

# Pediatric Bone Marrow Transplant Survival Prediction

Zoey Yu

# Brown University

Oct 24, 2024

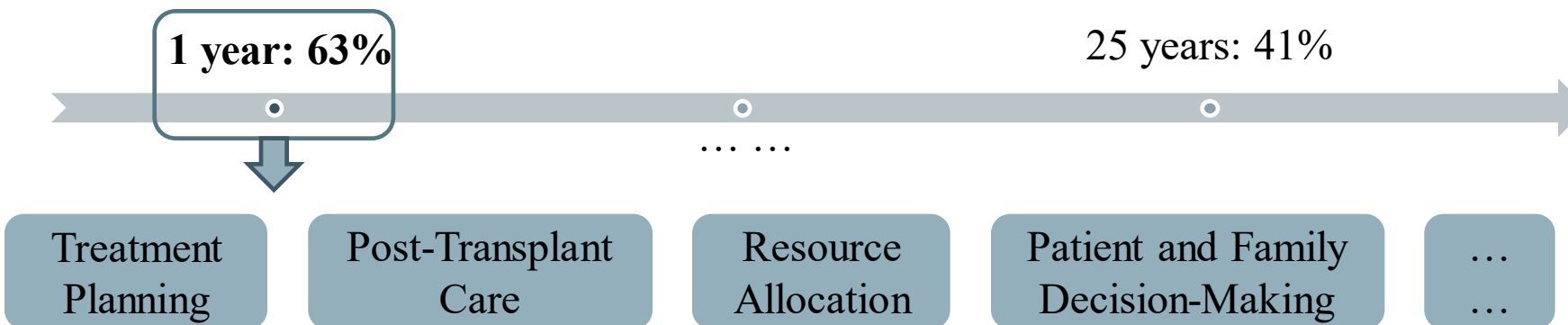


<https://github.com/Zoey-Yu98/data1030-midterm.git>



## Bone Marrow Transplant (BMT)

- To replace unhealthy bone marrow with healthy cells.
- One of the most effective treatments for blood related cancer and diseases (leukemia, lymphoma, and multiple myeloma)
- **BMTs have serious risks and low survival rate**

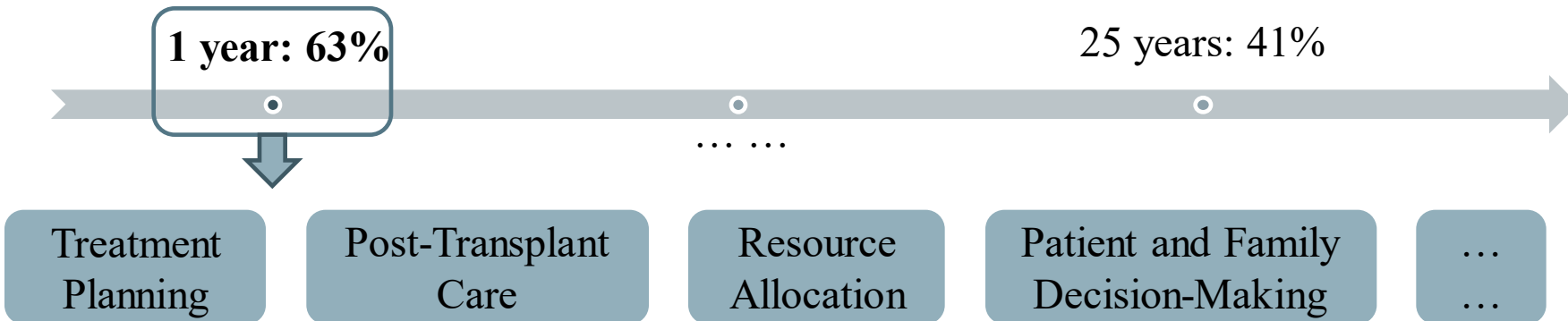




## Bone Marrow Transport (BMT)

### A Post-op 1-yr Survival Status Prediction → Decisions Making

- BMTs have serious risks and low survival rate



### Dataset Brief

- Hospital in Poland, from 2000 to 2010
- **187 Pediatric Patients** who underwent BMTs
- **37 Attributes**
  - **Pre-op Parameters** (e.g. Age, Gender, Blood Type, Disease, Antigen)
  - **Post-op Assessments** (e.g. Graft versus Host Disease (GvHD))
- **Classification Problem** (1 Year after Surgery, **Alive** or **Dead**)



