487	.
spay_neuterIntact	-0.66741	0.51303	0.01899	-35.153	< 2e-16	***
color_count2	0.10392	1.10951	0.01488	6.985	2.84e-12	***
color_count3	0.02813	1.02853	0.03509	0.802	0.422733	
color_shade_intensDark	0.12966	1.13844	0.03378	3.839	0.000124	***
color_shade_intensLight	0.09097	1.09524	0.03374	2.696	0.007015	**
color_shade_intensMedium	0.11213	1.11866	0.03271	3.428	0.000607	***

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

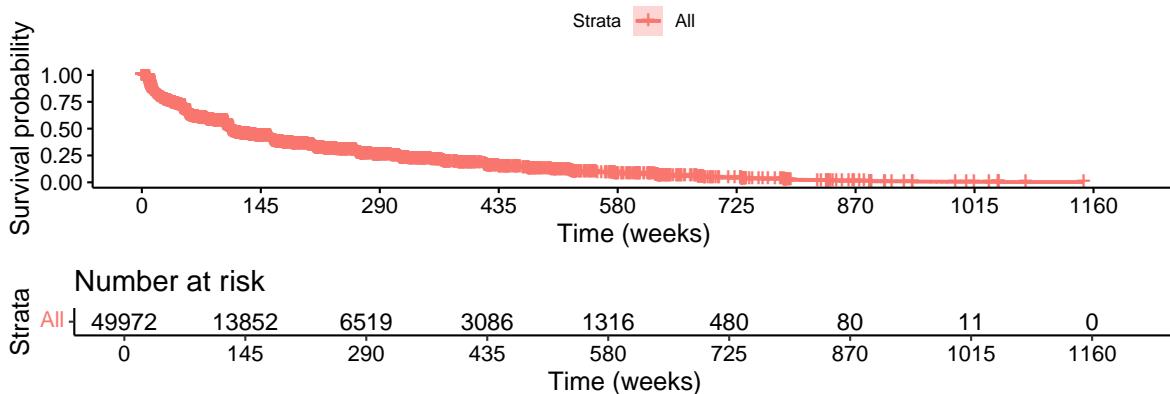
	exp(coef)	exp(-coef)	lower .95	upper .95
animal_typeCat	1.2655	0.7902	1.0972	1.4595
animal_typeDog	0.9853	1.0150	0.8550	1.1353
has_nameTRUE	0.9048	1.1052	0.8743	0.9363
sexMale	0.9814	1.0189	0.9603	1.0030
spay_neuterIntact	0.5130	1.9492	0.4943	0.5325
color_count2	1.1095	0.9013	1.0776	1.1423
color_count3	1.0285	0.9723	0.9602	1.1018

color_shade_intensDark	1.1384	0.8784	1.0655	1.2164
color_shade_intensLight	1.0952	0.9130	1.0251	1.1701
color_shade_intensMedium	1.1187	0.8939	1.0492	1.1927

Concordance= 0.615 (se = 0.002)
 Likelihood ratio test= 1936 on 10 df, p=<2e-16
 Wald test = 1707 on 10 df, p=<2e-16
 Score (logrank) test = 1752 on 10 df, p=<2e-16

Probability survival prediction

Cox model

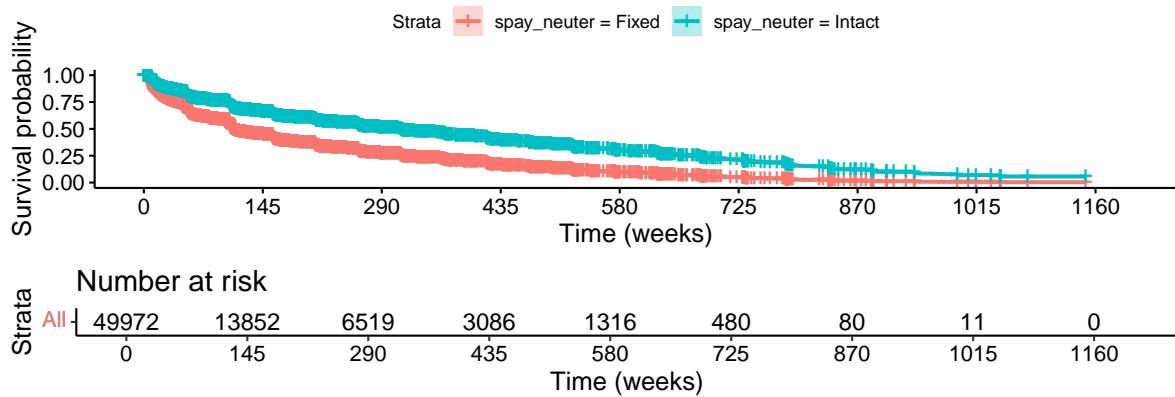


Call: survfit(formula = cox_model, data = data_df)

