STATISTICAL CHALLENGES IN COMPARING CHEMOTHERAPY AND BONE MARROW TRANSPLANTATION AS A TREATMENT FOR LEUKEMIA

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Comparison of survival for patients treated with either post remission chemotherapy or allogeneic bone marrow transplantation (BMT) for leukemias is considered. Two designs for the comparison are considered. The first is a genetic randomized clinical trial. For this type of trial, comparisons can be made either by an intent-to-treat analysis or by a time dependent covariate model. The second design compares data from a multicenter chemotherapy trial with data from a large transplant registry. Here analysis is complicated by the registry only observing patients who are transplanted so adjustments needs to be made for patients who die or relapse while waiting for transplant. Corrections suggested for this source of bias are a matching technique, inclusion of a time dependent covariate and a left truncated Cox model. We examine these techniques through a small Monte Carlo study and compare how much information is lost by using registry data as compared to a genetically randomized trial.

1. Introduction

Both chronic and acute leukemias are treated by one of two treatment modalities: intensive chemotherapy or bone marrow transplantation. Both treatment regimes have shown varying efficacies for different types of leukemia and for different disease states. A obvious question of clinical significance is which of the these two treatments is better. The comparison presents a number of statistical challenges in design and analysis. In this note we shall examine two designs one may use for comparison of a chemotherapy regime (CT) to an allogeneic bone marrow transplant (BMT). These methods are the so-called genetically randomized trial and the comparison of data from multicenter chemotherapy trials to bone marrow transplant data collected by a large registry.

In both types of studies the outcome of interest is the time to some terminal event. Both will typically start with a time origin at a time t_0 where the patient's disease is diagnosed or in remission. Of clinical interest is the time, measured from this point, to recurrence of the leukemia (Relapse), to death without recurrence of the leukemia (Death in Remission) or to the failure of the treatment when a patient either dies or relapses (Leukemia Free Survival, LFS). When comparing relapse rates, patients who die without recurrence of the leukemia are treated as censored observations while when death in remission is the event of interest

patients who relapse are treated as censored. Care must be taken in interpreting analyses based on relapse or death in remission since the censoring times are not independent. Most comparisons will focus on leukemia free survival rates since this best reflects the success rates of the treatments under study. The leukemia free survival rate is usually very close to the overall survival rate since patients tend to die very soon after relapsing.

The two types of studies share common statistical challenges. The first, once the terminal event is chosen, is the choice of an appropriate time scale. For patients with a suitable donor there is a waiting time from t_0 until the transplant is performed. This time may be relatively short if a donor is readily available and the patient is in reasonably good health except for the leukemia. It may be quite long if no donor is immediately available, if the patient needs additional treatment for conditions which preclude a transplant or for chronic leukemias where a patient may stay in a stable phase for a long time allowing transplant to be electively delayed. Some patients who have an available donor and are scheduled for a transplant may die or relapse while waiting for their transplant. Adjustments must be made for this loss in any analysis.

A second challenge is to account for differences in baseline characteristics between patients receiving the two treatments. These characteristics may have the same effect on outcome for both treatments (e.g., disease state, waiting time to remission), have different effects on outcome for the two treatments (e.g., white blood count at t_0) or affect outcome for only one of the treatments (e.g., Donor-recipient sex match for BMT patients). For patients given a bone marrow transplant there may also be a need to make adjustments for intermediate events that occur at random times in the course of a patient's recovery. For example, one may need to adjust for the occurrence of acute or chronic graft-versus-host disease. While these are important concerns, we shall focus on the first challenge of how to handle the different time scales for chemotherapy and transplant patients.

2. Prospective "Randomized" Trials

The "gold" standard for comparison of therapies in medicine is the randomized clinical trial. Here patients are assigned to treatment by some stochastic mechanism. This randomization serves to balance potential risk factors between the two treatments and remove potential physician and patient biases in selecting treatment.

