Equine Cryptorchid Stats

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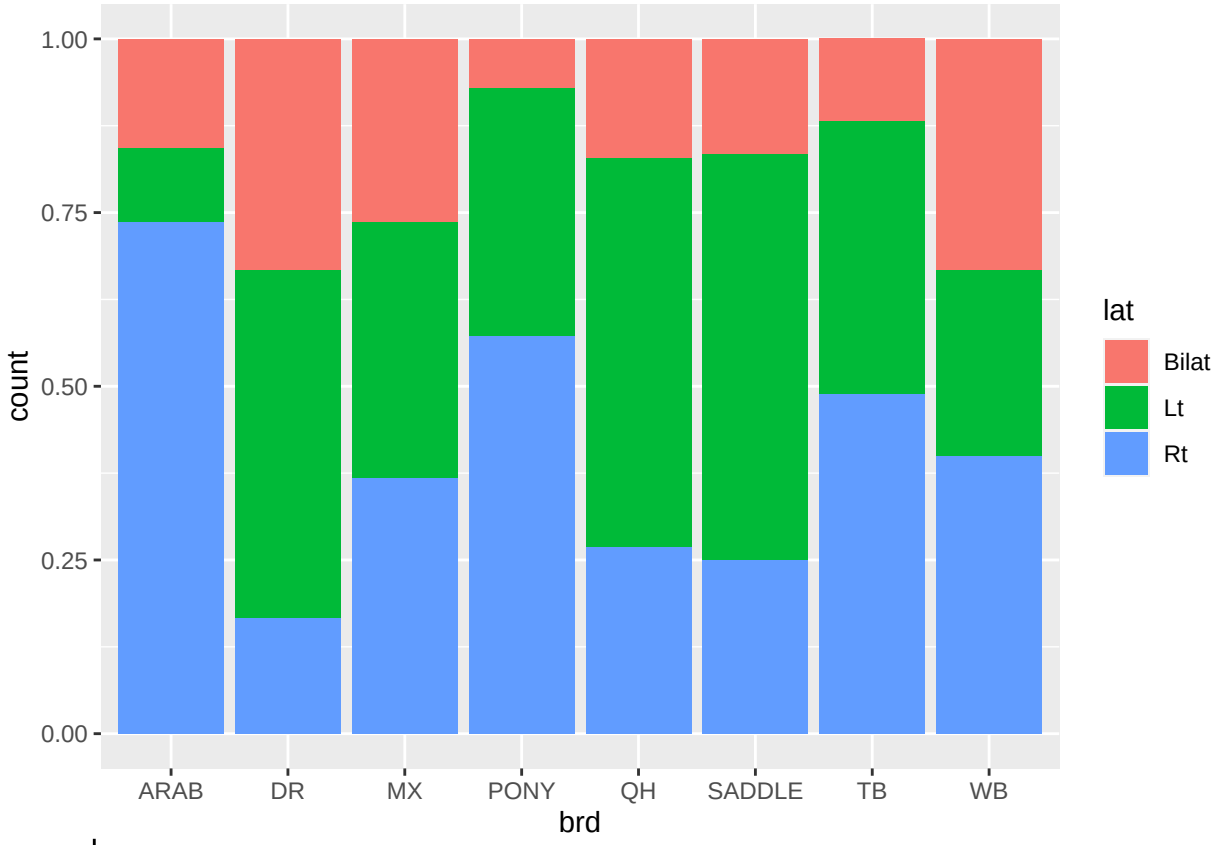
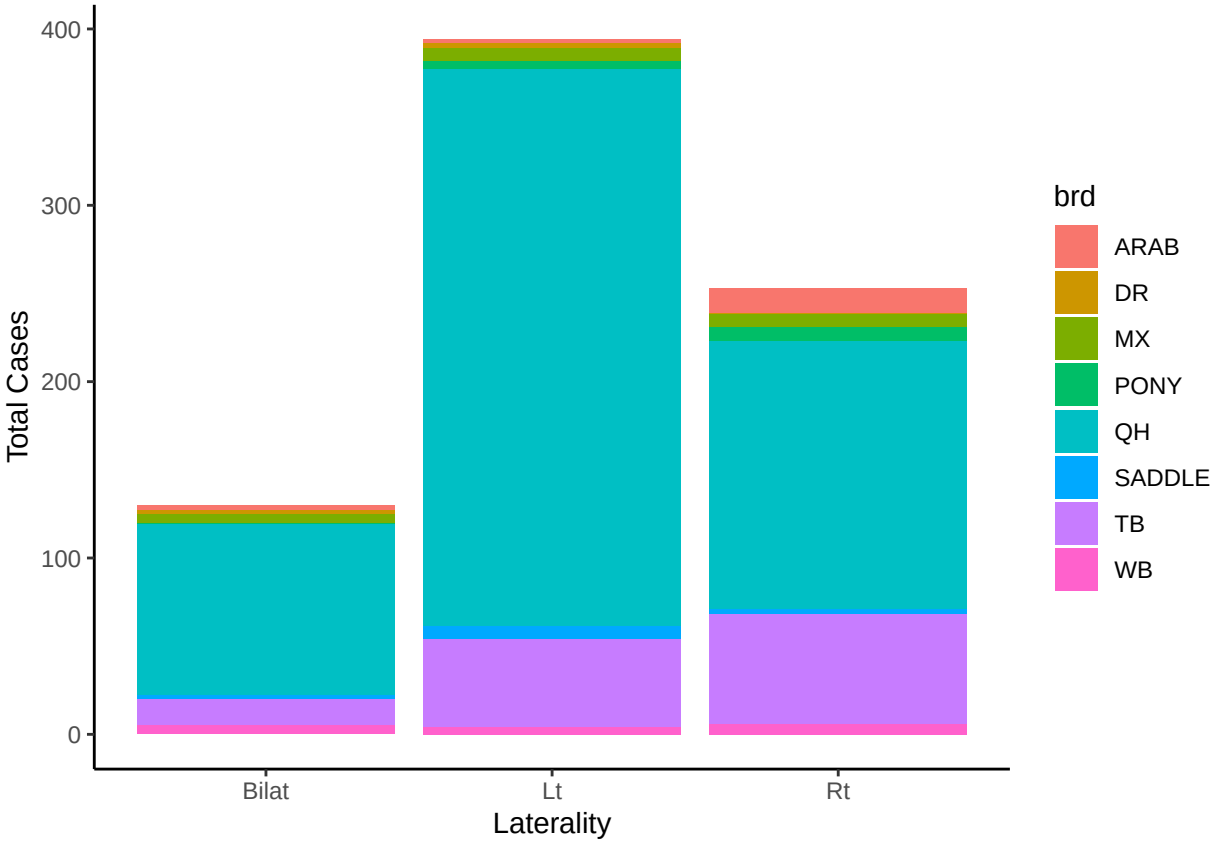
Evaluate the data graphically