**Source:** Sikora, M., Wróbel, Ł., & Gudyś, A. (2020). Bone marrow transplant: children [Dataset]. UCI Machine Learning Repository. <https://doi.org/10.24432/C5NP6Z>.

## Basic Understanding Of The Data

### 1. Data is iid within each feature

One patient

187 rows  
×  
37 columns

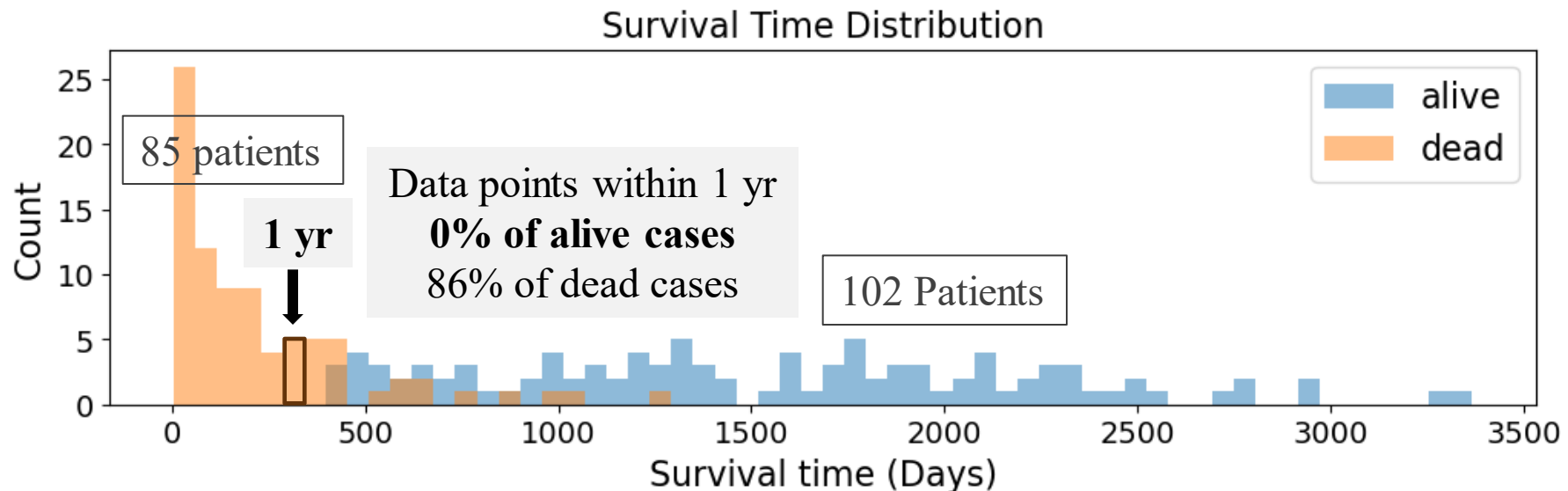
	Recipientgender	Stemcellsource	Donorage	Donorage35	IIIV	Disease	...	survival_time	survival_status
0	b'1'	b'1'	22.830137	b'0'	b'1'	b'ALL'		999.0	0.0
1	b'1'	b'0'	23.342466	b'0'	b'1'	b'ALL'		163.0	1.0
2	b'1'	b'0'	26.394521	b'0'	b'1'	b'ALL'	...	435.0	1.0
3	b'0'	b'0'	39.684932	b'1'	b'1'	b'AML'		53.0	1.0
4	b'0'	b'1'	33.358904	b'0'	b'0'	b'chronic'		2043.0	0.0
...	...	...	...	...	...	...		...	...

