

# Digital Complement

## Calling sequences and examples

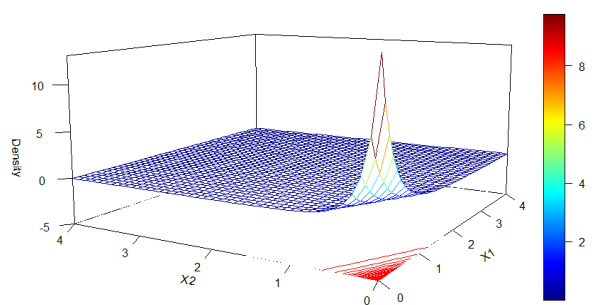
Multivariate Distribution	Calling sequence
Lomax ( $a = \text{parm1}, \theta = \text{parm2}$ )	<code>dmvlomax(x, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>pmvlomax(q, parm1 = 1, parm2 = rep(1, k))</code> <code>qmvlomax(p, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>rmvlomax(n, parm1 = 1, parm2 = rep(1, k))</code> <code>smvlomax(q, parm1 = 1, parm2 = rep(1, k))</code>
Mardia's Pareto Type I ( $a = \text{parm1}, \theta = \text{parm2}$ )	<code>dmvmpareto1(x, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>pmvmpareto1(q, parm1 = 1, parm2 = rep(1, k))</code> <code>qmvmpareto1(p, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>rmvmpareto1(n, parm1 = 1, parm2 = rep(1, k))</code> <code>smvmpareto1(q, parm1 = 1, parm2 = rep(1, k))</code>
Logistic ( $\mu = \text{parm1}, \sigma = \text{parm2}$ )	<code>dmvlogis(x, parm1 = rep(1, k), parm2 = rep(1, k), ...)</code> <code>pmvlogis(q, parm1 = rep(1, k), parm2 = rep(1, k))</code> <code>qmvlogis(p, parm1 = rep(1, k), parm2 = rep(1, k), ...)</code> <code>rmvlogis(n, parm1 = rep(1, k), parm2 = rep(1, k))</code> <code>smvlogis(q, parm1 = rep(1, k), parm2 = rep(1, k))</code>
Burr ( $a = \text{parm1}, d = \text{parm2}, c = \text{parm3}$ )	<code>dmvburr(x, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code> <code>pmvburr(q, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k))</code> <code>qmvburr(p, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code> <code>rmvburr(n, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k))</code> <code>smvburr(q, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k))</code>
Cook-Johnson's Uniform ( $a = \text{parm}$ )	<code>dmvunif(x, parm = 1, ...)</code> <code>pmvunif(q, parm = 1)</code> <code>qmvunif(p, parm = 1, dim = k, ...)</code> <code>rmvunif(n, parm = 1, dim = 1)</code> <code>smvunif(q, parm = 1)</code>
Generalized Lomax ( $a = \text{parm1}, \theta = \text{parm2}, l = \text{parm3}$ )	<code>dmvglomax(x, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code> <code>pmvglomax(q, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code> <code>qmvglomax(p, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code> <code>rmvglomax(n, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k))</code> <code>smvglomax(q, parm1 = 1, parm2 = rep(1, k), parm3 = rep(1, k), ...)</code>
$F$ ( $df = \text{df}$ )	<code>dmvf(x, df = rep(1, k + 1), ...)</code> <code>pmvf(q, df = rep(1, k + 1), ...)</code> <code>qmvf(p, df = rep(1, k + 1), ...)</code> <code>rmvf(n, df = rep(1, k + 1))</code> <code>smvf(q, df = rep(1, k + 1), ...)</code>
Inverted Beta ( $a = \text{parm1}, l = \text{parm2}$ )	<code>dmvinvbeta(x, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>pmvinvbeta(q, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>qmvinvbeta(p, parm1 = 1, parm2 = rep(1, k), ...)</code> <code>rmvinvbeta(n, parm1 = 1, parm2 = rep(1, k))</code> <code>smvinvbeta(q, parm1 = 1, parm2 = rep(1, k), ...)</code>

**Table 1:** Calling sequence for probability density calculation (dmv\*), cumulative distribution calculation (pmv\*), equicoordinate quantile calculation (qmv\*), random numbers generation (rmv\*), and survival function calculation (smv\*).

