

**Question 1 (20 marks)**

Please tick the option(s) that is/are always TRUE.

2 marks are awarded for every correctly ticked or unticked option.

- ☐ (EXAMPLE)  $2 + 1 = 0$
- ☒ (EXAMPLE)  $1 + 1 = 2$
- ☐ (a) In an Exponential regression setup, let  $\{Y_i\}_{i=1}^n$  denote independent observations with distribution  $Y_i \sim \text{Exponential}(g^{-1}(\mathbf{x}_i^T \boldsymbol{\theta}))$ , where  $g$  denotes the link function. Let  $\mu_i = E(Y_i)$ . Then, a suitable specification for  $g$  is  $g(\mu_i) = \log(\mu_i)$ , for  $\mu_i > 0$ .
- ☐ (b) Refer to part (a). Another suitable specification for  $g$  is  $g(\mu_i) = \sin(\mu_i)$ , for  $\mu_i > 0$ .
- ☐ (c) In a Binomial regression setup, let  $\{Y_i\}_{i=1}^n$  denote independent observations with distribution  $Y_i \sim \text{Binomial}(m_i, p_i)$ , where  $p_i = \Phi(\mathbf{x}_i^T \boldsymbol{\theta})$ ,  $\Phi$  denotes the standard normal CDF, and  $\boldsymbol{\theta} = (\theta_0, \theta_1, \theta_2)^T$  is a 3-dimensional column vector. We want to test  $H_0 : \theta_2 = 0$  against  $H_1 : \theta_2 \neq 0$ . Then, the Wald's test and the likelihood ratio test are equivalent.
- ☐ (d) Consider the saturated model for independent observations  $Y_i \sim N(\mu_i, \sigma^2)$  for  $i = 1, \dots, n$ . Then, the MLE for  $\mu_i$  is  $\tilde{\mu}_i = Y_i$  for  $i = 1, \dots, n$ .
- ☐ (e)  $\mathbf{X}$  is a  $n$  by  $p$  matrix such that  $r = r(\mathbf{X}) < p$ .  $\mathbf{C}$  is a full rank  $p$  by  $r$  matrix. Then,  $\mathbf{XC}$  is a full rank matrix.
- ☐ (f)  $\mathbf{X}$  is a  $n$  by  $p$  matrix such that  $n > p$  and  $r = r(\mathbf{X}) < p$ .  $\mathbf{C}$  is a  $p$  by  $r$  matrix such that  $\mathbf{XC}$  is a full rank matrix. Then,  $\mathbf{C}$  is a matrix with entries equal to either 0 or 1.
- ☐ (g)  $\mathbf{X}$  is the design matrix corresponding to the one-way ANOVA model with 3 levels:  $y_{ij} = \mu + \tau_i + \epsilon_{ij}$ , where  $i = 1, 2, 3$ ;  $j = 1, \dots, 7$ , and  $\epsilon_{ij} \sim N(0, \sigma^2)$ . Let

$$\mathbf{C} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}.$$

Then,  $\mathbf{XC}$  is a full rank matrix.

- ☐ (h)  $\mathbf{X}$  is the design matrix corresponding to the one-way ANOVA model with 4 levels:  $y_{ij} = \mu + \tau_i + \epsilon_{ij}$ , where  $i = 1, 2, 3, 4$ ,  $j = 1, \dots, 7$ , and  $\epsilon_{ij} \sim N(0, \sigma^2)$ . Let

$$\mathbf{C} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 0 \end{pmatrix}.$$

Then,  $\mathbf{XC}$  is a full rank matrix.

- ☐ (i) Consider the unit variance Gaussian density  $f(x; \mu) = (2\pi)^{-1/2} \exp\{-\frac{1}{2}(x - \mu)^2\}$ , for  $x \in \mathbb{R}$ , where the parameter is  $\mu \in \mathbb{R}$ . Then,  $f$  belongs to the exponential family of distributions.
- ☐ (j) Consider the Inverse-Gamma density  $f(x; \alpha, \beta) = (\beta^\alpha / \Gamma(\alpha))(x)^{-\alpha-1} \exp\{-\beta x\}$ , for  $x \geq 0$ , where the parameters are  $\alpha > 0$  and  $\beta > 0$ . Then,  $f$  belongs to the exponential family of distributions.

**Question 2 (18 marks)**

A drug company wishes to compare the percentage change in tumour size induced by three drugs in a clinical trial. Patients are randomly assigned to three drug groups A, B and C. Assume that patients' responses are independent of each other.