Target Variable  
1-yr survival status

alive

dead

**Survival Time:** Time of observation (if alive '0') or time of death (if dead '1') in days



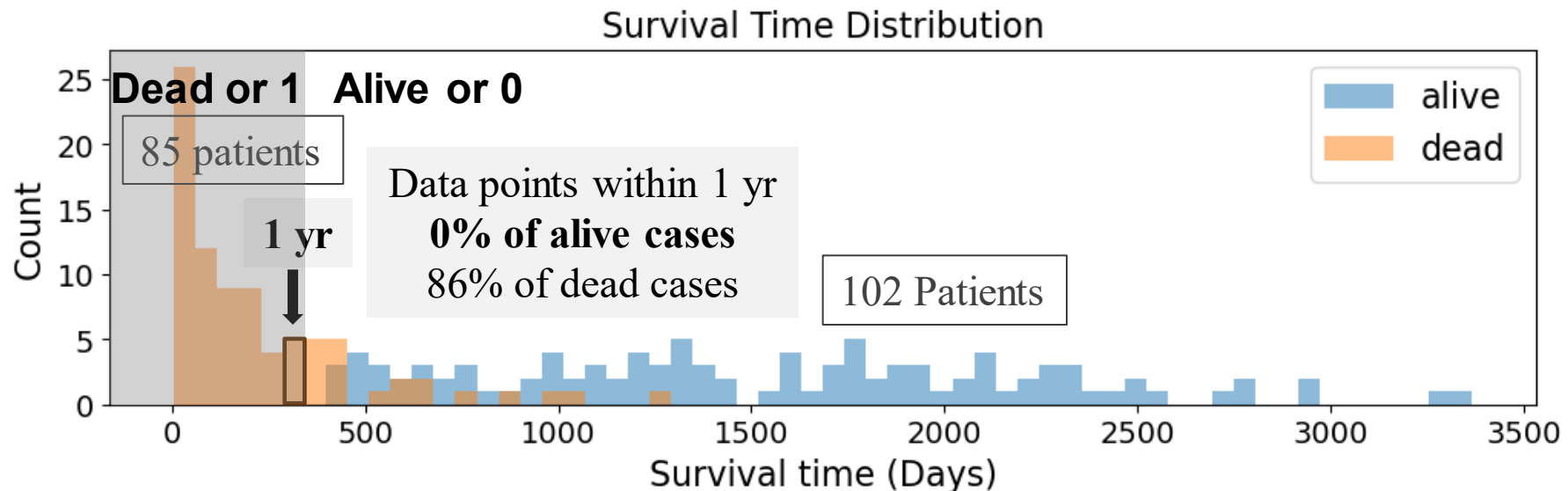


## Basic Understanding Of The Data

### 1. Data is iid within each feature

One patient		187 rows × 37 columns										
		Recipientgender	Stemcellsource	Donorage	Donorage35	IIIV	Disease	...	survival_time	survival_status	1_year_survival_status	
		0	b'1'	b'1'	22.830137	b'0'	b'1'	b'ALL'	999.0	0.0	0	
		1	b'1'	b'0'	23.342466	b'0'	b'1'	b'ALL'	163.0	1.0	1	
		2	b'1'	b'0'	26.394521	b'0'	b'1'	b'ALL'	...	435.0	1.0	0
		3	b'0'	b'0'	39.684932	b'1'	b'1'	b'AML'	53.0	1.0	1	
		4	b'0'	b'1'	33.358904	b'0'	b'0'	b'chronic'	2043.0	0.0	0	
		...	...	...	...	...	...	...	...	...		