The ideal randomized clinical trial of chemotherapy to allogeneic bone marrow transplantation would be based on a population of patients who had available, at time t_0, an appropriate donor. The patient would then be randomized to a chemotherapy regime or an immediate transplant. This would allow the LFS in the two arms of the trial to be analyzed by conventional statistical methods such as the log rank test or a proportional hazards regression model. It would eliminate the problem of accounting for the waiting time to transplant in the BMT sample. Such a trial would be easily interpretable by clinicians who are used to similar designs in the comparison of chemotherapy trials.

There are several problems with implementation of such a trial. First, there are logistical problems. These include, for example, the difficulty of having a pool of patients and/or donors available for an immediate transplant, scheduling problems inherent with the need for BMT patients to spend their initial recovery period in special rooms or beds, and the need, in some case, for attention to other conditions a patient may have at the time of diagnosis or remission. Second, there may be ethical problems associated with such a design. For a physician to put a patient on a randomized study he or she must believe that each

treatment is equally likely to be successful. A final problem is that, even if such studies can be implemented, they will involve small sample sizes that will only allow for detection of gross differences between the two treatments.

An alternative to the ideal randomized trial is a trial based on "genetic" randomization. Here sequential patients who meet the disease criterion are entered on study. Patients with a suitable donor are scheduled for a transplant while those without a donor are assigned to the chemotherapy arm. An assumption is made that the availability or non availability of a donor is sufficiently random that the results of such a trial will mimic a purely randomized trial.

There are two possible ways to analyze such a trial. While any of a variety of statistical methods can be used to compare the survival experience in the two arms (cf. Andersen et al (1993) for a survey) we shall focus on the Cox (1972) proportional hazards model. The most common type of analysis is based on an intent-to-treat analysis. Here patients are assigned to the appropriate arm at time t_0 and treatment is modeled by a fixed time covariate. Patients who die or relapse in the transplant arm without receiving a transplant are counted against transplant. The second type of analysis uses a time dependent covariate, $Z(t)$, with the value 1 after a patient is transplanted and 0 if the patient has yet to be transplanted or is in the chemotherapy arm. This is analogous to the type of analysis done on the Stanford Heart Transplant Study (c.f. Turnbull et al (1974)). Note that here patients with a donor who die or relapse prior to transplant are counted against the chemotherapy arm. For both types of analysis adjustments for possible covariates are made to both arms in the final Cox model.

Which type of analysis to use is open to debate (See Nowak (1994) for a recent discussion of these issues). The intent to treat analysis is simple for clinicians to understand. It uses the same time scale for both arms so that natural estimates of the LFS curves can be constructed. It handles deaths or relapses while waiting for transplant quite simply. The time-dependent covariate approach, on the other hand only puts patients in the transplant group after transplant. Since most transplant patients are treated similarly to chemotherapy patients until the time of transplant this may be appropriate. The approach may be more reasonable when some of the risk factors that need adjustment are clearly time dependent as well. For example the donor-recipient sex match is only relevant for patients actually transplanted not those whom we intend to transplant. In section 4 we shall compare the statistical performance of the two methods based on our Monte Carlo study.

Regardless of the analysis method there are several disadvantages to genetically randomized studies. First, they are typically small, single institutional studies so that only very gross differences in LFS can be found. Second, the genetic randomization may bias one or the other of the arms if survival is related to genotype or if genotype is related to some other factor that is itself related to survival. Lastly, this type of randomization does not insure balance between the two groups in other prognostic factors and may make adjustments for these factors difficult.

3. The Use Of Registry Data

An alternative to small randomized trials of chemotherapy versus transplantation is to make comparisons based on data from a registry of transplant patients and from multicenter chemotherapy trials. This approach, as noted by Davis (1988), allows for the pooling

of patients from many institutions in a natural way to greatly increase the power of the comparison between the two treatment modalities.

