This data is used in Chapter 11 to illustrate graphical methods for checking model assumptions following a proportional hazards regression analysis. In section 11.3, the martingale residuals are used to check overall model fit. In section 11.4, score residuals are used to check the proportional hazards assumption on disease-free survival for type of transplant. In section 11.5, the use of deviance residuals is illustrated for checking for outliers and, in section 11.6, the influence of individual observations is examined graphically.

In Chapter 12, this data set is used to illustrate the fit of parametric models using the accelerated failure-time model. The goodness of fit of these models is also discussed. Diagnostic plots for checking the fit of a parametric regression model using this data set are illustrated in section 12.5.

1.10 Bone Marrow Transplants for Hodgkin's and Non-Hodgkin's Lymphoma

The data in Table 1.5 was collected on 43 bone marrow transplant patients at The Ohio State University Bone Marrow Transplant Unit.

TABLE 1.5

Times to death or relapse (in days) for patients with bone marrow transplants for Hodgkin's and non-Hodgkin's lymphoma

Allo NHL		*Auto NHL*		*Allo HOD*		*Auto HOD*	
T_i	δ_i	T_i	δ_i	T_i	δ_i	T_i	δ_i
28	1	42	1	2	1	30	1
32	1	53	1	4	1	36	1
49	1	57	1	72	1	41	1
84	1	63	1	77	1	52	1
357	1	81	1	79	1	62	1
933	0	140	1			108	1
1078	0	176	1			132	1
1183	0	210	0			180	0
1560	0	252	1			307	0
2114	0	476	0			406	0
2144	0	524	1			446	0
		1037	0			484	0
						748	0
						1290	0
						1345	0

Details of this study can be found in Avalos et al. (1993). All patients had either Hodgkin's disease (HOD) or non-Hodgkin's lymphoma (NHL) and were given either an allogeneic (allo) transplant from an HLA-matched sibling donor or an autogeneic (auto) transplant where their own marrow was cleansed and returned to them after a high dose of chemotherapy. Of interest is a test of the null hypothesis of no difference in the leukemia-free-survival rate between patients given an allo or auto transplant, adjusting for the patient's disease state. This test, which requires stratification of the patient's disease is presented in section 7.5. The data, in Table 1.5, consists of the time on study for each patient, T_i, and the event indicator $\delta_i = 1$ if dead or relapsed; 0, otherwise.

1.11 Times to Death for Patients with Cancer of the Tongue

A study was conducted on the effects of ploidy on the prognosis of patients with cancers of the mouth. Patients were selected who had a paraffin-embedded sample of the cancerous tissue taken at the time of surgery. Follow-up survival data was obtained on each patient. The tissue samples were examined using a flow cytometer to determine if the tumor had an aneuploid (abnormal) or diploid (normal) DNA profile using a technique discussed in Sickle–Santanello et al. (1988). The following data in Table 1.6 is on patients with cancer of the tongue. Times are in weeks.

TABLE 1.6
Death times (in weeks) of patients with cancer of the tongue

Aneuploid Tumors:
Death Times: 1, 3, 3, 4, 10, 13, 13, 16, 16, 24, 26, 27, 28, 30, 30, 32, 41, 51, 65, 67, 70, 72, 73, 77, 91, 93, 96, 100, 104, 157, 167
Censored Observations: 61, 74, 79, 80, 81, 87, 87, 88, 89, 93, 97, 101, 104, 108, 109, 120, 131, 150, 231, 240, 400
Diploid Tumors:
Death Times: 1, 3, 4, 5, 5, 8, 12, 13, 18, 23, 26, 27, 30, 42, 56, 62, 69, 104, 104, 112, 129, 181
Censored Observations: 8, 67, 76, 104, 176, 231

The data is used in exercises.

the catheter. Compare these estimates to those obtained using the product-limit estimator.

(d) Fit a Weibull regression model to this data with a single covariate Z that indicates group membership. Test the hypothesis of no effect of catheter placement on the time to exit-site infection. Find estimates and 95% confidence intervals for the relative risk and the acceleration factor for exit-site infections. Provide an interpretation of these quantities.

12.3 In section 1.10, times to death or relapse (in days) are given for 23 non-Hodgkin's lymphoma (NHL) patients, 11 receiving an allogeneic (allo) transplant from an HLA-matched sibling donor and 12 patients receiving an autologous (auto) transplant. Also, data is given in Table 1.5 on 20 Hodgkin's lymphoma (HL) patients, 5 receiving an allogeneic (allo) transplant from an HLA-matched sibling donor and 15 patients receiving an autologous (auto) transplant. Because there is a potential for different efficacy of the two types of transplants for the two types of lymphoma, a model with a main effect for type of transplant, a main effect for disease type, and an interactive term is of interest.

(a) Using a Weibull regression model, analyze this data by performing a global test of no effect of transplant type and disease state on survival. Construct an ANOVA table to summarize estimates of the risk coefficients and the results of the one-degree-of-freedom tests for each covariate in the model. Estimate the covariance matrix of your estimates.

(b) Test the hypothesis of no disease-transplant type interaction using a likelihood ratio test.

(c) Find point estimates and 95% confidence intervals for the relative risk of death for an auto transplant NHL patient as compared to a NHL allo transplant patient.

(d) Test the hypothesis that the death rates are the same for HL allo transplants and NHL allo patients. Repeat this test for auto patients.

(e) Test the hypothesis that the death rates for auto transplant and allo transplant patients are the same against the alternative they are different for at least one disease group by a two-degree-of-freedom test of $H_o : h(t \mid \text{allo, NHL}) = h(t \mid \text{auto, NHL})$, $h(t \mid \text{allo, HL}) = h(t \mid \text{auto, HL})$.

(f) Compare your results to those found in Exercise 3 of Chapter 8 by using the semiparametric proportional hazards model.

12.4 Repeat Exercise 1 using the log logistic model. Compare your results to those found in that exercise. In part d, provide point and interval estimates of the acceleration factor and the relative odds.

Exercise 2 by making a quantile-quantile plot. Provide a crude estimate of the acceleration factor, and compare it to the estimate you found in Exercise 2.

12.13 In Exercise 1, you fit a Weibull regression model to explain the effect of ploidy on survival.

(a) Examine the fit of this model by making the appropriate plot of the Cox–Snell residuals.

(b) Examine the fit of this model by making the appropriate plot of the deviance residual's residuals.

(c) Repeat a and b for the log logistic regression model.

12.14 In Exercise 3, a Weibull regression model was fitted to the survival times of patients given a bone marrow transplant. The model included a covariate for type of transplant, type of disease and an interaction term.

(a) Examine the fit of this model by making the appropriate plot of the Cox–Snell residuals.

(b) Examine the fit of this model by making the appropriate plot of the deviance residuals.

(c) Repeat a and b for the log logistic regression model.