**Goal: Postoperatively, to predict 1-year survival status.**



## Basic Understanding Of The Data

### 1. Data is iid within each feature

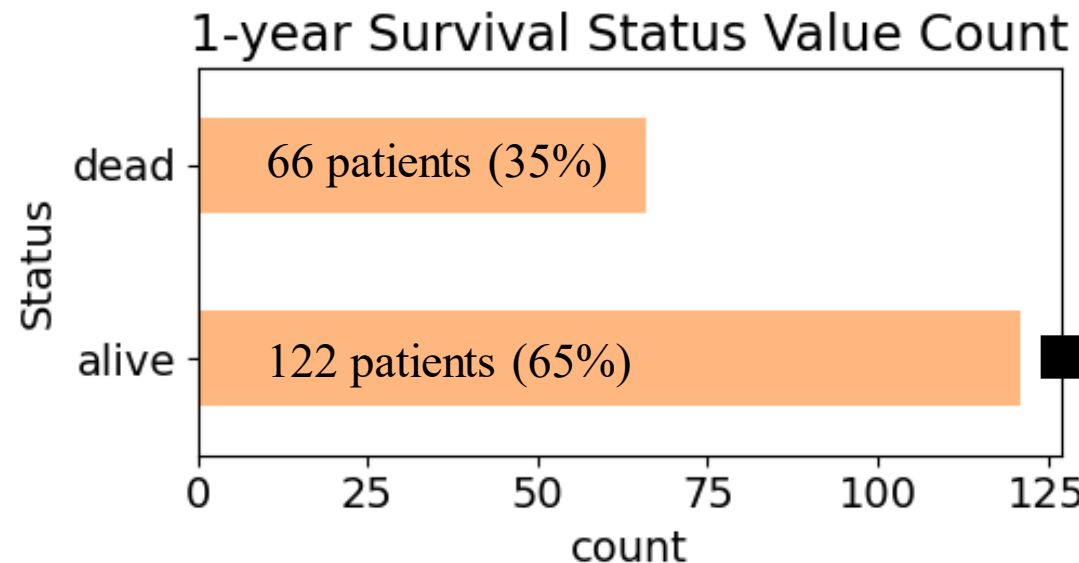
1. Data is iid within each feature

One patient

187 rows  
×  
37 columns

Recipientgender	Stemcellsource	Donorage	Donorage35	IIIV	Disease	...	survival_time	survival_status	1_year_survival_status
0	b'1'	b'1'	22.830137	b'0'	b'1'	b'ALL'	999.0	0.0	0
1	b'1'	b'0'	23.342466	b'0'	b'1'	b'ALL'	163.0	1.0	1
2	b'1'	b'0'	26.394521	b'0'	b'1'	b'ALL'	435.0	1.0	0
3	b'0'	b'0'	39.684932	b'1'	b'1'	b'AML'	53.0	1.0	1
4	b'0'	b'1'	33.358904	b'0'	b'0'	b'chronic'	2043.0	0.0	0
...	...	...	...	...	...	...	...	...	...

