# Integration in the hyper2 package 

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#### Abstract

The hyper 2 package presented a new formulation of the hyperdirichlet package, offering speed advantages and the ability to deal with higher-dimensional datasets. However, hyper2 was based on likelihood methods and as originally uploaded did not have the ability to integrate over the unit-sum simplex. This functionality has now been incorporated into the package which is documented here, by reproducing earlier analysis.


Keywords: Dirichlet distribution, hyperdirichlet, hyper2, combinatorics, R, multinomial distribution, constrained optimization, integration, simplex, unit-sum constraint.

## 1. Introduction

The hyper2 package (Hankin 2017) presented a new formulation of the hyperdirichlet distribution (Hankin 2010) which offered speed advantages over the original hyperdirichlet package, and the ability to deal with higher-dimensional datasets. However, hyper2 was based on likelihood methods and as originally uploaded did not have the ability to integrate over the unit-sum simplex. This functionality has now been incorporated into the package which is documented here, by reproducing earlier analysis.

## 2. Chess

Consider Table 1 in which matches between three chess players are tabulated; this dataset was analysed by Hankin (2010).

$$
C \frac{p_{1}^{30} p_{2}^{36} p_{3}^{22}}{\left(p_{1}+p_{2}\right)^{35}\left(p_{2}+p_{3}\right)^{35}\left(p_{1}+p_{3}\right)^{18}}
$$

(the symbol ' $C$ ' consistently stands for an undetermined constant). This likelihood function is provided in the hyper2 package as the chess dataset:

```
> data(chess)
> chess
Topalov^30 * (Topalov + Anand)^-35 * (Topalov + Karpov)^-18 * Anand^36
* (Anand + Karpov)^-35 * Karpov^22
```

We can calculate the normalizing constant:

| Topalov | Anand | Karpov | total |
| :---: | :---: | :---: | :---: |
| 22 | 13 | - | 35 |
| - | 23 | 12 | 35 |
| 8 | - | 10 | 18 |
| 30 | 36 | 22 | 88 |

Table 1: Results of 88 chess matches (dataset chess in the aylmer package) between three Grandmasters; entries show number of games won up to 2001 (draws are discarded). Topalov beats Anand 22-13; Anand beats Karpov 23-12; and Karpov beats Topalov 10-8

```
> B(chess)
```

[1] $1.442828 \mathrm{e}-28$
comparing well with the value given by the hyperdirichlet package of $1.47 \times 10^{-28}$. Hankin (2010) went on to calculate the $p$-value for $H_{0}: p=\left(\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right)$ as 0.395 , a calculation which may be performed in the hyper2 package as follows:

```
> f<- function(p){loglik(chess,indep(p)) > loglik(chess,c(1,1)/3)}
> probability(chess, disallowed=f,tol=0.01)
[1] 0.3785911
```

Again comparing well with the older result (smaller values of tol give closer agreement at the expense of increased computation time). Finally, we can calculate the probability that Topalov is a better player than Anand:

```
> T.lt.A <- function(p){p[1]<p[2]}
> probability(chess, disallowed=T.lt.A,tol=0.001)
[1] 0.7127539
```

again showing reasonable agreement with the 2010 value of 0.701 .

## 3. Verification

In a breathtaking display of arrogance and/or incompetence, Hankin (2010) did not actually provide any evidence that the integration suite of hyperdirichlet was accurate. Here I compensate for that inexcusable lapse by comparing numerical results with analytical formulae. Consider the standard Dirichlet distribution:

$$
\begin{equation*}
\frac{p_{1}^{\alpha_{1}-1} \ldots p_{k}^{\alpha_{k}-1}}{B\left(\alpha_{1}, \ldots, \alpha_{k}\right)} \tag{1}
\end{equation*}
$$

where it is understood that the $p_{i}>0$ and $\sum p_{i}=1$; here $B=\frac{\Gamma \sum \alpha_{i}}{\prod \Gamma \alpha_{i}}$ is the normalization constant. We can verify that hyper2: : B() is operating as expected for the case $\alpha_{1}=1, \alpha_{2}=$ $2, \alpha_{3}=3, \alpha_{4}=4$ :

```
> prod(gamma(1:4))/gamma(sum(1:4))
```