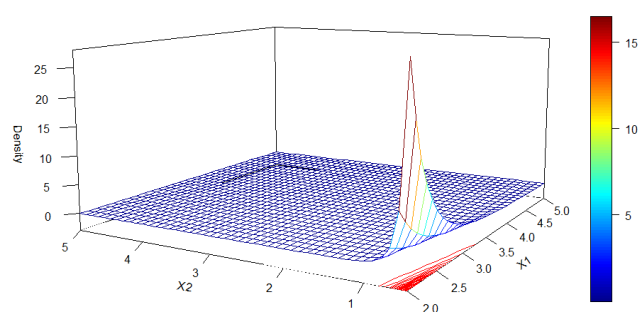
## Example code for maximum likelihood estimation of parameters

We define the following log-likelihood functions according to (??) for Mardia's Pareto Type I, Logistic, Burr, Cook-Johnson's uniform, generalized Lomax, and inverted beta distributions as follows.

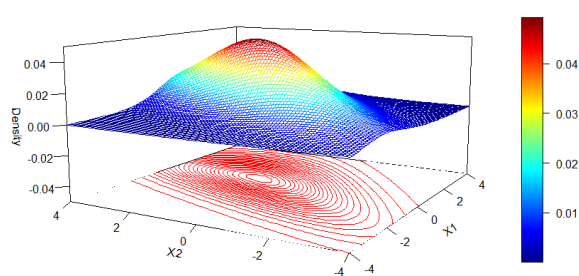
```
loglik.mpareto1 <- function(data, par) {
  ll <- sum(dmvmpareto1(data, parm1 = par[1], parm2 = par[-1], log = TRUE))
}
```



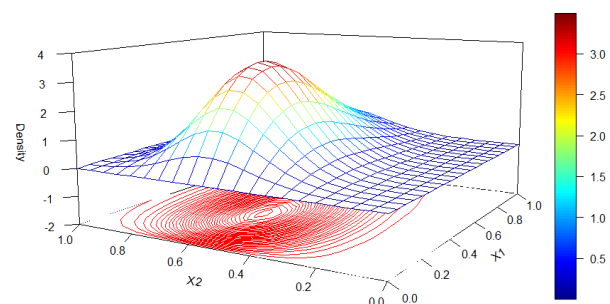
(a) Lomax



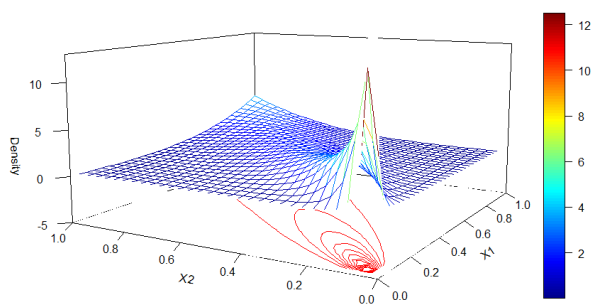
(b) Mardia's Pareto Type I



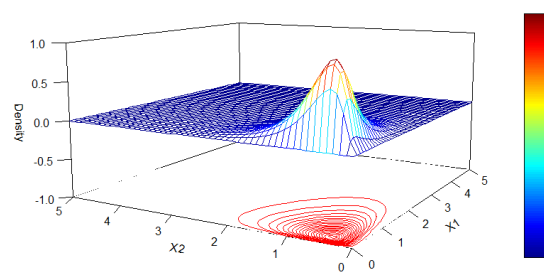
(c) Logistic



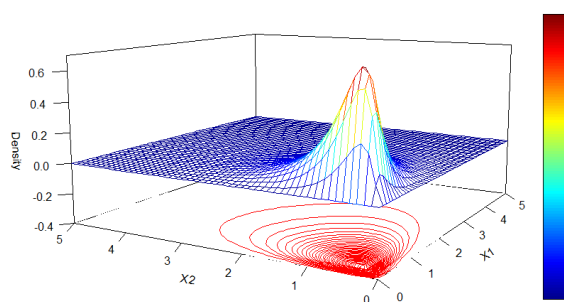
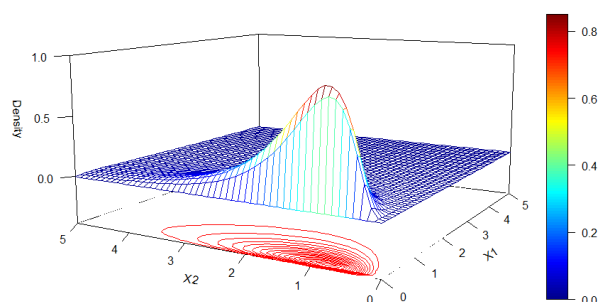
(d) Burr



(e) Cook-Johnson's Uniform



(f) Generalized Lomax

(g)  $F$ 

(h) Inverted Beta

Figure 1: Density surfaces created by the code in Table 2.