A source of data on bone marrow transplantation worldwide is the International Bone Marrow Transplant Registry (IBMTR). This registry, formed in 1972, collects data on successive transplants at 238 transplant centers in 42 countries. On the basis of surveys conducted by the IBMTR these teams account for about sixty percent of all the teams in the world performing allogeneic transplants. During the period 1989-1992 there were over 8,000 transplants reported to the registry. (See Bortin (1992) for additional details on the IBMTR).

Data on chemotherapy patients to be used in conjunction with transplant data from the IBMTR has come from several sources. For example, data from the German Multicenter ALL Trial has been used to study Acute Lymphoblastic Leukemia (ALL) in first remission (Horowitz el al (1991)), data from the Medical Research Council in Oxford has been used to study Acute Myelogenous Leukemia (AML) (Gale et al (1991)), data from Pediatric Oncology Group has been used to study ALL in second remission in children, and data from the Italian Cooperative Study Group has been used to study Chronic Myeloid Leukemia.

Analysis of these types of studies requires special care due to the different time scales in the cohorts. For the chemotherapy cohort the clock starts at t_0 and relapse or death after that point is observable. For the registry cohort only those patients receiving transplants are observed. As opposed to the genetic randomized trial, patients who would have been transplanted but died or relapsed prior to transplant are not observed. That is, we observe a left-truncated sample of patients in the BMT cohort. Notice that the problem is not that the time from t_0 to the terminal event is unobservable, but rather that patients must experience an intermediate event (BMT) to be included in the study cohort.

To handle a comparison where one sample is measured from a fixed time t_0 and the sample is left-truncated three methods have been suggested. The first is to ignore the truncation and proceed as for the genetic randomized trial. Here either a fixed-time covariate or time dependent covariate analysis can be used. This approach will clearly lead to bias estimates of the BMT LFS rates since only patients who survive long enough to have a transplant will be included in the sample.

A second approach to analysis is to use a matched pair analysis. Here, for each transplant patient a matched chemotherapy patient is selected who shares common values of a few important covariates and who lives leukemia-free at least as long as the waiting time to transplant of the BMT patient. Comparison between treatments is made by a stratified log rank test which produces a censored data version of the sign test (See Andersen et al (1993) Section V.3).

The match pair analysis is particularly appealing to physicians since it is easy to understand. It should adjust the comparisons for fixed time covariates and it should remove potential biases due to the delayed entry of patients into the transplant cohort. One major drawback of the approach, as our Monte Carlo study shows, is that the results are quite sensitive to how the matching is done. A second drawback is that some of the statistical power available in the two samples is lost. This occurs when patients are discarded when no match can be found or when the smaller event time of the matched pair corresponds to a censored observation.

The third method of analysis is to used a left-truncated version of the Cox proportional hazards model (cf. Mantel and Byar (1974)). Here we redefine the risk set for the BMT cohort at time t to be all those patients who are alive leukemia-free with a transplant prior to time t. Thus the BMT risk set is initially empty and as t increases patients are added

to the risk set as their transplant time occurs and are deleted from the risk set as they experience the event or are censored. This test is the left-truncated version of both the fixed time and time dependent Cox models of the genetically randomized trial.

4. Monte Carlo Comparisons

We report here results of a Monte Carlo study comparing various methods for treatment comparisons. A log logistic model was assumed for the time to death or relapse for patients in the chemotherapy group. That is, the hazard rate for a chemotherapy patient is

$$h_c(t) = \frac{k(t/\theta)^{k-1}}{\theta[1+(t/\theta)^{k-1}]}, \quad \text{for } t,\, q,\, k > 0. \tag{4.1}$$

This model has a hump shaped hazard rate that is typical shape of the hazard rate we see in these types of studies. Note that θ is the median time to death and/or relapse.