	Change in tumour size ( $y$ )					
Drug A:	7	-8	-10	-7	-9	
Drug B:	3	8	4	-4	-7	-6
Drug C:	-9	3	-4	-3	-2	-5

We consider a one-factor classification model  $y_{ij} = \mu + \tau_i + \epsilon_{ij}$ , where  $\epsilon_{ij} \sim N(0, \sigma^2)$  and  $i = 1, 2, 3; j = 1, \dots, n_i$

- (a) (4 marks) Express the one-factor ANOVA model in terms of its less-than-full-rank matrix form:  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$ . Provide full details of the entries and dimension of  $\mathbf{y}$ ,  $\mathbf{X}$ ,  $\boldsymbol{\beta}$ , and  $\boldsymbol{\epsilon}$ .

- (b) (4 marks) Use the below matrix to reparameterise your model in part (a) as a full-rank linear model:

$$\mathbf{C} = \begin{pmatrix} 0 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

Provide full details of the full-rank design matrix and coefficient vector in your reparameterised model. Also, express the coefficients in your full-rank linear model as linear combinations of  $\boldsymbol{\beta}$ .

- (c) (4 marks) Compute the sample means of observations from each group: Drug A, Drug B, Drug C.

- (d) (6 marks) A clinician hypothesize that all drug induces the same amount of change in tumour size. Verify that the clinician's hypothesis is testable and compute the corresponding test statistic. What is your conclusion at 5% significance level?

```
> vy1 <- c(7,-8,-10,-7,-9); sum((vy1 - mean(vy1))^2)
[1] 197.2
> vy2 <- c(3,8,4,-4,-7,-6); sum((vy2 - mean(vy2))^2)
[1] 189.3333
> vy3 <- c(-9,3,-4,-3,-2,-5); sum((vy3 - mean(vy3))^2)
[1] 77.33333
> c(qf(0.95,2,14),qf(0.95,1,14),qf(0.95,1,13))
[1] 3.738892 4.600110 4.667193
```

### Question 3 (16 marks)

Pearlie conducted an experiment to determine the influence of temperature (**Temp**) and moisture (**Moisture**) on the health (**Health**) of Bonsai trees. Three different temperature settings (Low, Medium, and High) and two moisture settings (Low, High) were considered. Health scores range between 0 to 10 with higher scores indicating better overall health.

- (a) (4 marks) In the initial phase of the experiment, she grew a total of  $n = 6$  bonsai plants – one plant under each combination of temperature-moisture settings. She used the following codes to fit an ANOVA model.

```
> names(BonsaiData)
[1] "Temp"      "Moisture"  "Health"
> BonsaiData$Health
[1] 4 6 3 2 9 7
> BonsaiData$Temp
[1] Low  Med  High Low  Med  High
Levels: High Low Med
> BonsaiData$Moisture
[1] "Low"  "Low"  "Low"  "High" "High" "High"
> summary(lm(Health~Temp))
```

Call:

```
lm(formula = Health ~ Temp)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	5.000	1.555	3.216	0.0487 *
TempLow	-2.000	2.198	-0.910	0.4300
TempMed	2.500	2.198	1.137	0.3381

---

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

Residual standard error: 2.198 on 3 degrees of freedom

Multiple R-squared: 0.5837, Adjusted R-squared: 0.3062

F-statistic: 2.103 on 2 and 3 DF, p-value: 0.2686

Provide details of the fitted reparameterised model in matrix form:  $\mathbf{y} = \tilde{\mathbf{X}}\boldsymbol{\gamma} + \boldsymbol{\epsilon}$ , where  $\tilde{\mathbf{X}}$  is a full-rank design matrix of dimension 6 by 3.

- (b) (6 marks) In the second phase of the experiment, Pearlie grew an additional four bonsai plants under various combinations of temperature and moisture settings. Data from both phases of the experiment are combined and used to refit the model in part (a). The ANOVA output of the re-fitted model is as follows:

```
> str(AdditionalBonsaiData)
'data.frame': 4 obs. of 3 variables:
 $ Temp      : chr  "Low" "Med" "High" "High"
 $ Moisture  : chr  "Low" "High" "Low" "High"
 $ Health    : num  3 7 2 7
> CombineData = rbind(BonsaiData, AdditionalBonsaiData)
> anova(lm(Health~Temp*Moisture, data=CombineData))
Analysis of Variance Table

