SUPPLEMENTAL MATERIAL

Supplemental Methods

I. Logistic regression

Methods

To further assess the strength of the association of power sheath and laser sheath with fibrosis score, we used a logistic regression model where a model selection process was applied for identifying key covariates. First, demographic and baseline clinical characteristics were entered into a logistic regression model one at a time, in which number of leads to be extracted, log transformed age of the oldest lead, and study center were forced in.

1) For power sheath, the variable "patient age" was identified to have a univariate association with the outcome (p-value < 0.20). The forced-in factors along with patient age were determined to be the covariates in the final multivariable logistic regression model.

2) For laser sheath, no variable was identified to have a univariate association with the outcome (p-value < 0.20). Therefore, what were forced in constructed the covariate set of the final multivariable logistic regression model.

Results

Table S1: Results for the multivariable logistic regression model for power sheath in which number of leads to be extracted, log transformed age of the oldest lead, and study center were forced in.

Variable	OR (95% CI)	P-value
Higher fibrosis score (fibrosis score 3&4 vs. 1&2)	2.78 (1.22, 6.31)	0.015
Number of leads to be extracted	2.15 (1.35, 3.43)	0.001
Age of the oldest lead (log transformed)	3.40 (1.88, 6.13)	<.001
Patient age	0.97 (0.95, 0.996)	0.024

Table S2: Results for the multivariable logistic regression model for laser sheath in which number of leads to be extracted, log transformed age of the oldest lead, and study center were forced in.

Variable	OR (95% CI)	P-value
Higher fibrosis score (fibrosis score 3&4 vs. 1&2)	2.33 (0.93, 5.84)	0.073
Number of leads to be extracted	1.61 (1.09, 2.37)	0.016
Age of the oldest lead (log transformed)	3.55 (1.93, 6.54)	<.001

II. Rank ANCOVA

Methods

Hettmansperger and McKean linear model aligned rank test has been implemented for the single covariate and one-way ANCOVA case, where it was stated that the test could be extended to the multiple covariate case. Basically, a robust regression model (PROC ROBUSTREG in SAS) was constructed to derive robust residuals which were then ranked from low to high (PROC RANK in SAS), followed by weighting the ranked residuals. A parametric ANOVA was subsequently performed on the weighted ranked residuals to obtain the aligned rank test statistic and the associated p-value. In the robust regression, model selection was conducted using the criteria of AICR and BICR (i.e. AIC and BIC for robust regression) to generate a final covariate set.

Given that random seed was involved in performing the robust regression with multiple covariates, iterations were run (N=1000 was applied, each with a different random seed), and the aligned rank test statistics generated in each iteration were averaged for the final aligned rank test.

SAS Code

```
* Model selection is conducted using the variable selection criteria of AICR and BICR, to generate
  a final covariate set for extract_duration and fluoroscopy_duration respectively;
proc robustreg data=lead_fibrosis method=mm;
  model <duration_variable> = <set of dempographic and baseline clinical characteristics>;
run;


* When performing PROC ROBUSTREG for multiple covariates that involves random seed, iterations are
  necessary - run 1000 iterations and get the average of the aligned rank test statistic and the
  corresponding Chi-square test p-value;

* Set up the dataset for the aligned rank test statistic with the initial value 0,
  for use of appending the test statistics generated in the iterations;
data initial;
  input HettMckeanChisqValue 8.;
  datalines;
  0
  ;
run;
data ma_HM0;
  set initial;
  format HettMckeanChisqValue 12.8;
run;

%macro mvrank (var=, cov=, grp=, run_count=);

%do i=1 %to &run_count;
proc robustreg data=lead_fibrosis method=mm seed=&i;
  model &var = &cov;  /*regress the covariates on the duration variable*/
  output out=res&i r=residual;
run;

proc rank data=res&i out=rank&i;
  var residual;
run;

data weight&i;
  set rank&i nobs=n;
  rename residual=RankedResidual;
  weight=12**.5*(residual/(n+1)-.5);  /*pre-specified weight is calculated*/
run;

proc glm data=weight&i;
  class &grp;
  model weight = &grp;
  ods output modelanova=ma&i(where=(hypothesistype=3));
run;
```

```
data ma&i;
  set ma&i;
  rename ss=HettMckeanChisqValue;
  ProbChisq=sdf('chisquare', ss, df);
  criticalValueChisq=quantile('chisquare', .95, df);
run;

title "The Hettmansperger and McKean Nonparametric One-Way ANCOVA (alighed rank test) Procedure for &var vs. &grp";
proc print data=ma&i noobs;
  var Dependent Source DF HettMckeanChisqValue ProbChisq CriticalValueChisq;
run;
title '';


data ma_HM&i;
  set ma&i;
  keep HettMckeanChisqValue;
run;

* Obtain the set of aligned rank test statistics from the iterations;
%let ilag = %SYSEVALF(&i - 1);
proc append base=ma_HM&i data=ma_HM&ilag;
run;

%end;


data ma_HM&run_count;
  set ma_HM&run_count;
  if HettMckeanChisqValue eq 0 then delete;
run;
proc print data=ma_HM&run_count; run;

proc means data=ma_HM&run_count noprint;
  var HettMckeanChisqValue;
  output out=avg_ss;
run;

data ss;
  set avg_ss;
  if _STAT_ in ('N', 'MIN', 'MAX', 'STD') then delete;
  ProbChisq=sdf('chisquare', HettMckeanChisqValue, 1);
run;
proc print data=ss; run;

%mend mvrank;

%mvrank (var=extract_duration, cov=<covariate set>, grp=higher_fibrosis, run_count=1000);
%mvrank (var=fluoroscopy_duration, cov=<covariate set>, grp=higher_fibrosis, run_count=1000);
```