Multivariate Distribution	Command	Output
Lomax ( $a = 5, \theta_1 = 0.5, \theta_2 = 1$ )	<code>dplot2(dfun = function(x) dmvlomax(x, parm1 = 5, parm2 = c(0.5, 1)), x1 = seq(0, 4, 0.1), x2 = seq(0, 4, 0.1), xlim = c(-5, 13))</code>	Figure 1 (a)
Mardia's Pareto Type I ( $a = 5, \theta_1 = 0.5, \theta_2 = 2$ )	<code>dplot2(dfun = function(x) dmvmppareto1(x, parm1 = 5, parm2 = c(0.5, 2)), x1 = seq(2, 5, 0.1), x2 = seq(0.5, 5, 0.1), xlim = c(-3, 28))</code>	Figure 1 (b)
Logistic ( $\mu_1 = 0.5, \mu_2 = 1, \sigma_1 = 1, \sigma_2 = 1.5$ )	<code>dplot2(dfun = function(x) dmvmlogis(x, parm1 = c(0.5, 1), parm2 = c(1, 1.5)), x1 = seq(-4, 4, 0.1), x2 = seq(-4, 4, 0.1), xlim = c(-0.05, 0.05))</code>	Figure 1 (c)
Burr ( $a = 3, d_1 = 1, d_2 = 3, c_1 = 2, c_2 = 5$ )	<code>dplot2(dfun = function(x) dmvm Burr(x, parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5)), x1 = seq(0, 1, 0.05), x2 = seq(0, 1, 0.05), xlim = c(-2, 4))</code>	Figure 1 (d)
Cook-Johnson's Uniform ( $a = 0.3$ )	<code>dplot2(dfun = function(x) dmvmunif(x, parm = 0.3), x1 = seq(0, 1, 1 / 30), x2 = seq(0, 1, 1 / 30), xlim = c(-5, 13))</code>	Figure 1 (e)
Generalized Lomax ( $a = 5, \theta_1 = 0.5, \theta_2 = 1, l_1 = 2, l_2 = 4$ )	<code>dplot2(dfun = function(x) dmvmglomax(x, parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4)), x1 = seq(0, 5, 0.1), x2 = seq(0, 5, 0.1), xlim = c(-1, 1))</code>	Figure 1 (f)
$F$ ( $df = (4, 6, 9)$ )	<code>dplot2(dfun = function(x) dmvmf(x, df = c(4, 6, 9)), x1 = seq(0, 5, 0.1), x2 = seq(0, 5, 0.1), xlim = c(-0.4, 0.7))</code>	Figure 1 (g)
Inverted Beta ( $a = 4, l_1 = 2, l_2 = 6$ )	<code>dplot2(dfun = function(x) dmvinvbeta(x, parm1 = 4, parm2 = c(2, 6)), x1 = seq(0, 5, 0.1), x2 = seq(0, 5, 0.1), xlim = c(-0.4, 1))</code>	Figure 1 (h)

Table 2: Example code for creating bivariate density plot.

Bivariate Distribution	Command	Output ( $x_1, x_2$ )
Lomax ( $a = 5, \theta_1 = 0.5, \theta_2 = 1$ )	<code>rmvlomax(n = 2, parm1 = 5, parm2 = c(0.5, 1))</code>	1.0174406 0.7076480 0.3686253 0.7826978
Mardia's Pareto Type I ( $a = 5, \theta_1 = 0.5, \theta_2 = 2$ )	<code>rmvmppareto1(n = 2, parm1 = 5, parm2 = c(0.5, 2))</code>	3.017441 0.8538240 2.368625 0.8913489
Logistic ( $\mu_1 = 0.5, \mu_2 = 1, \sigma_1 = 1, \sigma_2 = 1.5$ )	<code>rmvmlogis(n = 2, parm1 = c(0.5, 1), parm2 = c(1, 1.5))</code>	-0.5019906 -0.9980586 -0.6524945 -2.8979116
Burr ( $a = 3, d_1 = 1, d_2 = 3, c_1 = 2, c_2 = 5$ )	<code>rmvm Burr(n = 2, parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5))</code>	0.9107865 0.8260570 0.6045062 0.8764837
Cook-Johnson's Uniform ( $a = 0.3$ )	<code>rmvmunif(n = 2, parm = 0.3, dim = 2)</code>	0.38036196 0.24878181 0.03596575 0.08862409
Generalized Lomax ( $a = 5, \theta_1 = 0.5, \theta_2 = 1, l_1 = 2, l_2 = 4$ )	<code>rmvmglomax(n = 2, parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4))</code>	0.6928037 1.281699 0.7038999 1.184839
$F$ ( $df = (4, 6, 9)$ )	<code>rmvmf(n = 2, df = c(4, 6, 9))</code>	1.145489 1.517436 1.523112 2.211925
Inverted Beta ( $a = 4, l_1 = 2, l_2 = 6$ )	<code>rmvinvbeta(n = 2, parm1 = 4, parm2 = c(2, 6))</code>	0.4282041 1.878369 0.4697152 2.459994