Response: Health
          Df Sum Sq Mean Sq F value    Pr(>F)
Temp          2  28.583   14.2917   19.0556 0.009022 **
Moisture       1  10.012    10.0119   13.3492 0.021701 *
Temp:Moisture  2   14.405     7.2024    9.6032 0.029710 *
Residuals     4    3.000     0.7500
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> c(qf(0.95,2,4), qf(0.98,2,4), qf(0.95,1,4), qf(0.98,1,4))
[1]  6.944272  12.142136   7.708647  14.039615
```

Use the R output to test  $H_0$ : no interaction effect between temperature and moisture at 5% significance level. Include the null distribution of the test statistic, the value of your test statistic and conclusion in your answer.

- (c) (6 marks) Using the combined data from the two phases, Pearlie fitted a two-way ANOVA without interaction. The ANOVA output of the model is as follows:

```
> anova(lm(Health~Temp+Moisture,data=CombineData))
Analysis of Variance Table
```

```
Response: Health
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Temp	2	28.583	14.2917	4.9268	0.05421 .
Moisture	1	10.012	10.0119	3.4514	0.11257
Residuals	6	17.405	2.9008		

```
---
```

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

```
> c(qf(0.95,2,6),qf(0.98,2,6),qf(0.95,1,6),qf(0.98,1,6))
```

```
[1] 5.143253  8.052094  5.987378  9.876365
```

Use the R output to test  $H_0$  : *no Moisture effect* at 5% significance level. Include the null distribution of the test statistic, the value of your test statistic and conclusion in your answer.

**Question 4 (14 marks)**

The data frame `beetle` contains data on the concentration, `x`, of insecticides given to groups of beetles of size, `m`, and the subsequent number that died, `y`. Here is a table of the `beetle` data frame:

x	1.6907	1.7242	1.7552	1.7842	1.8113	1.8369	1.8610	1.8839
m	59	60	62	56	63	59	62	60
y	6	13	18	28	52	53	61	60

A binomial model is to be used to model the log odds of a beetle dying. At concentration  $x_i$ , the log odds are assumed to be  $\eta_i = \beta_1 + \beta_2 x_i$ , with parameters  $\beta = (\beta_1, \beta_2)$ .

- (a) (6 marks) Write down the canonical link of a Binomial regression model. Write down the domain and range of the link function, and verify that it is a monotonic function.



- (b) (3 marks) We found that the maximum likelihood estimates of  $\beta$  is  $\hat{\beta} = \begin{bmatrix} -60.71746 & 34.27033 \end{bmatrix}^T$  and the inverse of the corresponding Fisher Information matrix is:

$$\mathcal{I}(\hat{\beta})^{-1} = \begin{bmatrix} 26.839771 & -15.0821509 \\ -15.082151 & 8.4805597 \end{bmatrix}$$

Find the 90% confidence interval for  $\beta_1$ . Is  $-60$  a plausible value for  $\beta_1$  at this confidence level?

```
> c(qnorm(0.95), qnorm(0.975))  
[1] 1.644854    1.959964
```

- (c) (5 marks) Find the 95% confidence interval for the probability that a beetle dies at insecticide concentration 1.7.

**Question 5 (22 marks)**

The data `moons` contains the diameter, mass, distance from the sun, and number of moons for 13 planets, gas giants, and dwarf planets in our solar system. The variables are

- **Name:** a character variable with the name of the planet, gas giant, or dwarf planet
- **Distance:** distance from sun, relative to earth's
- **Diameter:** diameter of the planet, relative to earth's
- **Mass:** mass, relative to earth's
- **Moons:** number of moons

The first 3 rows of the data are shown below:

Name	Distance	Diameter	Mass	Moons
Mercury	0.39	0.382	0.0600	0
Venus	0.72	0.949	0.8200	0
Earth	1.00	1.000	1.0000	1

We want to see if the number of moons of a planet is related to its size. We will use Poisson regression (with log link) to model the number of moons of a planet.