For a patient in the transplant group we first generate a random transplant time, X, from the following density function

$$f(x) = \begin{cases} \phi x & \text{if } 0 \le x < 8 \\ \alpha \exp(-\gamma x) & \text{if } x \ge 8 \end{cases} \tag{4.2}$$

Once a transplant time is generated, the LFS time for the transplant patient is generated from the following conditional proportional hazards model:

$$h_T(t|X) = \begin{cases} \exp(\beta_1) h_c(t) & \text{if } t < X \\ \exp(\beta_2) h_c(t) & \text{if } t \ge X \end{cases} \tag{4.3}$$

Here the parameter β_1 models pre-transplant differences between the two samples and β_2 the effect of transplant.

Type I censoring was used in the study. Patients were entered into the study at a date E generated from a uniform [0,86] distribution. Patients were censored if $T+E$ was greater than 92 units where T is their LFS time. This insures that all patients have at least six units of follow-up.

Two sets of parameters are reported in this note. In model I we have $\phi = 0.009375, \gamma = 0.1071, \alpha = 0.1767, k = 2$ and $\theta = 10$. In model II we have $\phi = 0.015625, \gamma = 0.25, \alpha = 0.9236, k = 3$ and $\theta = 20$. Model I corresponds to a long waiting time to transplant with 30% of the transplants taking place prior to 8 time units, while model II corresponds to more early transplants with a median time to transplant of 8. When there is no difference in efficacy between the transplant and chemotherapy cohorts Model I has 11% censoring in both samples and 55% of the event times in the BMT group occurring prior to transplant, while Model II has 20% censoring and 13% early events.

For each of 1000 replicates a sample of n_c chemotherapy (CT) and n_b BMT patients is generated from each of the models. This sample models the complete data or genetically randomized sample. From this sample a truncated sample is constructed which consists of only those BMT patients who survived long enough to be transplanted.

We first consider the various methods for constructing a matched sample. Eligible matches for a BMT patient transplanted at time X are chemotherapy patients with an on study time $T > X$. Six matching techniques were considered. They are

Method 1: Pick a CT patient at random. Select at random a BMT patient from eligible BMT patients yet to be matched.

Method 2: Pick a BMT patient at random. Select at random a CT patient from the pool of eligible CT patients yet to be matched.

Method 3: Pick the BMT patient with the longest time to transplant. Match at random with a CT patient. Repeat with the BMT patient with the 2nd longest waiting time, etc.

Method 4: Pick BMT patient with the shortest time to transplant. Match at random with a CT patient. Repeat with the BMT patient with the 2nd smallest waiting time, etc.

Method 5: Pick CT patient with the smallest time on study. Match with an eligible BMT patient if possible. Repeat with the CT patient with the second smallest study time, etc.

Method 6: Pick CT patient with the longest time on study. Match with an eligible BMT patient if possible. Repeat with the CT patient with the second longest study time.

Table 1 give the estimated powers of a 0.05 level sign test (based on the score statistic from a stratified Cox regression model) for the six matching methods. Entries with a "+" or "−" are estimated significance levels more than two standard deviations away from the nominal 0.05 level. For those with a "+" the excess number of rejections was due to the one sided matched pairs test providing evidence that the LFS time was longer in the BMT cohort, while those with a "−" rejection was in favor of the CT cohort having longer LFS. The only method of matching which seems to provide the correct null significance level is method 4 which matches chemo patients to the smallest waiting time to BMT first. This method also seems to give the fewest number of matched pairs. Method 6 is matching too many long lived Chemo patients to short lived BMT patients. Methods 1,2,3 and 5 are matching too many long lived BMT patients to short lived chemo patients. Our extended Monte Carlo study showed that results are not an artifact of small sample sizes but hold for samples as large as 1000 in each arm. In our power study we shall use method 4 as the matching method.