**Goal: Postoperatively, to predict 1-year survival status.**

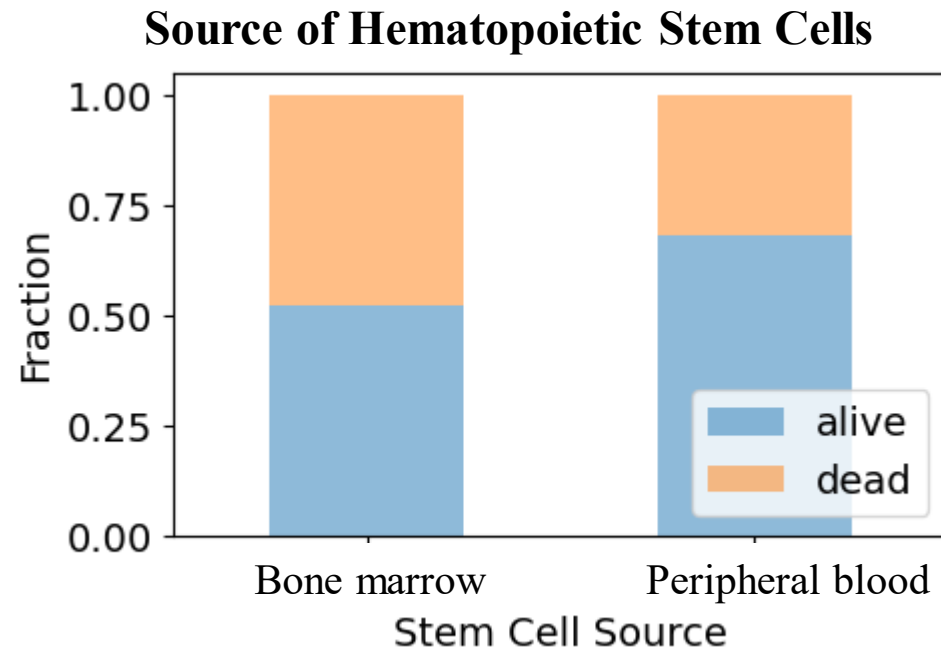


baseline accuracy of  
our classification model

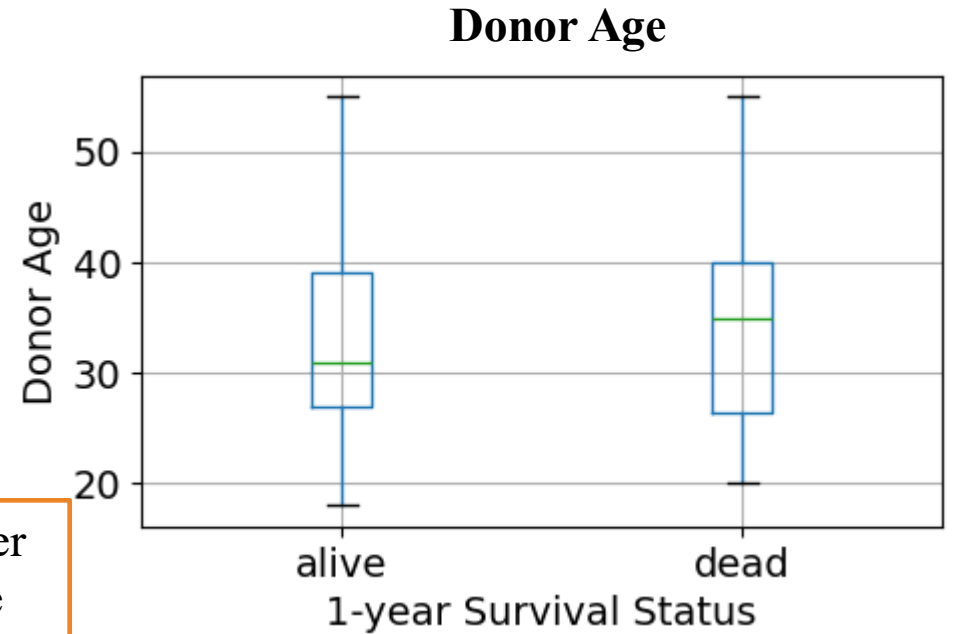
## Basic Understanding Of The Data

### 2. Some important correlations between features and the target variable

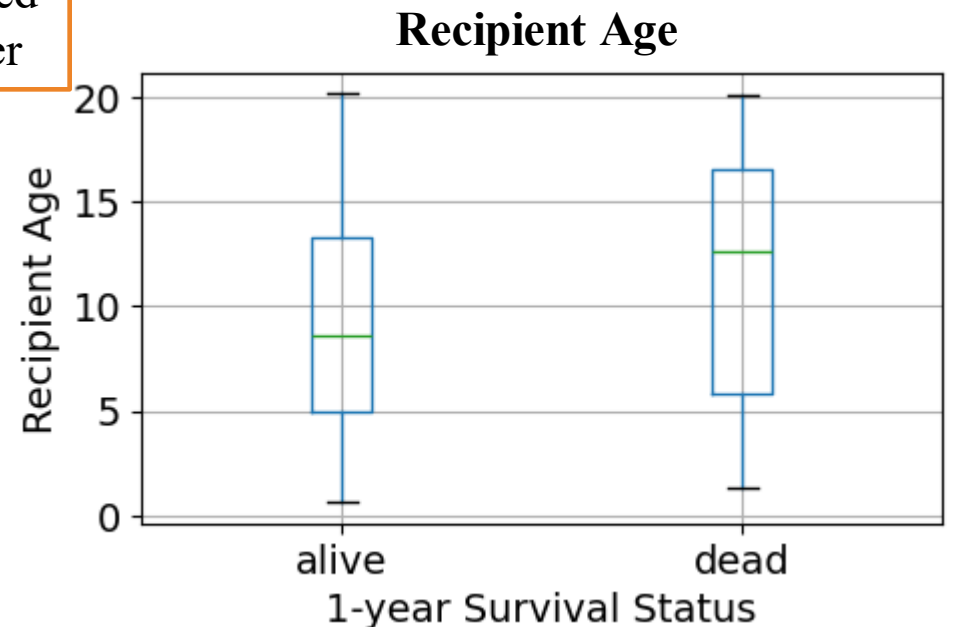