Table 3: Example code for random numbers generation from bivariate distributions with `set.seed(2019)` and  $n = 2$ .

```

loglik.logis <- function(data, par) {
  mu <- par[1:(length(par) / 2)]
  sigma <- par[(length(par)/2 + 1):(length(par))]
  ll <- sum(dmvlogis(data, parm1 = mu, parm2 = sigma, log = TRUE))
}

loglik.burr <- function(data, par) {
  a <- par[1]
  d <- par[2:(length(par) + 1) / 2]
  c <- par[(length(par) + 1) / 2 + 1:(length(par))]
  ll = sum(dmvm Burr(data, parm1 = a, parm2 = d, parm3 = c, log = TRUE))
}

```

Bivariate Distribution and Quantiles	Command	Output
Lomax ( $a = 5, \theta_1 = 0.5, \theta_2 = 2$ ) ( $x_1, x_2$ ) = (1, 0.5)	pmvlomax(q = c(1, 0.5), parm1 = 5, parm2 = c(0.5, 1)) smvlomax(q = c(1, 0.5), parm1 = 5, parm2 = c(0.5, 1)) qmvlomax(p = 0.5, parm1 = 5, parm2 = c(0.5, 1))	0.7678755 0.03125 0.3928917
Mardia's Pareto Type I ( $a = 5, \theta_1 = 0.5, \theta_2 = 2$ ) ( $x_1, x_2$ ) = (3, 1)	pmvmpareto1(q = c(3, 1), parm1 = 5, parm2 = c(0.5, 2)) smvmpareto1(q = c(3, 1), parm1 = 5, parm2 = c(0.5, 2)) qmvmpareto1(p = 0.5, parm1 = 5, parm2 = c(0.5, 2))	0.8473028 0.01024 2.297463
Logistic ( $\mu_1 = 0.5$ , $\mu_2 = 1, \sigma_1 = 1, \sigma_2 = 1.5$ ) ( $x_1, x_2$ ) = (1, 2)	pmvlogis(q = c(1, 2), parm1 = c(0.5, 1), parm2 = c(1, 1.5)) smvlogis(q = c(1, 2), parm1 = c(0.5, 1), parm2 = c(1, 1.5)) qmvlogis(p = 0.5, parm1 = c(0.5, 1), parm2 = c(1, 1.5))	0.4717097 0.188494 1.6041
Burr ( $a = 3, d_1 = 1$ , $d_2 = 3, c_1 = 2, c_2 = 5$ ) ( $x_1, x_2$ ) = (0.5, 1)	pmvburr(q = c(0.5, 1), parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5)) smvburr(q = c(0.5, 1), parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5)) qmvburr(p = 0.5, parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5))	0.4854017 0.01302666 0.6853613
Cook-Johnson's Uniform ( $a = 0.3$ ) ( $x_1, x_2$ ) = (0.5, 0.75)	pmvunif(q = c(0.5, 0.75), parm = 0.3) smvunif(q = c(0.5, 0.75), parm = 0.3) qmvunif(p = 0.5, parm = 0.3, dim = 2)	0.4782716 0.2282716 0.598348
Generalized Lomax ( $a = 5$ , $\theta_1 = 0.5$ , $\theta_2 = 1, l_1 = 2, l_2 = 4$ ) ( $x_1, x_2$ ) = (0.5, 1)	pmvglomax(q = c(0.5, 1), parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4)) smvglomax(q = c(0.5, 1), parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4)) qmvglomax(p = 0.5, parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4))	0.2645588 0.2832001 1.050651
F ( $df = (4, 6, 9)$ ) ( $x_1, x_2$ ) = (1, 2)	pmvf(q = c(1, 2), df = c(4, 6, 9)) smvf(q = c(1, 2), df = c(4, 6, 9)) qmvf(p = 0.5, df = c(4, 6, 9))	0.4418794 0.2296895 1.448382
Inverted Beta ( $a = 4, l_1 = 2, l_2 = 6$ ) ( $x_1, x_2$ ) = (1, 2)	pmvinvbeta(q = c(1, 2), parm1 = 4, parm2 = c(2, 6)) smvinvbeta(q = c(1, 2), parm1 = 4, parm2 = c(2, 6)) qmvinvbeta(p = 0.5, parm1 = 4, parm2 = c(2, 6))	0.5873188 0.1245114 1.568017

