

Q1 What is your team name?

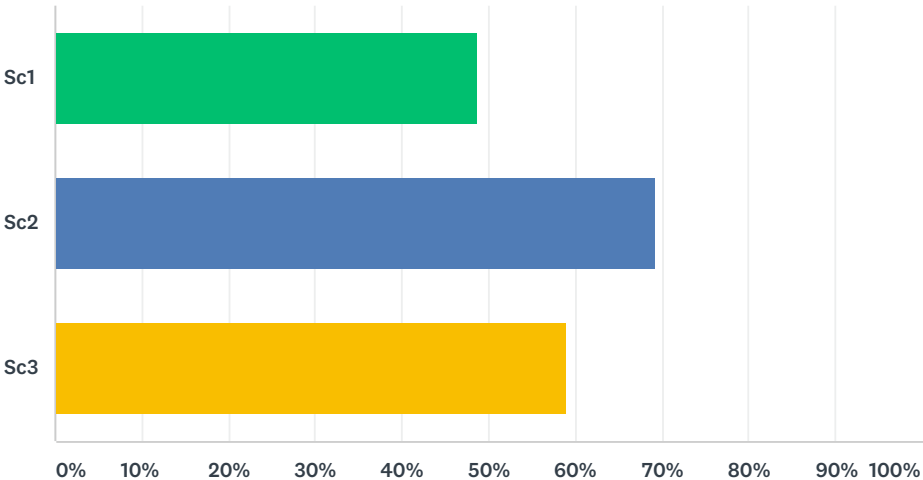
Answered: 39 Skipped: 0

Q2 How many people made up your team?

Answered: 39 Skipped: 0

Q3 In which subchallenges did you participate ? (Choose all that apply)
Please complete the questions related to subchallenge you participated in accordingly.