- (a) (6 marks) We first fit a model that assumes the number of moons does not depend on any other variable in the data (Model 0). Next, we fit a model for the number of moons with predictors Diameter and Mass. We call this Model 1. The following R output is provided.

```
model0 <- glm(Moons~1,family = poisson(link = 'log'),data = moons)
model1 <- glm(Moons~ Mass + Diameter,family = poisson(link = 'log'),data = moons)
summary(model1)

# Call:
# glm(formula = Moons ~ Mass + Diameter, family = poisson(link = "log"),
#      data = moons)
#
# Deviance Residuals:
#      Min       1Q   Median       3Q      Max
# -2.45936  -2.05425  -0.91278   0.27366   4.32665
#
# Coefficients:
#              Estimate Std. Error z value Pr(>|z|)
# (Intercept)  0.71322809  0.19912109   3.5819 0.0003411 ***
# Mass        -0.00401033  0.00094609  -4.2388 2.247e-05 ***
# Diameter     0.41803308  0.03270228  12.7830 < 2.2e-16 ***
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# (Dispersion parameter for poisson family taken to be 1)
#
#      Null deviance: 388.2529  on 12  degrees of freedom
# Residual deviance:  44.8173  on 10  degrees of freedom
# AIC: 84.8331
#> c(qchisq(0.95,10), qchisq(0.95,2),qnorm(0.975))
# [1] 18.307038  5.991465  1.959964
```

Compared to Model 0, is Model 1 a better model for predicting the number of moons? Conduct an appropriate hypothesis test at 10% significance level and state clearly the test you use, the test statistic value, its null distribution, and the conclusion. *Hint: the Null deviance in the R output corresponds to the deviance of Model 0. The residual deviance corresponds to the deviance of Model 1.*

- (b) (5 marks) Use the R output in part (a) to answer this part: Test  $H_0 : \beta_{Diameter} = 0$  at 5% significance level. State the test statistic, null distribution of your test statistic, p-value, and the conclusion.

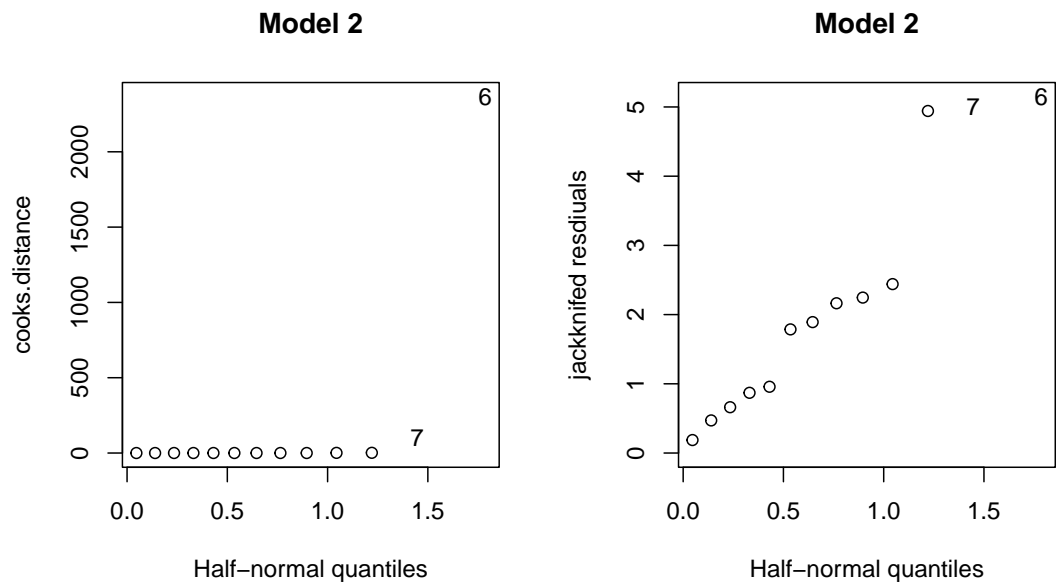
- (c) (7 marks) We suspect that distance from sun is also useful in predicting the number of moons of a planet. We then add `Distance` to our model, and call this new model Model 2. The model's summary is shown below (with `MISSING` output):

```
model2 <- glm(Moons~ Mass + Diameter + Distance, family = poisson(link = 'log'),
data = moons)
summary(model2)

# Call:
# glm(formula = Moons ~ Mass + Diameter + Distance, family = poisson(link = "log"),
#      data = moons)
#
# Deviance Residuals:
#      Min       1Q   Median       3Q      Max
# -2.34540  -1.73936  -0.87962   0.27045   4.40580
#
# Coefficients:
#              Estimate Std. Error  z value Pr(>|z|)
# (Intercept) MISSING1    0.33261090   0.9390  0.34776
# Mass        -0.00392976  0.00094607 MISSING2 3.271e-05 ***
# Diameter     0.44500885 MISSING3     11.6350 < 2.2e-16 ***
# Distance     0.01410618 MISSING4      1.7067  0.08788 .
# ---
# Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#
# (Dispersion parameter for poisson family taken to be MISSING5)
#
#      Null deviance: MISSING6  on 12  degrees of freedom
# Residual deviance:  41.8974  on MISSING7  degrees of freedom
```

Compute all `MISSING` output

- (d) (4 marks) The figure below shows the half-normal plots of Cook's distance (left panel) and jackknife residuals (right panel) from Model 2. Can you identify any influential observations or outliers from the two plots?