Table 1: Null Powers Of A 0.05 Level Test Based On Matched Pairs

		n_c	n_b	n_c	n_b	n_c	n_b	n_c	n_b
		50	50	50	100	100	50	100	100
METHOD 1	Model I	0.171+		0.341+		0.146+		0.353+	
	Model II	0.084+		0.097+		0.086+		0.150+	
METHOD 2	Model I	0.081+		0.294+		0.060		0.092+	
	Model II	0.054		0.100+		0.052		0.069+	
METHOD 3	Model I	0.137+		0.721+		0.061		0.164+	
	Model II	0.070+		0.204+		0.051		0.099+	
METHOD 4	Model I	0.037		0.045		0.053		0.045	
	Model II	0.051		0.046		0.054		0.042	
METHOD 5	Model I	0.995+		0.936+		1.000+		1.000+	
	Model II	0.326+		0.095+		0.999+		0.580+	
METHOD 6	Model I	0.253−		0.043		0.743−		0.453−	
	Model II	0.066−		0.077−		0.814−		0.094−	

+ BMT > Chemo − BMT < Chemo

Table 2 compares the null performance of five possible test statistics. The first two are based on the complete sample and the remaining three on the truncated sample where patients with events prior to transplant in the BMT group are truncated. For the complete sample data the two tests are a scores test based on the Cox proportional hazards model with either a fixed covariate reflecting an intent to give the patient a transplant or a time dependent covariate with the value 1 if the patient has been transplanted and 0 otherwise. These two tests are also performed on truncated sample ignoring the fact the data is left truncated. Finally, a test based on the left truncated version of the Cox model is presented. Percentages with a "+" are more than two standard errors above 5%.

Table 2: Percent Of Samples Rejecting Null Hypothesis Based On A 5% Level Test

		COMPLETE SAMPLE				TRUNCATED SAMPLE TRUNCATION IGNORED					
		Fixed Time Covariate (Intent To Treat)		Time Dependent Covariate		Fixed Time Covariate		Time Dependent Covariate		Left Truncated Cox Model	
		Model	Model	Model	Model	Model	Model	Model	Model	Model	Model
n_c	n_b	I	II	I	II	I	II	I	II	I	II
50	50	6.7+	5.2	4.8	5.6	56.1+	8.7+	10.0+	6.2	6.1	5.5
50	100	6.4	5.9	6.3	5.0	56.0+	8.4+	8.8+	5.8	7.3+	4.7
100	50	4.4	5.8	5.7	4.8	74.1+	11.0+	29.3+	8.9+	4.9	5.3
100	100	5.1	5.0	5.2	5.2	85.1+	12.9+	15.0+	6.8+	4.8	4.7

From Table 2 we see that if we ignore the fact that the registry data is left truncated for large samples or for heavy truncation (Model I) both the fixed time and time dependent covariate approach reject the hypothesis of no difference in LFS too often. With the single exception of the $n_b = 50$, $n_c = 100$ case the left truncated Cox model holds its level. Both methods of analysis on the complete data sample perform within their nominal levels. Our study showed that this pattern holds for larger sample sizes and other censoring and truncation patterns.

The power study reported in Table 3 uses only those statistics that had the appropriate null levels. That is the two Cox models on the complete sample and the left truncated and matched pairs (Method 4) Cox models on the truncated samples.

The power study reveals several general patterns. When β_2 is not zero, for truncated samples the left truncated Cox model has higher power than the matched pairs Cox model. When β_2 is zero both tests give an average power not significantly different from the nominal 0.05 level test as is expected since they have no information on individuals who fail prior to transplant where the true differences lie. In this case the time dependent covariate approach in the complete sample has low power as well.

When $\beta_1 = 0$ so that there is no difference between BMT and Chemo patients prior to transplant the time dependent covariate approach in the complete sample out performs the intent to treat approach. There is only a slight drop in power when the left truncated Cox model is used in the reduced sample. There is a substantial drop in power using the matched pairs analysis. When the signs of β_1 and β_2 are the same, the intent to treat analysis has the highest power, while the left truncated Cox model out performs the time dependent covariate model. Again there is a substantial drop in power using the matched pairs analysis. When the signs of β_1 and β_2 are reversed the hazard rate of the BMT group

will cross that of the chemo group. Here the time dependent covariate model has better power then the intent to treat model and the left truncated Cox analysis power is close to the time dependent covariate model. As the truncation percentage increases we see a greater difference between the time dependent covariate analysis in the complete sample and that in the truncated sample. Finally, when $\beta_2 = 0$ both techniques based on the truncated sample have no ability to detect differences between the two treatments and the time dependent covariate approach has little power as well.