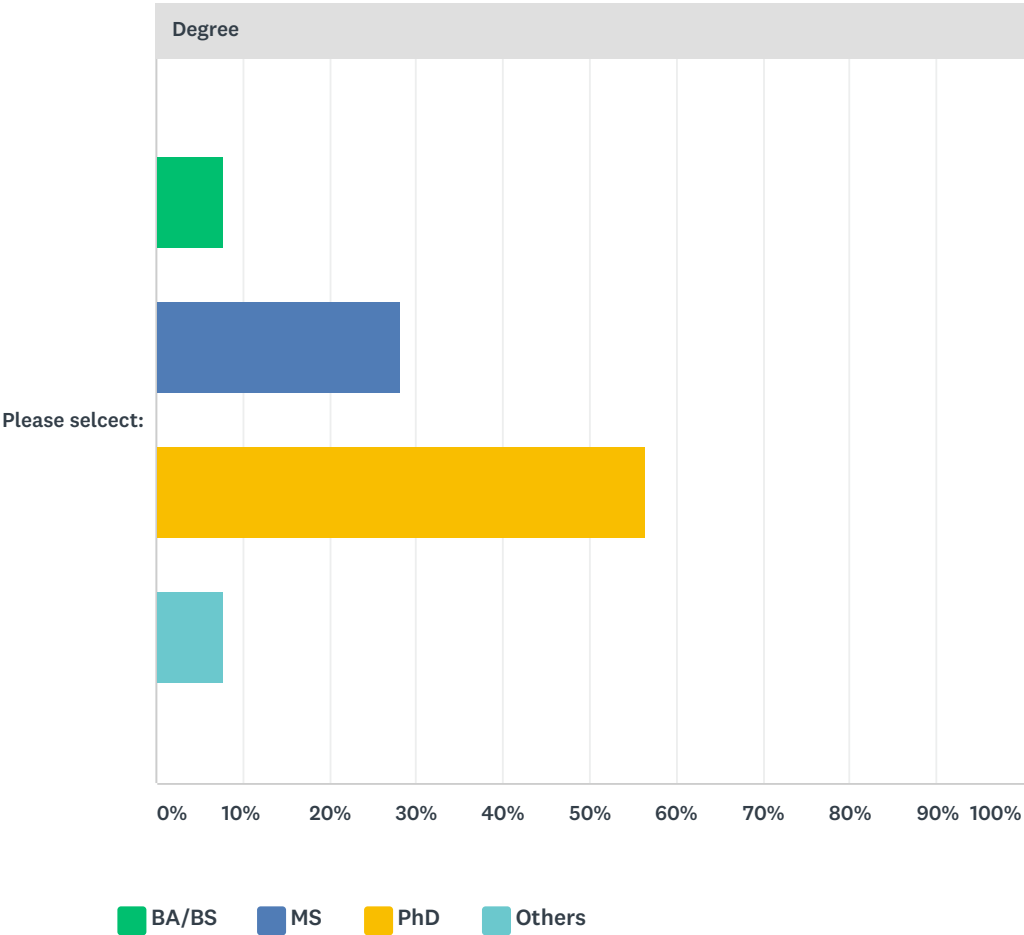
Answered: 39 Skipped: 0

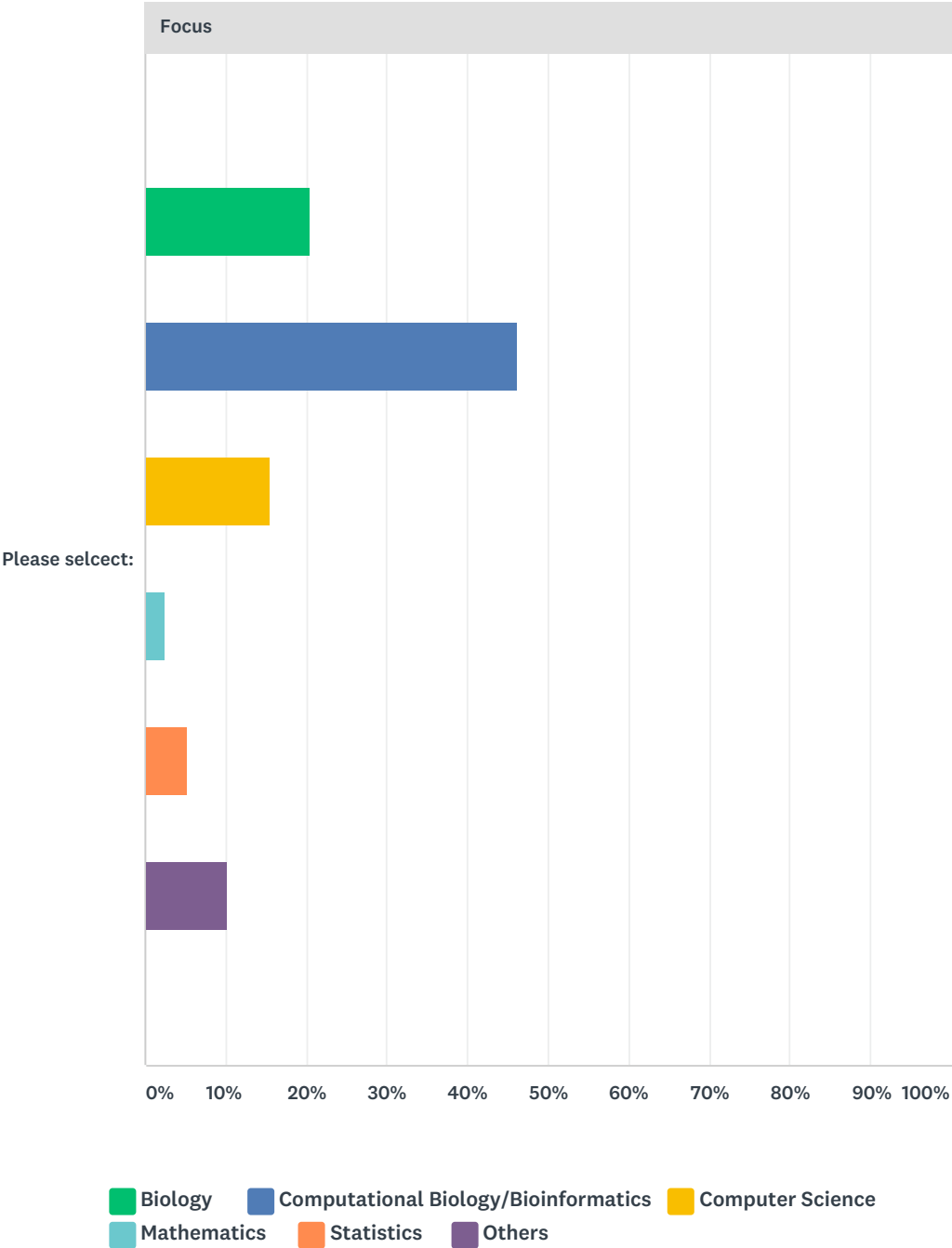


ANSWER CHOICES	RESPONSES	
Sc1	48.72%	19
Sc2	69.23%	27
Sc3	58.97%	23
Total Respondents: 39		

