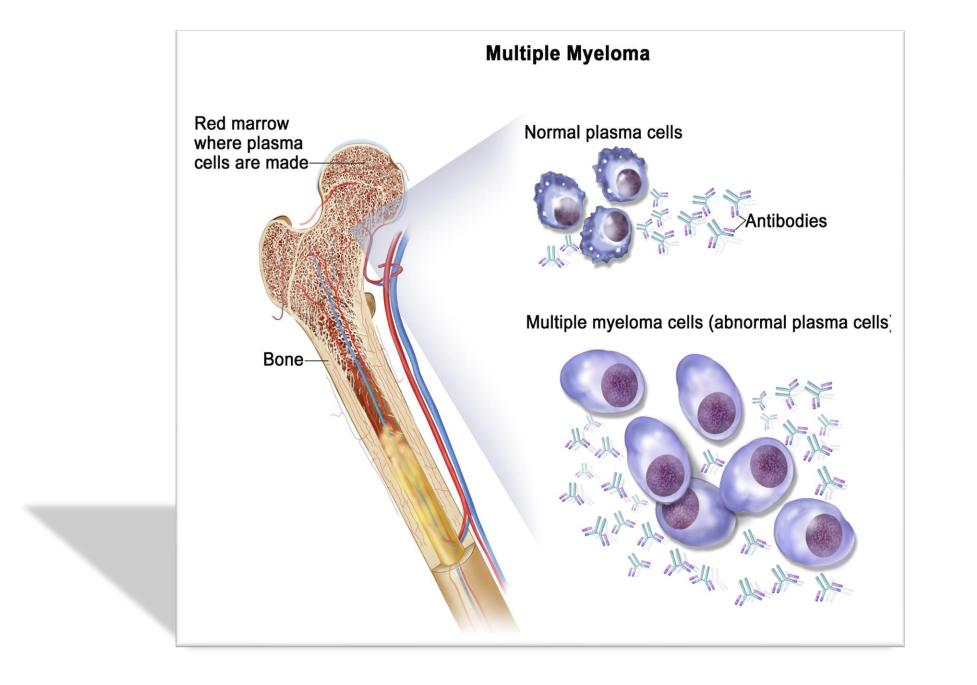
## WHAT CAUSES MULTIPLE MYELOMA CANCER? MMC

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Development of Multiple Myeloma



The High-Quality Analytical **Model That Answers These Questions Is** 

Usefulness of the Results to MMC Patients

> Once a patient is diagnosed with MMC, 1) the medical doctor can accurately predict the survival time of the patient given the

- Use developed a real data-driven statistical model to answer the following questions:
  - What are the individual risk factors that cause multiple myeloma cancer (MMC)?
  - What are the interactions of risk factors that cause MMC?
  - III. Given the risk factors and interactions of a given MMC patient, can we predict the survival time of the patient?
  - IV. Can we rank the individual risk factors and the interactions according to the percentage contribution to the death times of MMC patients? V. Can we identify the values of the risk factors to maximize the survival time of an MMC patient?

 $log(\hat{t}_i) = -4.377 - 1.097X_1 + 0.332X_{3normal}$  $-0.949X_{4present} + 0.016X_5 + 0.562X_{6female}$  $-0.586X_{8present} + 0.022X_{11} - 1.268X_{13none}$ +4.  $151X'_{16}$  - 0.  $252X_7 * X'_{14}$ ,

for

 $X_{i} = \begin{cases} 1 - e^{-X_{i}'}, & \text{if } x < 0, \\ -1 + e^{X_{i}'} & \text{otherwise, for } i = 14, 16. \end{cases}$ 

This Statistical Model Answer the Relative Questions of MMC.

- risk factors we have identified.
- The medical doctor can tell whether a 2) patient needs critical treatment attention based on the risk factors identified with the patient upon being diagnosed with the MMC.
- A patient can be advice on what he/she needs to do to maximize his/her survival time.
- The MMC patients can be informed of the key risk factors that caused his/her cancer.
- Knowing this information about the risk 5) factors, the physician can prescribe applicable drug treatment to the patient.

The Ranking of the Percentage (%) of **Contribution of Risk Factors to the Survival** Time of MMC

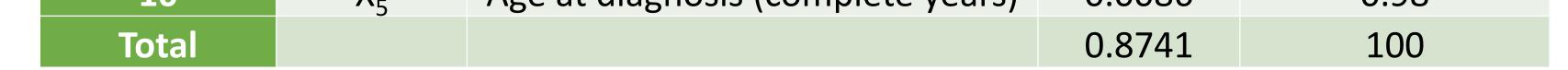
Detail Analysis of **This Research** 

## Acknowledgement

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Rank	variable	Description	R <sup>2</sup>	% Contribution
		Bence Jone protein in urine at		
1	X <sub>13</sub>	diagnosis 1-present, 2-none	0.2672	30.57
2	X <sub>1</sub>	Log BUN at diagnosis	0.2052	23.48
		Infections at diagnosis 0 none, 1		
3	X <sub>4</sub>	present	0.0949	10.86
		% Myeloid cells in peripheral		
4	X <sub>11</sub>	blood at diagnosis	0.089	10.18
		Serum calcium (mgm%) at		
5	X' <sub>16</sub>	diagnosis	0.0661	7.56
		Fractures at diagnosis 0 none, 1		
6	X <sub>8</sub>	present	0.0613	7.01
	$X_7 \& X'_{_{14}}$	Log WBC at diagnosis and Total		
7	<b>'</b> 14	serum protein at diagnosis	0.0379	4.34
8	Х <sub>6</sub>	Gender 1 male, 2 female	0.0329	3.76
		Platelets at diagnosis 0 abnormal,		
9	X <sub>3</sub>	1 normal	0.011	1.26
10	X <sub>5</sub>	Age at diagnosis (complete years)	0.0086	0.98

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  - of Multiple Myeloma." Health Science Journal, Volume 14, IPHSJ-19-2974.
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## [KEY WORDS: Data driven; Machine learning techniques; Statistical modeling; Multiple myeloma cancer; Health science; Public Health]

## The ASA Biopharmaceutical Section Regulatory – Industry Statistics Workshop (Sept 22-25, 2020)