[1] $3.306878 \mathrm{e}-05$

```
> B(dirichlet(alpha=1:4))
```

[1] $3.306878 \mathrm{e}-05$
Further, consider a Dirichlet distribution with $\alpha_{1}=\alpha_{2}=\alpha_{3}=\alpha_{4}=3$. Then, by symmetry, the probability that $p_{1}<p_{2}$ should be exactly $\frac{1}{2}$ :

```
> f<- function(p){p[1]<p[2]}
> H <- dirichlet(alpha=rep (2,4))
> probability(H,f,tol=0.1)
```

[1] 0.5045785
Further, $\mathrm{P}\left(p_{1}<p_{2}<p_{3}\right)$ should be exactly $\frac{1}{6}$ :

```
> g <- function(p){(p[1]<p[2]) & (p[2]<p[3])}
```

> 1-probability(H,disallowed=g,tol=0.1)
[1] 0.1644873

## 4. More results: icons dataset

Consider the icons dataset, shown in table 2, and the following hypotheses, again following Hankin (2010), and reproduced here for convenience.

```
> data("oneill") # load the dataset
> icons
NB^32 * (NB + L + THC + OA)^-20 * (NB + L + THC + WAIS)^-15 * (NB + L +
OA + WAIS )^-9 * (NB + PB + THC + OA)^-18* (NB + PB + THC + WAIS)^-18 *
(NB + PB + OA + WAIS)^-8* L^24* (L + PB + THC + OA)^-11 * (L + PB +
THC + WAIS)^-16 * (L + PB + OA + WAIS)^-18* PB^30* THC^24* OA^14 *
WAIS^9
> maxp(icons)
    NB
    L PB THC
    OA WAIS
0.25230411 0.17364433 0.22458188 0.17011281 0.11068604 0.06867083
```

For reference, the other hypotheses were:

| icon |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| NB | L | PB | THC | OA | WAIS | total |
| 5 | 3 | - | 4 | - | 3 | 15 |
| 3 | - | 5 | 8 | - | 2 | 18 |
| - | 4 | 9 | 2 | - | 1 | 16 |
| 1 | 3 | - | 3 | 4 | - | 11 |
| 4 | - | 5 | 6 | 3 | - | 18 |
| - | 4 | 3 | 1 | 3 | - | 11 |
| 5 | 1 | - | - | 1 | 2 | 9 |
| 5 | - | 1 | - | 1 | 1 | 8 |
| - | 9 | 7 | - | 2 | 0 | 18 |
| 23 | 24 | 30 | 24 | 14 | 9 | 124 |

Table 2: Experimental results from O'Neill (2007) (dataset icons in the package): respondents' choice of 'most concerning' icon of those presented. Thus the first row shows results from respondents presented with icons NB, L, THC, and WAIS; of the 15 respondents, 5 chose NB as the most concerning (see text for a key to the acronyms). Note the " 0 " in row 9 , column 6: this option was available to the 18 respondents of that row, but none of them actually chose WAIS

- $H_{1}: p_{1} \geqslant \frac{1}{6}$
- $H_{2}: p_{1} \geqslant \max \left\{p_{2}, \ldots p_{6}\right\}$
- $H_{3}: p_{5}+p_{6} \geqslant \frac{1}{3}$
- $H_{4}: \max \left\{p_{5}, p_{6}\right\} \geqslant \min \left\{p_{1}, p_{2}, p_{3}, p_{4}\right\}$
$>f 1<-$ function $(p)\{p[1]>1 / 6\}$
$>f 2<-$ function $(p)\{p[1]>\max (f i l l u p(p)[-1])\}$
$>f 3<-$ function $(p)\{\operatorname{sum}(f i l l u p(p)[5: 6])>1 / 3\}$
$>f 4<-$ function $(p)\{\max (f i l l u p(p)[1: 2])>\min (f i l l u p(p)[3: 6])\}$
Here I will analyse just the first hypothesis, that is $H_{1}: p_{1} \leqslant \frac{1}{6}$ using the integration facilities of the hyper2 package, and compare with previous results. Here we perform a Bayesian analysis, made possible by the efficient coding of hyper2:

```
> probability(icons, disallowed=function(p){p[1] > 1/6}, tol=0.1)
```