time	n.risk	n.event	survival	std.err	lower	95% CI	upper	95% CI
52	29309	12989	0.714	0.0193	0.677		0.752	

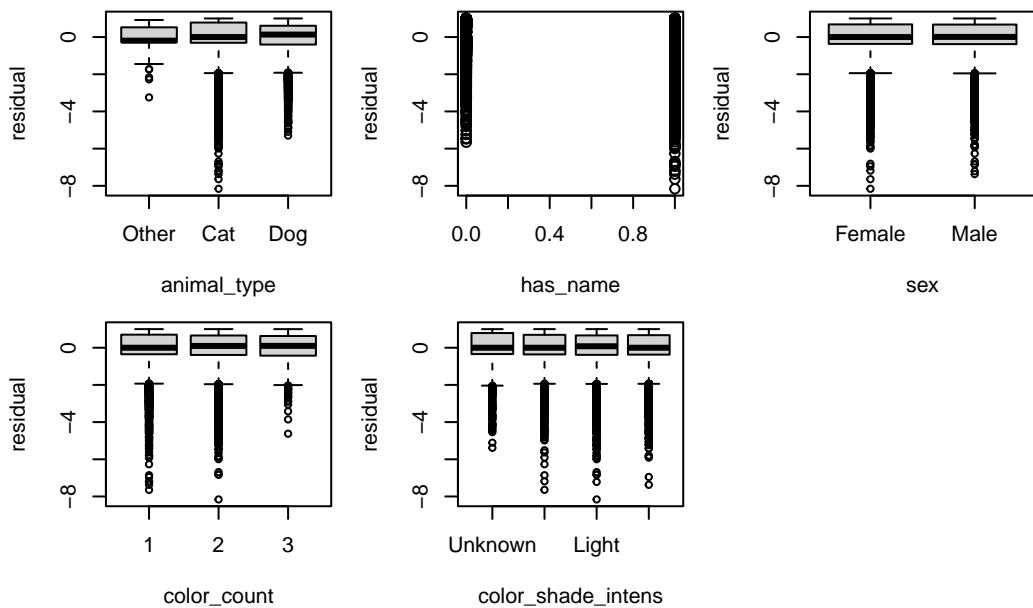
New data point prediction for one point changing only the spay_neuter variable

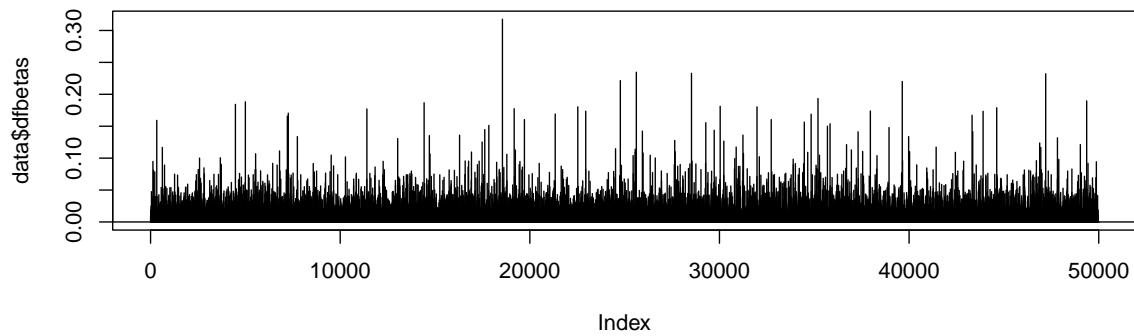
Cox model prediction depending on spay_neuter