Table 3: Percent Of 1000 Samples Which Reject H_0 Based On A 5% Level Test

							COMPLETE SAMPLE		TRUNCATED SAMPLE	
n_b	n_c	Percent Censored Chemo	Percent Censored BMT	Percent Truncated	β_1	β_2	Intent To Treat	Time Dependent Covariate	Left Truncated Cox Model	Match Pairs
50	50	11	19	56	.000	-.693	24.8	58.9	55.7	30.9
50	50	21	35	13	.000	-.693	69.1	78.2	76.6	46.6
50	50	11	7	56	.000	.693	22.8	73.7	69.3	29.7
50	50	21	13	13	.000	.693	77.1	87.5	86.2	53.4
50	50	11	16	39	-.693	.000	39.5	13.0	5.5	6.5
50	50	20	21	9	-.693	.000	6.5	5.5	5.5	5.4
50	50	11	27	39	-.693	-.693	85.7	39.7	62.0	33.8
50	50	20	36	9	-.693	-.693	82.3	76.5	79.9	49.3
50	50	11	11	39	-.693	.693	7.2	95.2	75.0	41.0
50	50	21	14	9	-.693	.693	67.9	92.6	86.0	55.1
50	50	11	6	73	.693	.000	58.9	7.5	6.7	3.9
50	50	21	20	21	.693	.000	8.3	5.4	4.1	5.4
50	50	11	10	73	.693	-.693	22.4	58.0	41.5	19.5
50	50	21	32	21	.693	-.693	44.9	85.0	77.2	47.0
50	50	11	4	73	.693	.693	90.4	36.1	57.8	20.2
50	50	21	11	21	.693	.693	88.9	77.1	84.4	52.5
50	100	11	19	56	.000	-.693	30.2	63.9	61.7	29.2
50	100	21	35	13	.000	-.693	81.8	88.6	88.0	44.7
50	100	11	7	56	.000	.693	30.1	77.7	77.4	33.2
50	100	21	13	13	.000	.693	88.8	94.3	94.2	59.3
50	100	11	16	39	-.693	.000	47.5	8.0	5.6	4.8
50	100	20	21	9	-.693	.000	5.6	5.6	5.4	4.6
50	100	11	27	39	-.693	-.693	95.2	59.3	74.7	41.5
50	100	20	36	9	-.693	-.693	91.7	87.6	89.4	50.5
50	100	11	11	39	-.693	.693	4.6	95.8	88.4	43.5
50	100	21	14	9	-.693	.693	78.5	95.5	94.3	55.0
50	100	11	6	73	.693	.000	71.8	5.1	5.9	4.4
50	100	21	20	21	.693	.000	11.6	5.8	5.7	3.9
50	100	11	10	73	.693	-.693	28.7	57.5	48.0	20.0
50	100	21	32	21	.693	-.693	58.6	89.2	86.5	48.1
50	100	11	4	73	.693	.693	97.8	49.6	64.0	21.0
50	100	21	11	21	.693	.693	96.2	88.1	91.5	50.2

Table 3 (Continued): Percent Of 1000 Samples Which Reject H_0 Based On A 5% Level Test