[1] 0.01501733

See how the disallowed region is the expected bit of the parameter space. Thus the probability that the $p_{i}$ are unexpected (that is, $\left.p_{1}<1 / 6\right)$ is about $1.5 \%$ or conversely, $P\left(H_{1}\right) \simeq 0.985$. The likelihood ratio reported was about 2.608 , which would correspond to a $p$-value of about

```
> pchisq(2*2.608,df=1,lower.tail=FALSE)
```

[1] 0.02237997
or just over $2 \%$ under an asympotic distribution; thus this frequentist technique gives comparable strength of evidence for $H_{1}$ to the Bayesian approach.

## 5. Incomplete survey data

This section performs the analysis originally presented in Altham and Hankin (2010). The data, given here in table 4 arises from 69 medical malpractice claims, and are the two surgeons' answers to the question: was there a communication breakdown in the hand-off between physicians caring for the patient?

| Reviewer 1 | Reviewer 2 |  |  |  |
| :--- | :---: | :---: | :---: | :---: |
|  | Yes | No | Missing | Total |
| Yes | 26 | 1 | 2 | 29 |
| No | 5 | 18 | 9 | 32 |
| Missing | 4 | 4 | 0 | 8 |
| Total | 35 | 23 | 11 | 69 |

Table 3: Two surgeon reviews of malpractice claims data

| Reviewer 1 | Reviewer 2 |  |  |  |
| :--- | :---: | :---: | :---: | :---: |
|  | Yes | No | Missing | Total |
| Yes | $y_{11}$ | $y_{10}$ | $z_{1+}$ | $y_{1+}+z_{1+}$ |
| No | $y_{01}$ | $y_{00}$ | $z_{0+}$ | $y_{0+}+z_{0+}$ |
| Missing | $u_{+1}$ | $u_{+0}$ | 0 | $u_{++}$ |
| Total | $y_{+1}+u_{+1}$ | $y_{+0}+u_{+0}$ | $z_{++}$ | $n$ |

Table 4: Notation for the data
We may implement an appropriate likelihood function as follows:

```
> H <- hyper2(d=4)
> pnames(H) <- c("t00","t10", "t01", "t11")
> H["t00"] <- 18
> H["t10"] <- 01
> H["t01"] <- 05
> H["t11"] <- 26
> H[c("t11","t10")] <- 2
> H[c("t01","t00")] <- 9
> H[c("t11","t01")] <- 4
> H[c("t10","t00")] <- 4
>H
t00^18 * (t00 + t10)^4 * (t00 + t01)^9 * t10 * (t10 + t11)^2 * t01^5 *
(t01 + t11)^4 * t11^26
```

(object H is provided as handover in the package). Then we may estimate the probability that reviewer 2 is more likely to give a 'yes' than reviewer 1 as follows:

```
> free <- maxp(H,give=TRUE)
> m <- fillup(free$par)
> names(m) <- pnames(H)
> m
t00 rrrerrern
> free$value
[1] -64.14538
```

Then the constrained optimization:

```
> obj <- function(p){-loglik(H,p)} # objective func
> gr <- function(p){-gradient(H,p)} # gradient, needed for speed
> UI <- rbind(diag(3),-1) #UI and CI specify constraints
> CI <- c(rep (0,3),-1) # p_i >= 0 and sum p_i <= 1
```

We will test $H_{A}: p_{2}<p_{3}$ using the method of support.

```
> ml_HA <- constrOptim(theta=c(0.1,0.2,0.1), f = obj,grad=gr,
+ ui = rbind(UI,c(0,1,-1)), # p2 > p3
+ ci = c(CI,0))
> ml_HA$value
[1] 66.14453
```

Thus the support for $H_{A}$ is

```
> ml_HA$value - free$value
```

[1] 130.2899
thus agreeing almost exactly with Altham and Hankin (2010).

## References

Altham PME, Hankin RKS (2010). "Using recently developed software on a 2 x 2 table of matched pairs with incompletely classified data." Journal of the Royal Statistical Society, series $C, \mathbf{5 9}(2), 377-379$.

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