**Table 4:** Example code for computation of CDF, survival function, and equicoordinate quantile from bivariate distributions.

```
loglik.uniform <- function(data, par) {
  ll = sum(dmvunif(data, parm = par, log = TRUE))
}

loglik.glomax <- function(data, par) {
  a = par[1]
  theta = par[2:((length(par) + 1) / 2)]
  L = par[((length(par) + 1) / 2 + 1):(length(par))]
  ll = sum(dmvglomax(data, parm1 = a, parm2 = theta, parm3 = L, log = TRUE))
}

loglik.invbeta <- function(data, par) {
  a = par[1]
  l = par[-1]
  ll = sum(dmvinvbeta(data, parm1 = a, parm2 = l, log = TRUE))
}
```

Next, in order to create a data set in each case, we draw random sample of size  $n = 300$ . In each case, the random sampling is done by setting `set.seed(1)` in advance but not shown in the following code.

```

bvtMP1 <- rmvmpareto1(n = 300, parm1 = 5, parm2 = c(0.5, 2))

bvtlogis <- rmvlogis(n = 300, parm1 = c(0.5, 1), parm2 = c(1, 1.5))

bvtburr <- rmv Burr(n = 300, parm1 = 3, parm2 = c(1, 3), parm3 = c(2, 5))

bvtuniform <- rmvunif(n = 300, parm = 0.3, dim = 2)

bvtglomax <- rmvglomax(n = 300, parm1 = 5, parm2 = c(0.5, 1), parm3 = c(2, 4))

bvtinvtbeta <- rmvinvtbeta(n = 300, parm1 = 4, parm2 = c(2, 6))

```

The following code performs the maximum likelihood estimation for our sample data sets with appropriate optimization methods and constraints as described in Table ?? . The output `est$convergence = 0` shows that, in each case, the convergence is successfully achieved, and `est$par` are the resulting estimated parameters.

- **Mardia's Pareto Type I** ( $a = 5, \theta_1 = 0.5, \theta_2 = 2$ ):

```

> minParm2 = 1 / apply(bvtMP1, 2, min)
> est = constrOptim(theta = c(10, 10, 10), f = loglik.mpareto1, grad = NULL,
+                   data = bvtMP1, ui = diag(3), ci = c(0, minParm2),
+                   control = list(fnscale = -1))
> est$convergence
[1] 0
> est$par
[1] 4.6386220 0.4997126 1.9978535

```

- **Logistic** ( $\mu_1 = 0.5, \mu_2 = 1, \sigma_1 = 1, \sigma_2 = 1.5$ ):

```

> est = optim(par = rep(10, 4), fn = loglik.logis, data = bvtlogis,
+            control = list(fnscale = -1))
> est$convergence
[1] 0
> est$par
[1] 0.3919998 0.8973157 0.9757377 1.5597609

```

- **Burr** ( $a = 3, d_1 = 1, d_2 = 3, c_1 = 2, c_2 = 5$ ):

```

> est = constrOptim(theta = rep(10, 5), f = loglik.burr, grad = NULL,
+                   data = bvtburr, ui = diag(5), ci = rep(0, 5),
+                   control = list(fnscale = -1))
> est$convergence
[1] 0
> est$par
[1] 3.9149862 0.6488968 2.0685892 1.9271949 5.0769719

```

- **Cook-Johnson's uniform** ( $a = 0.3$ ):

```

> est = optimize(f = loglik.uniform, data = bvtuniform,
+               interval = c(0, 100000), maximum = TRUE)
> est$maximum
[1] 0.3106469

```

- **Generalized Lomax** ( $a = 5, \theta_1 = 0.5, \theta_2 = 1, l_1 = 2, l_2 = 4$ ):

```

> est = constrOptim(theta = rep(10, 5), f = loglik.glomax,
+                   grad = NULL, data = bvtglomax, ui = diag(5),
+                   ci = rep(0, 5), control = list(fnscale = -1))
> est$convergence

```

```
[1] 0
> est$par
[1] 3.918698 0.546744 1.791263 1.703105 5.217363
```

- **Inverted Beta** ( $a = 4, l_1 = 2, l_2 = 6$ ):

```
> est = constrOptim(theta = rep(10, 3), f = loglik.invbeta, grad = NULL,
+                   data = bvtinvbeta, ui = diag(3), ci = rep(0, 3),
+                   control = list(fnscale = -1))
> est$convergence
[1] 0
> est$par
[1] 3.671536 1.824509 5.464654
```