Appendix 4: Model validation

Model validation check with Martingale Residuals



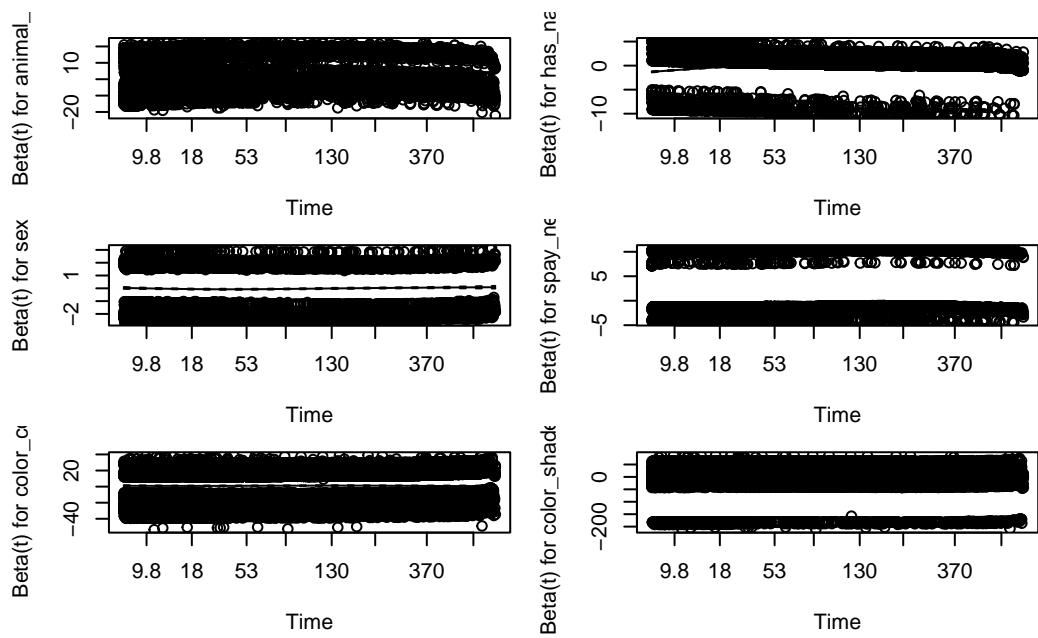


We could try to identify data with these highest values, remove them and redo the all process to eventually check if the model assumptions are satisfied.

Model validation check with Proportionality of hazards

Schoenfeld residuals

	chisq	df	p
animal_type	3125.4	2	< 2e-16
has_name	986.9	1	< 2e-16
sex	24.3	1	8.2e-07
spay_neuter	29.8	1	4.7e-08
color_count	258.6	2	< 2e-16
color_shade_intens	297.1	3	< 2e-16
GLOBAL	3789.7	10	< 2e-16



The figure indicates violation of proportionality of the hazards.

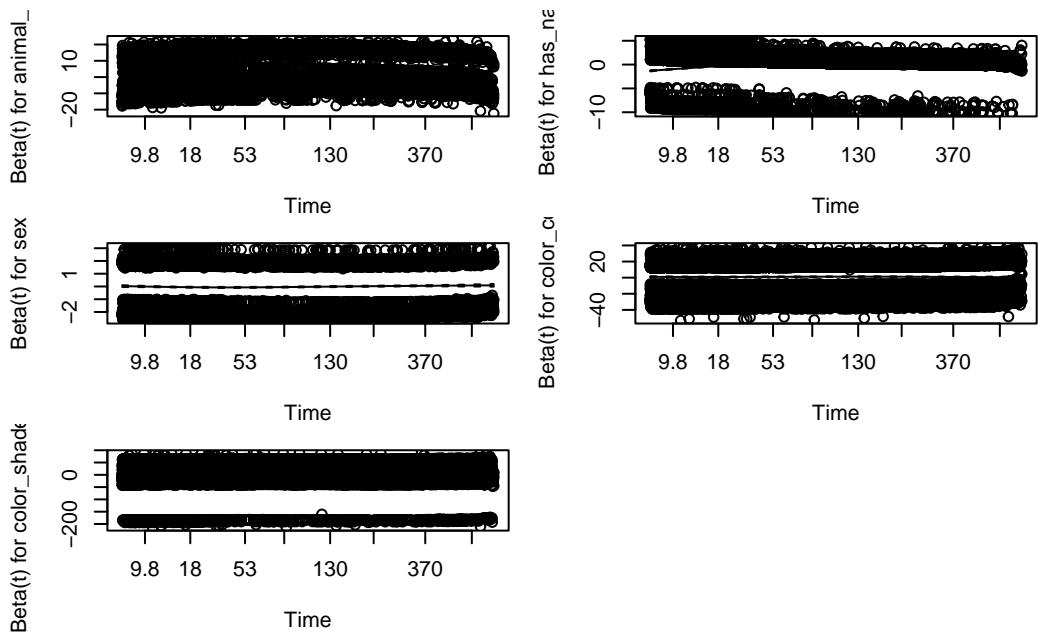
It is not better by trying to fix it with stratification.

```
fit <- coxph(Surv(time_to_outcome, outcome) ~ animal_type + has_name + sex + color_count + color_shade_intens)

residual.sch <- cox.zph(fit)
residual.sch
```