Q4 Please select your highest degree conferred and focus ? (PhD, MS, BS/BA) (e.g. PhD computational biology)

Answered: 39 Skipped: 0



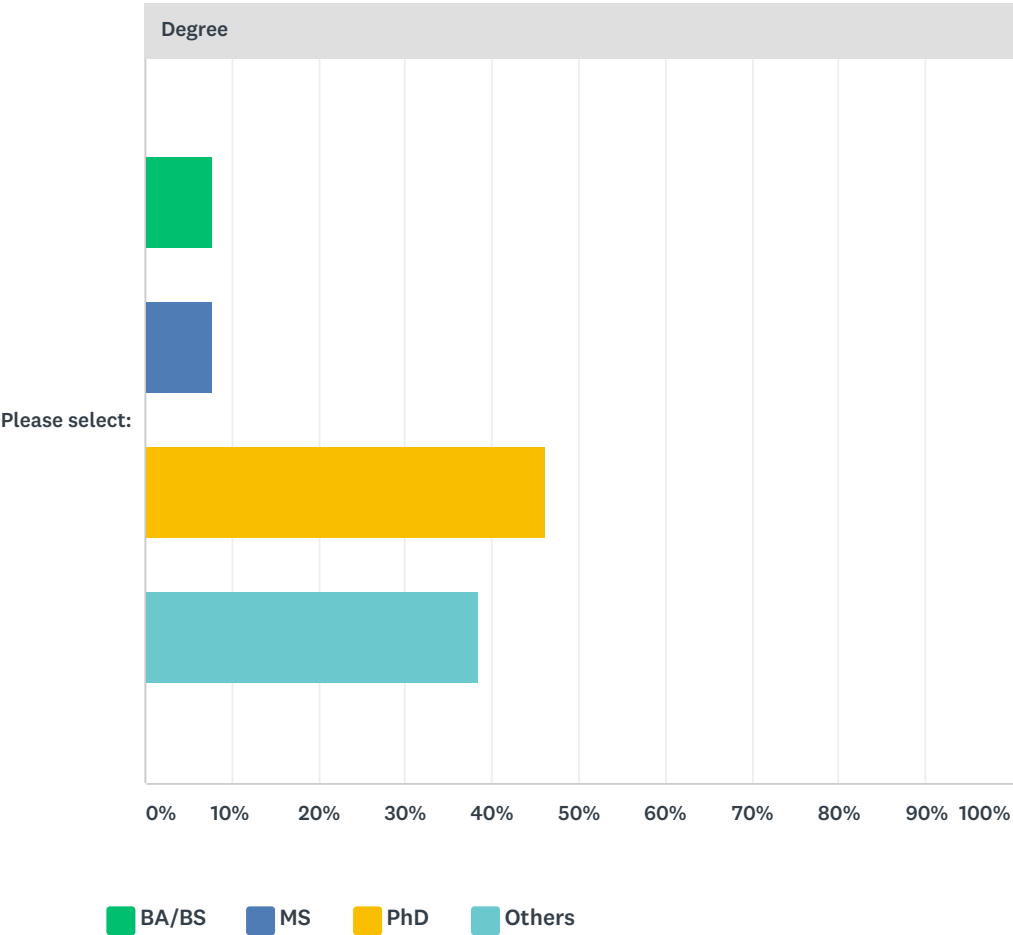


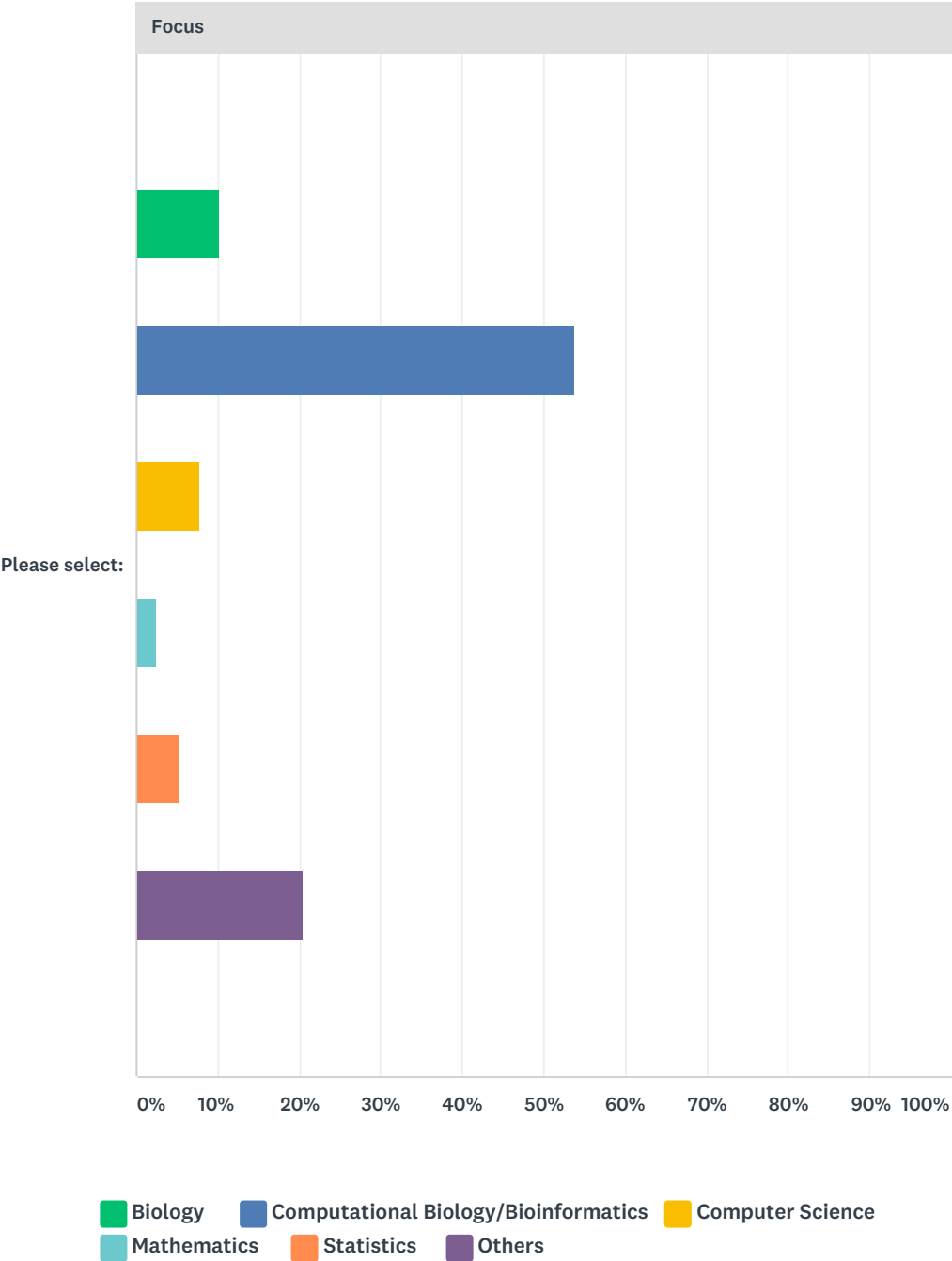
Degree							
	BA/BS	MS	PHD	OTHERS	TOTAL		
Please select:	7.69%	28.21%	56.41%	7.69%			
	3	11	22	3			39

Focus							
	BIOLOGY	COMPUTATIONAL BIOLOGY/BIOINFORMATICS	COMPUTER SCIENCE	MATHEMATICS	STATISTICS	OTHERS	TOTAL
Please select:	20.51%	46.15%	15.38%	2.56%	5.13%	10.26%	
	8	18	6	1	2	4	39

Q5 Please select your ongoing (if any) degree and focus ? (PhD, MS, BS/BA) (e.g. PhD computational biology)

Answered: 39 Skipped: 0





Degree							
	BA/BS	MS	PHD	OTHERS	TOTAL		
Please select:	7.69%	7.69%	46.15%	38.46%			
	3	3	18	15			39