							COMPLETE SAMPLE		TRUNCATED SAMPLE	
n_b	n_c	Percent Censored Chemo	Percent Censored BMT	Percent Truncated	β_1	β_2	Intent To Treat	Time Dependent Covariate	Left Truncated Cox Model	Match Pairs
100	50	11	19	56	.000	-.693	27.2	79.9	73.2	45.1
100	50	21	35	13	.000	-.693	84.0	92.2	91.3	52.6
100	50	11	7	56	.000	.693	31.2	91.8	84.5	33.2
100	50	21	13	13	.000	.693	86.3	96.0	93.6	53.6
100	50	11	16	39	-.693	.000	48.3	34.1	4.8	4.6
100	50	20	21	9	-.693	.000	6.6	8.0	5.3	5.7
100	50	11	27	39	-.693	-.693	95.4	37.6	80.8	44.9
100	50	20	36	9	-.693	-.693	93.3	86.2	92.0	52.4
100	50	11	11	39	-.693	.693	9.1	100.0	88.0	48.9
100	50	21	14	9	-.693	.693	79.7	98.9	93.4	54.0
100	50	11	6	73	.693	.000	68.5	15.9	5.2	5.4
100	50	21	20	21	.693	.000	8.5	9.6	5.4	5.0
100	50	11	10	73	.693	-.693	21.8	91.9	64.7	34.5
100	50	21	32	21	.693	-.693	54.2	96.6	89.1	52.3
100	50	11	4	73	.693	.693	96.1	43.0	77.1	41.4
100	50	21	11	21	.693	.693	94.4	84.7	91.7	57.9
100	100	11	19	56	.000	-.693	42.6	88.3	85.6	53.8
100	100	21	35	13	.000	-.693	93.0	97.0	96.3	78.4
100	100	11	7	56	.000	.693	41.2	95.4	95.4	55.3
100	100	21	13	13	.000	.693	97.9	99.6	99.4	83.7
100	100	11	16	39	-.693	.000	63.9	20.9	5.5	5.0
100	100	20	21	9	-.693	.000	8.8	5.3	5.8	5.5
100	100	11	27	39	-.693	-.693	98.6	65.7	88.6	57.1
100	100	20	36	9	-.693	-.693	98.3	96.4	97.7	79.0
100	100	11	11	39	-.693	.693	7.4	99.9	96.4	63.9
100	100	21	14	9	-.693	.693	93.5	99.9	99.4	84.5
100	100	11	6	73	.693	.000	85.3	8.1	5.3	4.7
100	100	21	20	21	.693	.000	11.3	6.1	4.7	5.0
100	100	11	10	73	.693	-.693	35.0	88.8	73.5	36.5
100	100	21	32	21	.693	-.693	72.9	99.0	96.6	73.0
100	100	11	4	73	.693	.693	99.8	63.2	86.4	42.3
100	100	21	11	21	.693	.693	99.3	97.3	98.7	81.3

5. Conclusions

The results of our limited simulation study seem to suggest that the use of registry data, if properly analyzed, results in little loss of information over a genetically randomized trial if

the survival experience of the transplant group pretransplant is comparable to that of the chemotherapy group. The most powerful analysis of studies of this type is that based on a method that accounts for delayed entry of BMT patients in the risk set at the time of transplant and not on matching. In fact, matching, if done inappropriately, may lead to erroneous conclusions with a rather high probability.

For complete samples we see that the time dependent covariate approach has the best power if the two groups mortality experience is similar prior to transplant. In discussing our Monte Carlo model with investigators in this area we were told that, after adjustments for initial covariates, the pretransplant hazard rates should be similar in the two groups. Which analysis to use depends on the assumptions to be made by the investigator. Note that in complete samples these are testable assumption.

In our Monte Carlo study we ignored other possible covariates that need to be adjusted for. We believe that after these adjustments similar conclusions should hold.

A picture or a survival curve is often worth as much to clinical investigators as a formal test. A product-limit estimator of survival curve can be computed using the left truncated data from a registry. This curve is an estimator of the conditional survival of a patient who was transplanted (see Andersen et al (1993) for details). The product-limit estimator based on the chemotherapy data is an estimator of an unconditional survival curve. An other summary survival curve is due to Begg et al (1984) which provides an estimator of the conditional probability of survival for a chemo patient given this time is larger that a randomly selected transplant time. This method while it has merits ignores the right truncated nature of the time to transplant in the BMT group. Further investigation into the merits of these estimates or into alternative methods of summarizing this data is warranted.

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