	chisq	df	p
animal_type	3115.8	2	< 2e-16
has_name	1110.6	1	< 2e-16
sex	25.1	1	5.5e-07
color_count	258.0	2	< 2e-16
color_shade_intens	298.3	3	< 2e-16
GLOBAL	3781.4	9	< 2e-16

```
par(mfrow = c(3, 2), mar = c(4, 4, 1, 1), oma = c(0, 0, 2, 0))
plot(residual.sch)
```



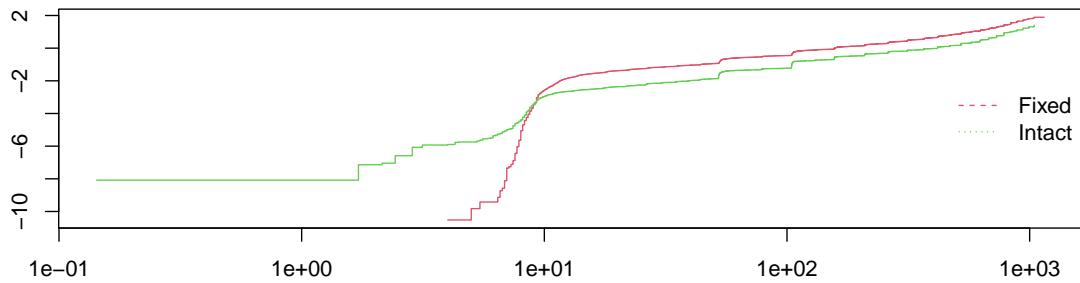
Let's look at KM model as well.

```
fit.KM<-survfit(Surv(time_to_outcome, outcome)~spay_neuter, data=data)
fit.KM
```

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ spay_neuter,
  data = data)
```

	n	events	median	0.95LCL	0.95UCL
spay_neuter=Fixed	37011	29865	105	105	105
spay_neuter=Intact	12961	3312	210	209	243

```
plot(fit.KM, fun ="cloglog", col=2:3)
legend("right", legend=sort(unique(data$spay_neuter)), col=2:3, lty=2:3, horiz=FALSE, bty
```



The figure indicates violation of proportionality of the hazards.

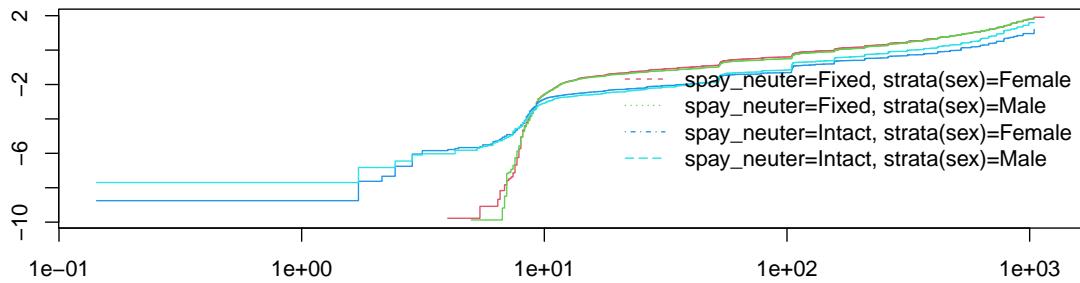
Let's try to fix it with stratification

```
fit.KM_strata<-survfit(Surv(time_to_outcome, outcome)~spay_neuter+strata(sex),data=data)
fit.KM_strata
```

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ spay_neuter +
  strata(sex), data = data)
```

	n	events	median	0.95LCL	0.95UCL
spay_neuter=Fixed, strata(sex)=Female	17594	14348	104	104	105
spay_neuter=Fixed, strata(sex)=Male	19417	15517	105	105	105
spay_neuter=Intact, strata(sex)=Female	6335	1419	264	261	314
spay_neuter=Intact, strata(sex)=Male	6626	1893	203	170	209

```
plot(fit.KM_strata, fun ="cloglog", col=2:5)
legend("right", legend=sort(names(fit.KM_strata$strata)), col=2:5, lty=2:5, horiz=FALSE,
```



The figure still indicates violation of proportionality of the hazards.