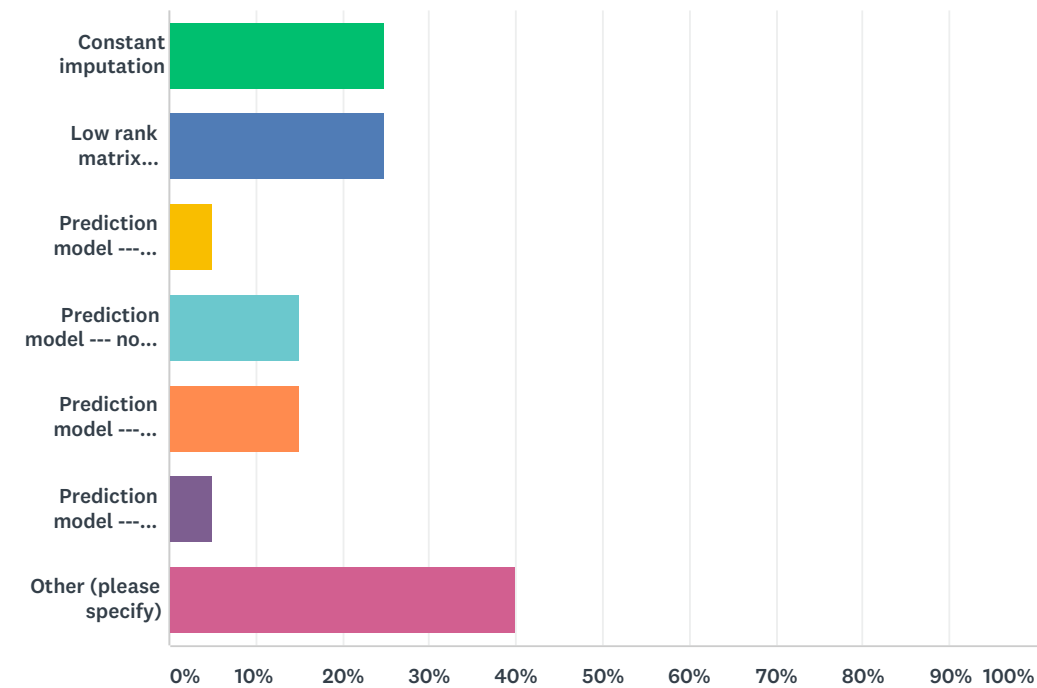
Focus							
	BIOLOGY	COMPUTATIONAL BIOLOGY/BIOINFORMATICS	COMPUTER SCIENCE	MATHEMATICS	STATISTICS	OTHERS	TOTAL
Please select:	10.26%	53.85%	7.69%	2.56%	5.13%	20.51%	
	4	21	3	1	2	8	39

Q6 What is the key location of your team (City, State/Country, or Institution) ?

Answered: 39 Skipped: 0

Q7 Describe your method. (Choose all that apply)

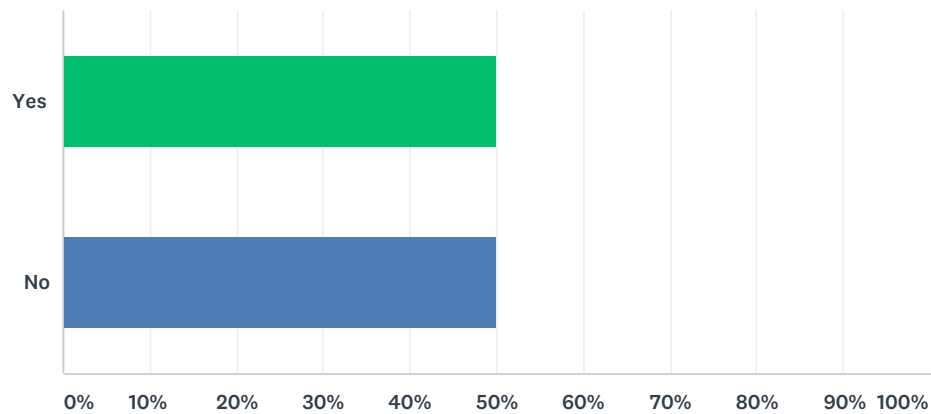
Answered: 20 Skipped: 19



ANSWER CHOICES	RESPONSES	
Constant imputation	25.00%	5
Low rank matrix completion	25.00%	5
Prediction model --- clustering method (i.e. KNN)	5.00%	1
Prediction model --- non linear regression (i.e. Tree model)	15.00%	3
Prediction model --- Linear regression (i.e. LASSO regression)	15.00%	3
Prediction model --- Comprehensive model(i.e. Neural Network)	5.00%	1
Other (please specify)	40.00%	8
Total Respondents: 20		