**Pre-op**



BMT sourced from peripheral blood worked better than from bone marrow.



Lower  
Age  
Worked  
Better



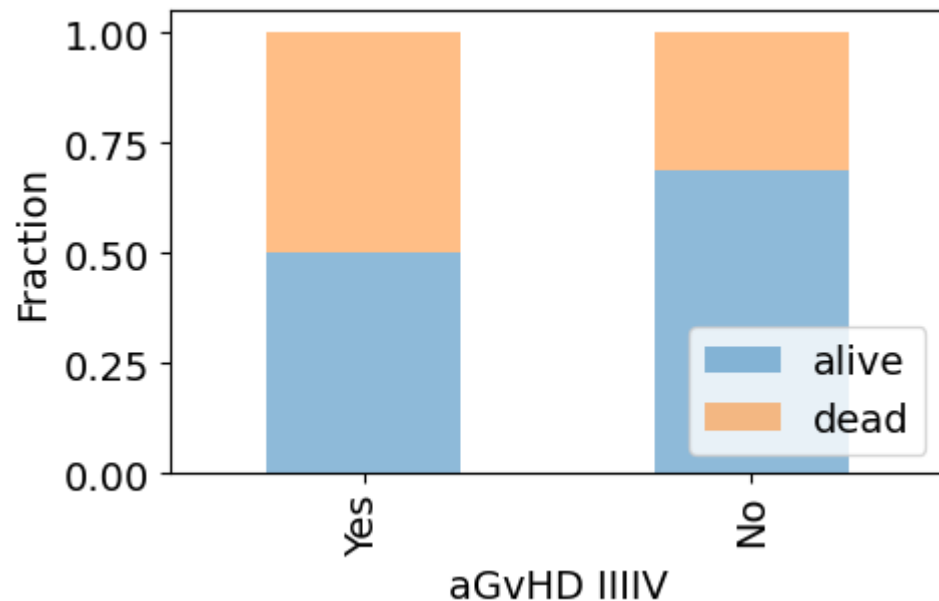


## Basic Understanding Of The Data

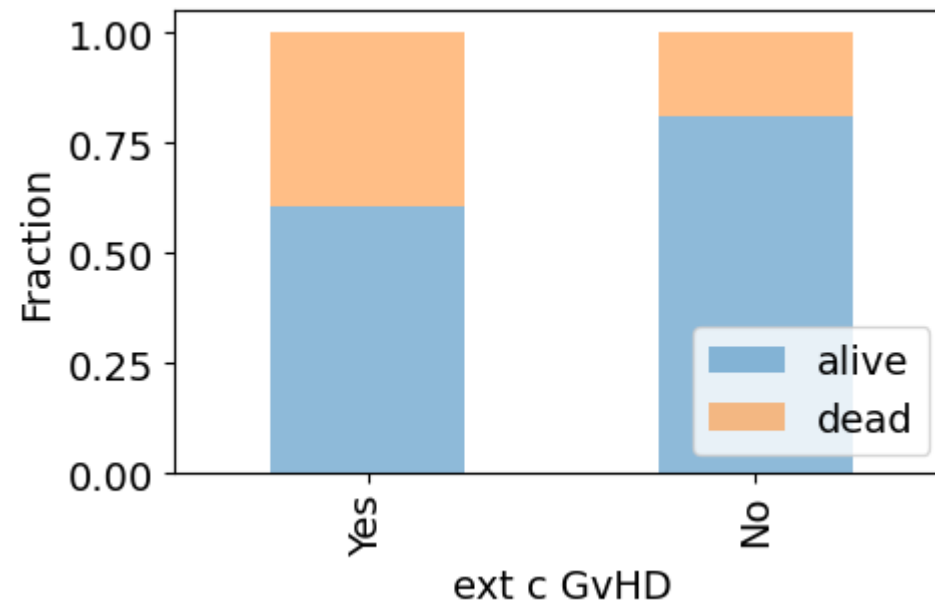
### 2. Some important correlations between features and the target variable