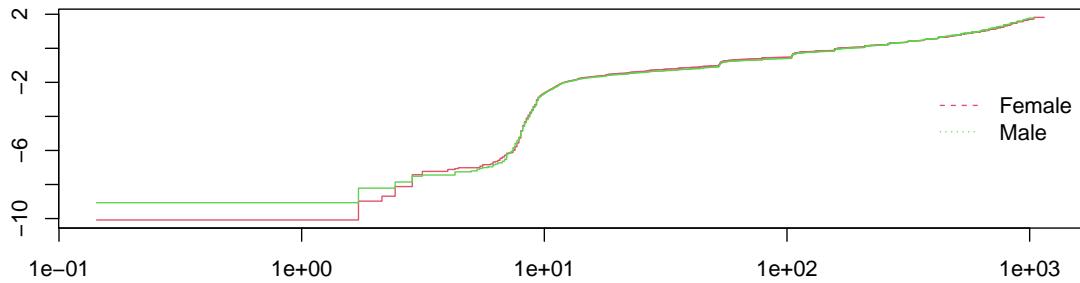
Let's try by using sex first.

```
fit.KM<-survfit(Surv(time_to_outcome, outcome)~sex, data=data)
fit.KM
```

Call: survfit(formula = Surv(time_to_outcome, outcome) ~ sex, data = data)

	n	events	median	0.95LCL	0.95UCL
sex=Female	23929	15767	105	105	106
sex=Male	26043	17410	106	106	107

```
plot(fit.KM, fun ="cloglog", col=2:3)
legend("right", legend=sort(unique(data$sex)), col=2:3, lty=2:3, horiz=FALSE, bty='n')
```



The figure indicates violation of proportionality of the hazards.

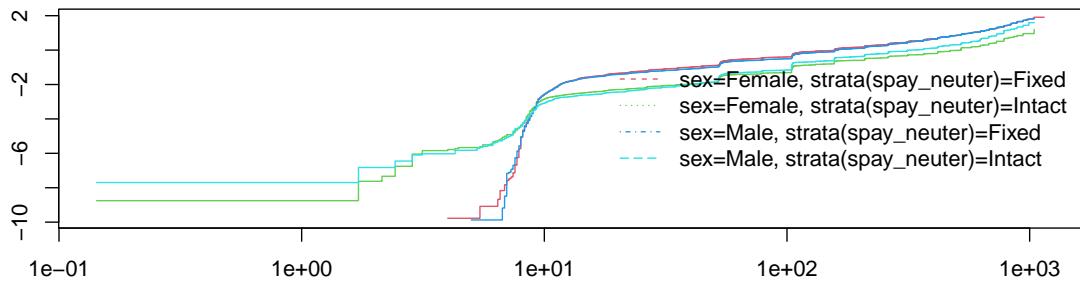
Let's try to fix it with stratification

```
fit.KM_strata<-survfit(Surv(time_to_outcome, outcome)~sex+strata(spay_neuter),data=data)
fit.KM_strata
```

```
Call: survfit(formula = Surv(time_to_outcome, outcome) ~ sex + strata(spay_neuter),
  data = data)
```

	n	events	median	0.95LCL	0.95UCL
sex=Female, strata(spay_neuter)=Fixed	17594	14348	104	104	105
sex=Female, strata(spay_neuter)=Intact	6335	1419	264	261	314
sex=Male, strata(spay_neuter)=Fixed	19417	15517	105	105	105
sex=Male, strata(spay_neuter)=Intact	6626	1893	203	170	209

```
plot(fit.KM_strata, fun ="cloglog", col=2:5)
legend("right", legend=sort(names(fit.KM_strata$strata)), col=2:5, lty=2:5, horiz=FALSE,
```



The figure still indicates violation of proportionality of the hazards.