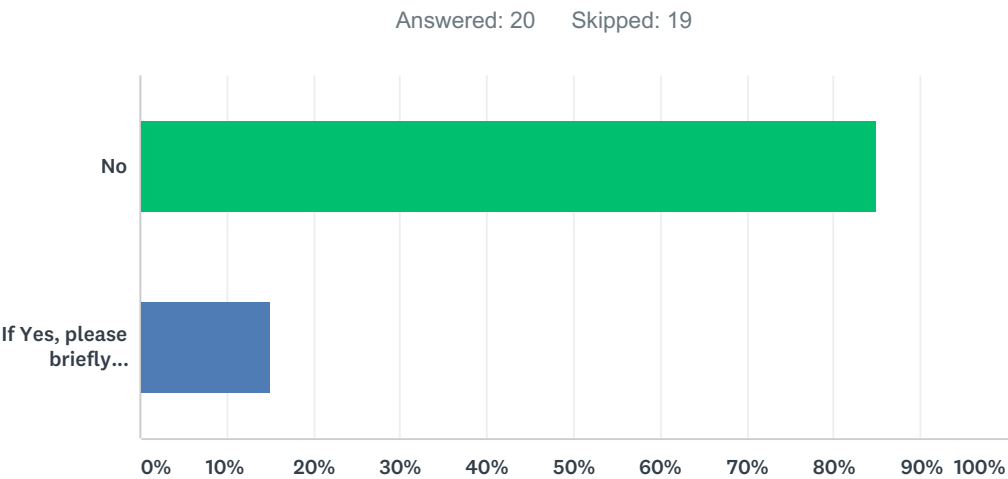
Q8 Did you use iterative algorithm to update imputation in your model?

Answered: 20 Skipped: 19



ANSWER CHOICES		RESPONSES	
Yes		50.00%	10
No		50.00%	10
TOTAL			20

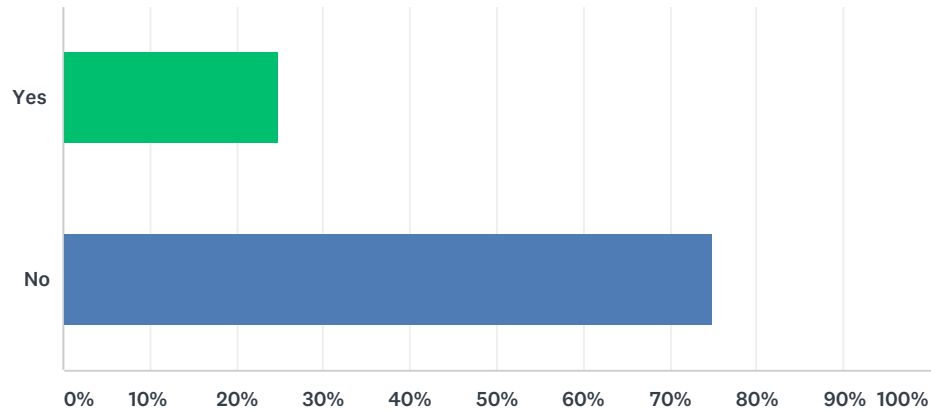
Q9 Does your method provide confidence scores for the imputed values?



ANSWER CHOICES	RESPONSES	
No	85.00%	17
If Yes, please briefly describe the procedure used to generate the confidence score:	15.00%	3
TOTAL		20

Q10 Does your method treat biological missing and technical missing differently?