**Question 6 (10 marks)**

A large postal survey on the psychology of debt was conducted with 381 participants. The data is imported in R under the name **debt**. In this data, the frequency of credit card use is a three-level factor ranging from never, through occasionally to regularly. We are interested in building a model for predicting credit card use as a function of the other variables. The variables in the data are:

- **ccarduse**: how often did s/he use credit cards (a factor of 3 levels: never, occasionally, regularly)
- **children**: number of children in household
- **manage**: self-rating of money management skill (high values=high skill)
- **locintrn**: score on a locus of control scale (high values=internal)
- **prodebt**: score on a scale of attitudes to debt (high values=favourable to debt)
- **singpar**: is the respondent a single parent ? (a factor with levels: 0 = No, 1 = Yes)

We will fit multinomial logit models to this data.

- (a) (6 marks) We first assume that frequency of credit card use depends on all other variables except `manage`. We call this Model A. The summary of Model A is shown below.

```
# Call:
# multinom(formula = ccarduse ~ children + locintrn + prodebt +
#           singpar, data = debt)
#
# Coefficients:
#             (Intercept)  children  locintrn  prodebt  singpar1
# occasionally    -2.06177 -0.114668  0.0211954  0.407830 -0.432893
# regularly       -5.77064 -0.210404  0.4371748  0.955684 -0.463336
#
# Std. Errors:
#             (Intercept)  children  locintrn  prodebt  singpar1
# occasionally    0.926473  0.116407  0.142538  0.185453  0.531529
# regularly       1.082938  0.127205  0.158297  0.199827  0.591830
```

According to model A, what is the probability of a person to “never”, “occasionally” and “regularly” use their credit card, given that this person has 2 children, locus of control score 2, attitudes to debt score 3.0 and a single parent ?



- (b) (4 marks) We now add variable `manage` to Model A and call this Model B. The new model's summary is shown below. At significant level 5%, test the adequacy of model B.

The deviance of Model A and Model B are 734.3599 and 726.31306 respectively.

```
modelB <- multinom(ccarduse ~ ., debt)
summary(modelB,digits = 6)
# Call:
# multinom(formula = ccarduse ~ ., data = debt)
#
# Coefficients:
#               (Intercept)   children   manage   locintrn   prodebt   singpar1
# occasionally    -3.61581 -0.0930887  0.316138 -0.00812246  0.516055 -0.372842
# regularly       -7.55512 -0.1875308  0.373647  0.39712055  1.073635 -0.402110
#
# Std. Errors:
#               (Intercept) children   manage locintrn   prodebt singpar1
# occasionally    1.18869 0.118150 0.150050 0.143516 0.193305 0.535481
# regularly       1.34353 0.128873 0.160573 0.159870 0.208181 0.600022
> c(qchisq(0.95,2),qchisq(0.95,12),qchisq(0.95,369))
[1]  5.991465 21.026070 414.792164
```