#### Post-op

Development of acute GvHD stage III or IV



Development of extensive chronic GvHD



Acute or extensive GvHD increased the risk of death, though it was not always fatal.

## Splitting Of The Data

**iid data splitting:** `from sklearn.model_selection import train_test_split`

	Training Set	Validation Set	Test Set
% of patients	60 %	20 %	20 %
# of patients	112	37	38

## Missing Data

Features	Fraction of NA	Features	Fraction of NA	Features	Fraction of NA
<u>R</u> blood type	0.005348	<u>D</u> CMV infection	0.010695	extensive chronic GvHB	0.165775
<u>R</u> blood cell Rh	0.010695	<u>R</u> CMV infection	0.074866	CD3+/CD34+	0.026738
Blood type match	0.005348	Antigen difference	0.005348	CD3+ dose	0.026738
Serological compatibility	0.085561	Allele difference	0.005348	<u>R</u> HSC before surgery	0.010695

Fraction of points with missing values (NA) : 0.24064171122994651

R = recipient    D = donor

HSC = hematopoietic stem cells (CD34+ cells)

## Dealing with Missing Data --- Clarify The Data Type

Features	Type	Features	Type	Features	Type
<u>R</u> blood type	Categorical	<u>D</u> CMV infection	Categorical	extensive chronic GvHB	Categorical
<u>R</u> blood cell Rh	Categorical	<u>R</u> CMV infection	Categorical	CD3+/CD34+	Continuous
Blood type match	Categorical	Antigen difference	Ordinal	CD3+ dose	Continuous
Serological compatibility	Ordinal	Allele difference	Ordinal	<u>R</u> HSC before surgery	Continuous

Most of them are **categorical** (non ordinal), some are **ordinal**, and some are **continuous**

## Dealing with Missing Data --- **Categorical** (Not Ordinal) Data

Features	Type	Features	Type	Features	Type
<u>R</u> blood type	<b>Categorical</b>	<u>D</u> CMV infection	<b>Categorical</b>	extensive chronic GvHB	<b>Categorical</b>
<u>R</u> blood cell Rh	<b>Categorical</b>	<u>R</u> CMV infection	<b>Categorical</b>	CD3+/CD34+	Continuous
Blood type match	<b>Categorical</b>	Antigen difference	<b>Ordinal</b>	CD3+ dose	Continuous
Serological compatibility	<b>Ordinal</b>	Allele difference	<b>Ordinal</b>	<u>R</u> HSC before surgery	Continuous

Learned in class: the BEST thing we can do is to **treat missing values as another category**

E.g. **Blood type:**

- Unlikely the hospital did not have blood type tested
- Over 30 blood group systems in addition to ABO and Rh
  - E.g. Duffy, K antigen (or Kell), Lutheran, and Kidd blood groups

**SimpleImputer (strategy='constant')**

## Dealing with Missing Data --- Ordinal Data

Features	Type	Features	Type	Features	Type
<u>R</u> blood type	Categorical	<u>D</u> CMV infection	Categorical	extensive chronic GvHB	Categorical
<u>R</u> blood cell Rh	Categorical	<u>R</u> CMV infection	Categorical	CD3+/CD34+	Continuous
Blood type match	Categorical	Antigen difference	Ordinal	CD3+ dose	Continuous
Serological compatibility	Ordinal	Allele difference	Ordinal	<u>R</u> HSC before surgery	Continuous

Learned in class: the BEST thing we can do is to **treat missing values as another category**

How should they be ordered?