Create contingency table to look at total numbers and evaluate whether there are any differences between groups

```
##
##          Bilat  Lt  Rt
##   ARAB       3   2  14
##   DR         2   3   1
##   MX         5   7   7
##   PONY       1   5   8
##   QH        97 316 152
##   SADDLE     2   7   3
##   TB        15  50  62
##   WB         5   4   6
```

```
## Warning in chisq.test(cont_table): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  cont_table
## X-squared = 52.049, df = 14, p-value = 2.759e-06
```

```
##
##  Fisher's Exact Test for Count Data with simulated p-value (based on
##  2000 replicates)
##
## data:  cont_table
## p-value = 0.0004998
## alternative hypothesis: two.sided
```

There are statistical differences in the total numbers between groups

To evaluate differences between groups, a multinomial model was used and all pairs compared at each level - bilateral, right sided, left sided

```
## # weights:  27 (16 variable)
## initial  value 853.621748
## iter  10 value 758.901683
## final  value 758.318248
## converged
```

```
## Call:
## multinom(formula = lat ~ brd, data = t1, weights = freq, Hess = T,
##     model = T)
##
## Coefficients:
##    (Intercept)   brdARAB     brdDR      brdMX   brdPONY   brdSADDLE      brdTB
## Lt   1.1810332 -1.586681 -0.775605 -0.8445417 0.4286778  0.07174181 0.02293932
## Rt   0.4491737  1.091260 -1.142430 -0.1126813 1.6305627 -0.04371046 0.96991206
```

```
##         brdWB
## Lt -1.4042365
## Rt -0.2668569
##
## Std. Errors:
##    (Intercept)   brdARAB     brdDR     brdMX  brdPONY brdSADDLE     brdTB
## Lt   0.1160770 0.9202582 0.9202114 0.5969365 1.101698 0.8101441 0.3164500
## Rt   0.1299547 0.6493379 1.2316422 0.5997895 1.068714 0.9220779 0.3157277
##        brdWB
## Lt 0.6807942
## Rt 0.6193135
##
## Residual Deviance: 1516.636
## AIC: 1548.636
```

```
## lat = Bilat:
##  contrast    estimate     SE df t.ratio p.value
##  ARAB - QH   -0.01378 0.0851 16  -0.162  0.9993
##  DR - QH      0.16166 0.1931 16   0.837  0.8793
##  MX - QH      0.09147 0.1023 16   0.895  0.8556
##  PONY - QH   -0.10027 0.0706 16  -1.420  0.5698
##  SADDLE - QH -0.00502 0.1087 16  -0.046  1.0000
##  TB - QH     -0.05357 0.0327 16  -1.636  0.4446
##  WB - QH      0.16166 0.1227 16   1.317  0.6309
##
## lat = Lt:
##  contrast    estimate     SE df t.ratio p.value
##  ARAB - QH   -0.45404 0.0734 16  -6.183  0.0001
##  DR - QH     -0.05929 0.2052 16  -0.289  0.9952
##  MX - QH     -0.19087 0.1126 16  -1.695  0.4127
##  PONY - QH   -0.20215 0.1298 16  -1.558  0.4889
##  SADDLE - QH  0.02404 0.1438 16   0.167  0.9992
##  TB - QH     -0.16559 0.0481 16  -3.441  0.0188
##  WB - QH     -0.29264 0.1161 16  -2.521  0.1115
##
## lat = Rt:
##  contrast    estimate     SE df t.ratio p.value
##  ARAB - QH    0.46783 0.1027 16   4.554  0.0020
##  DR - QH     -0.10237 0.1533 16  -0.668  0.9364
##  MX - QH      0.09940 0.1122 16   0.886  0.8594
##  PONY - QH    0.30242 0.1336 16   2.264  0.1749
##  SADDLE - QH -0.01903 0.1264 16  -0.151  0.9994
##  TB - QH      0.21916 0.0481 16   4.555  0.0020
##  WB - QH      0.13098 0.1279 16   1.024  0.7945
##
## P value adjustment: dunnettx method for 7 tests
```