Table XII: Discrete Distributions

Probability Distribution and Parameter Values	Probability Mass Function	Moment-Generating Function	Mean $E(X)$	Variance $\text{Var}(X)$	Examples
<b>Bernoulli</b> $0 < p < 1$ $q = 1 - p$	$p^x q^{1-x}, x = 0, 1$	$q + pe^t$	$p$	$pq$	Experiment with two possible outcomes, say success and failure, $p = P(\text{success})$
<b>Binomial</b> $n = 1, 2, 3, \dots$ $0 < p < 1$	$\binom{n}{x} p^x q^{n-x},$ $x = 0, 1, \dots, n$	$(q + pe^t)^n$	$np$	$npq$	Number of successes in a sequence of $n$ Bernoulli trials, $p = P(\text{success})$
<b>Geometric</b> $0 < p < 1$ $q = 1 - p$	$q^{x-1} p,$ $x = 1, 2, \dots$	$\frac{pe^t}{1 - qe^t}$	$\frac{1}{p}$	$\frac{q}{p^2}$	The number of trials to obtain the first success in a sequence of Bernoulli trials
<b>Hypergeometric</b> $x \leq n, x \leq N_1$ $n - x \leq N_2$ $N = N_1 + N_2$ $N_1 > 0, N_2 > 0$	$\frac{\binom{N_1}{x} \binom{N_2}{n-x}}{\binom{N}{n}}$		$n \frac{\binom{N_1}{1}}{\binom{N}{1}}$	$n \frac{\binom{N_1}{1} \binom{N_2}{1}}{\binom{N}{1} \binom{N}{1}} \frac{(N-n)}{(N-1)}$	Selecting $r$ objects at random without replacement from a set composed of two types of objects
<b>Negative Binomial</b> $r = 1, 2, 3, \dots$ $0 < p < 1$	$\binom{x-1}{r-1} p^r q^{x-r},$ $x = r, r+1, \dots$	$\frac{(pe^t)^r}{(1 - qe^t)^r}$	$\frac{r}{p}$	$\frac{rq}{p^2}$	The number of trials to obtain the $r$ th success in a sequence of Bernoulli trials
<b>Poisson</b> $0 < \lambda$	$\frac{\lambda^x e^{-\lambda}}{x!},$ $x = 0, 1, \dots$	$e^{\lambda(e^t - 1)}$	$\lambda$	$\lambda$	Number of events occurring in a unit interval, events are occurring randomly at a mean rate of $\lambda$ per unit interval
<b>Uniform</b> $m > 0$	$\frac{1}{m}, x = 1, 2, \dots, m$		$\frac{m+1}{2}$	$\frac{m^2 - 1}{12}$	Select an integer randomly from $1, 2, \dots, m$

Table XIII: Continuous Distributions

Probability Distribution and Parameter Values	Probability Density Function	Moment-Generating Function	Mean $E(X)$	Variance $\text{Var}(X)$	Examples
<b>Beta</b> $0 < \alpha$ $0 < \beta$	$\frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha)\Gamma(\beta)} x^{\alpha-1} (1-x)^{\beta-1},$ $0 < x < 1$		$\frac{\alpha}{\alpha + \beta}$	$\frac{\alpha\beta}{(\alpha + \beta + 1)(\alpha + \beta)^2}$	$X = X_1/(X_1 + X_2)$ , where $X_1$ and $X_2$ have independent gamma distributions with same $\theta$
<b>Chi-square</b> $r = 1, 2, \dots$	$\frac{x^{r/2-1} e^{-x/2}}{\Gamma(r/2) 2^{r/2}},$ $0 < x < \infty$	$\frac{1}{(1 - 2t)^{r/2}}, t < \frac{1}{2}$	$r$	$2r$	Gamma distribution, $\theta = 2$ , $\alpha = r/2$ ; sum of squares of $r$ independent $N(0, 1)$ random variables
<b>Exponential</b> $0 < \theta$	$\frac{1}{\theta} e^{-x/\theta}, 0 \leq x < \infty$	$\frac{1}{1 - \theta t}, t < \frac{1}{\theta}$	$\theta$	$\theta^2$	Waiting time to first arrival when observing a Poisson process with a mean rate of arrivals equal to $\lambda = 1/\theta$
<b>Gamma</b> $0 < \alpha$ $0 < \theta$	$\frac{x^{\alpha-1} e^{-x/\theta}}{\Gamma(\alpha)\theta^\alpha},$ $0 < x < \infty$	$\frac{1}{(1 - \theta t)^\alpha}, t < \frac{1}{\theta}$	$\alpha\theta$	$\alpha\theta^2$	Waiting time to $\alpha$ th arrival when observing a Poisson process with a mean rate of arrivals equal to $\lambda = 1/\theta$
<b>Normal</b> $-\infty < \mu < \infty$ $0 < \sigma$	$\frac{e^{-(x-\mu)^2/2\sigma^2}}{\sigma\sqrt{2\pi}},$ $-\infty < x < \infty$	$e^{i\mu t + \sigma^2 t^2/2}$	$\mu$	$\sigma^2$	Errors in measurements; heights of children; breaking strengths
<b>Uniform</b> $-\infty < a < b < \infty$	$\frac{1}{b-a}, a \leq x \leq b$	$\frac{e^{ib} - e^{ia}}{i(b-a)}, t \neq 0$ $1, t = 0$	$\frac{a+b}{2}$	$\frac{(b-a)^2}{12}$	Select a point at random from the interval $[a, b]$