To treat missing values **as the highest category**

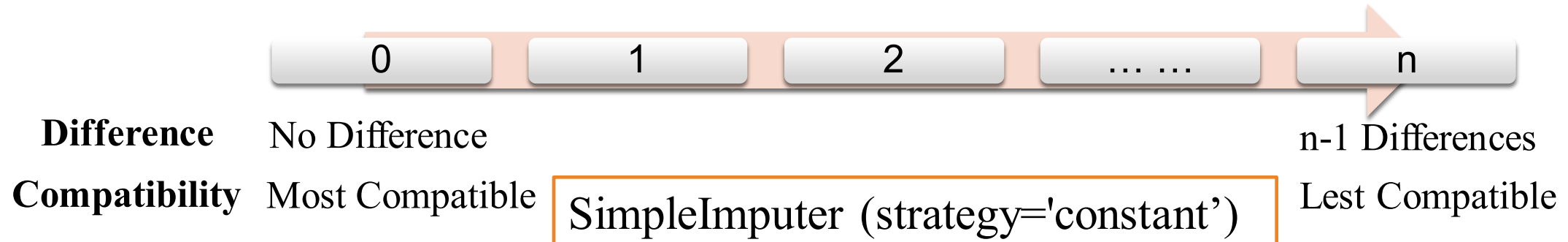
## Dealing with Missing Data --- Ordinal Data

Features	Type	Features	Type	Features	Type
<u>R</u> blood type	Categorical	<u>D</u> CMV infection	Categorical	extensive chronic GvHB	Categorical
<u>R</u> blood cell Rh	Categorical	<u>R</u> CMV infection	Categorical	CD3+/CD34+	Continuous
Blood type match	Categorical	Antigen difference	Ordinal	CD3+ dose	Continuous
Serological compatibility	Ordinal	Allele difference	Ordinal	<u>R</u> HSC before surgery	Continuous

Learned in class: the BEST thing we can do is to **treat missing values as another category**

How should they be ordered?

To treat missing values **as the highest category**



R = recipient    D = donor

HSC = hematopoietic stem cells (CD34+ cells)



## Dealing with Missing Data --- Continuous Data

Features	Type	Features	Type	Features	Type
<u>R</u> blood type	Categorical	<u>D</u> CMV infection	Categorical	extensive chronic GvHB	Categorical
<u>R</u> blood cell Rh	Categorical	<u>R</u> CMV infection	Categorical	CD3+/CD34+	Continuous
Blood type match	Categorical	Antigen difference	Ordinal	CD3+ dose	Continuous
Serological compatibility	Ordinal	Allele difference	Ordinal	<u>R</u> HSC before surgery	Continuous

**For now, based on our current knowledge:**

**SimpleImputer (strategy='mean')**

Will change to better method when we learn more in the class.

## High Correlation (Redundant) Data Reduction

**Donor age**, Donor age 35; **Recipient age**, Recipient age 10, Recipient age int

Fit\_Transformation X\_Train

SimpleImputer + OneHotEncoder

**Features =**

- gender, age, matching, Disease, judging-related features

SimpleImputer + StandardScaler

**Features =**

- Dosed for CD34+, CD3+
- Body mass
- Recovery time for some side effects

SimpleImputer + Ordinal Encoder

**Features =**

- leveled status, matching grade, age groups-related features

MinMaxScaler

**Features =**

- donor age, recipient age

Transformation  $X_{\text{val}}$  and  $X_{\text{test}}$

Data Ready for Machine Learning!

```
X_train.shape  
(112, 36)
```

```
X_train_prep.shape  
(112, 68)
```

THANK YOU

Zoey “Ziyan” Yu

Ziyan\_yu@brown.edu

PhD Candidate in Chemistry

Brown University

Oct 24, 2024