There are no differences in the occurence of bilateral cryptorchidism

There are differences in L v R for Arabians and TB vs QH

Remove bilateral from model and repeat

```
## # weights:  9 (8 variable)
## initial  value 448.466226
## iter  10 value 411.509817
## final  value 411.509278
## converged
```

```
## Call:
## multinom(formula = lat ~ brd, data = t2, weights = freq)
##
## Coefficients:
##                 Values  Std. Err.
## (Intercept)  0.7318601 0.09870916
## brdARAB     -2.6777060 0.76232837
## brdDR        0.3667616 1.15891462
## brdMX       -0.7318207 0.54356029
## brdPONY     -1.2018677 0.57857048
## brdSADDLE    0.1154860 0.69709624
## brdTB       -0.9469630 0.21417866
## brdWB       -1.1373484 0.65300237
##
## Residual Deviance: 823.0186
## AIC: 839.0186
```

```
## lat = Rt:
##  contrast    estimate     SE df t.ratio p.value
##  ARAB - QH     0.5502 0.0855  8   6.438  0.0011
##  DR - QH      -0.0748 0.2176  8  -0.344  0.9913
##  MX - QH       0.1752 0.1354  8   1.294  0.6562
##  PONY - QH     0.2906 0.1367  8   2.126  0.2637
##  SADDLE - QH  -0.0248 0.1465  8  -0.169  0.9991
##  TB - QH       0.2288 0.0517  8   4.423  0.0114
##  WB - QH       0.2752 0.1564  8   1.759  0.4130
##
## lat = Lt:
##  contrast    estimate     SE df t.ratio p.value
##  ARAB - QH    -0.5502 0.0855  8  -6.438  0.0011
##  DR - QH       0.0748 0.2176  8   0.344  0.9913
##  MX - QH      -0.1752 0.1354  8  -1.294  0.6562
##  PONY - QH    -0.2906 0.1367  8  -2.126  0.2637
##  SADDLE - QH   0.0248 0.1465  8   0.169  0.9991
##  TB - QH      -0.2288 0.0517  8  -4.423  0.0114
##  WB - QH      -0.2752 0.1564  8  -1.759  0.4130
##
## P value adjustment: dunnettx method for 7 tests
```

Same results, probably more relevant model

Print odds ratios and confidence intervals

These are the odds of a unilateral crypt being left sided (vs QH)

```
## # A tibble: 7 x 4
##   breed     odds.ratio lower_CI upper_CI
##   <chr>          <dbl>    <dbl>    <dbl>
## 1 brdARAB       0.0687   0.0154    0.306
## 2 brdDR         1.44     0.149    14.0
## 3 brdMX         0.481    0.166     1.40
## 4 brdPONY       0.301    0.0967    0.934
## 5 brdSADDLE     1.12     0.286     4.40
## 6 brdTB         0.388    0.255     0.590
## 7 brdWB         0.321    0.0892    1.15
```

Forestplot of the data - this is the odds ratio for a unilateral crypt horse

to be left-sided vs. a Quarterhorse. Arabians and Thoroughbreds (and likely Ponies) are

significantly less likely to present as left-sided than Quarterhorses - or those 3 are

significantly more likely to present as right sided than QH.