Answered: 20 Skipped: 19



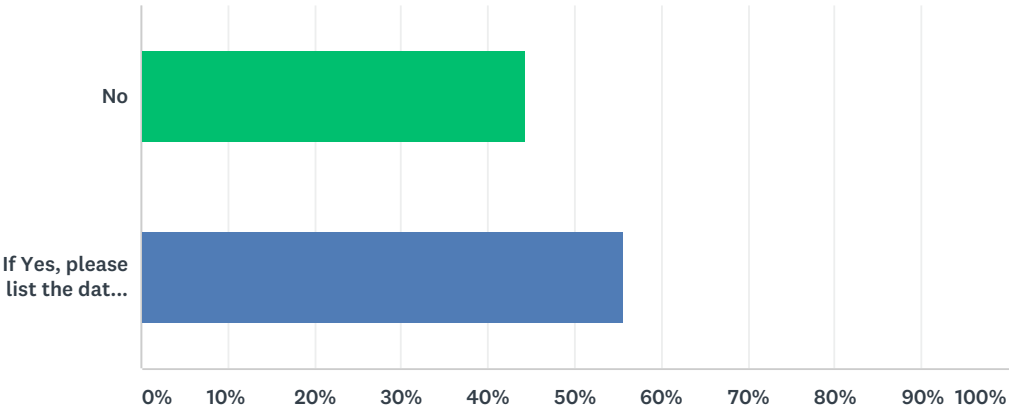
ANSWER CHOICES	RESPONSES	
Yes	25.00%	5
No	75.00%	15
TOTAL		20

Q11 What is the computational complexity of your method (time and nodes) ?

Answered: 15 Skipped: 24

Q12 Did you use multiple data types to make your predictions?

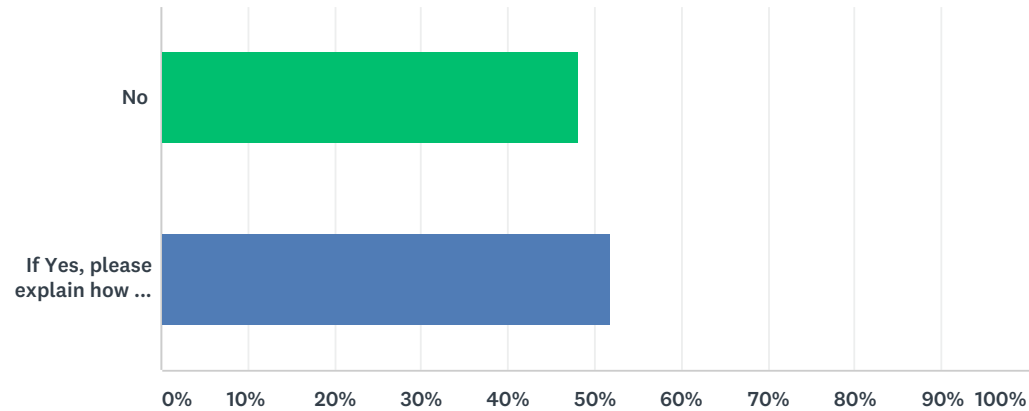
Answered: 27 Skipped: 12



ANSWER CHOICES		RESPONSES	
No		44.44%	12
If Yes, please list the data types:		55.56%	15
TOTAL			27

Q13 Did you normalize or standardize the data before carrying any analysis?

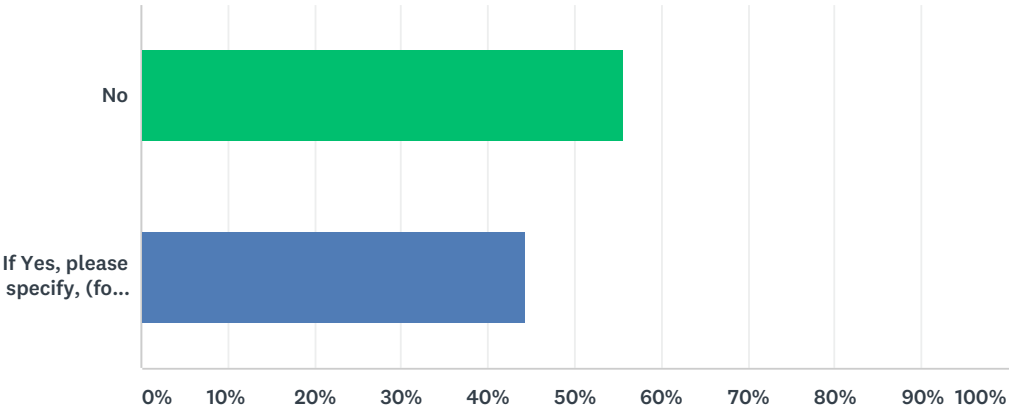
Answered: 27 Skipped: 12



ANSWER CHOICES		RESPONSES	
No		48.15%	13
If Yes, please explain how you normalized each data type.		51.85%	14
TOTAL			27

Q14 Did you use external data / prior knowledge to build your model?
(e.g. pathway databases)

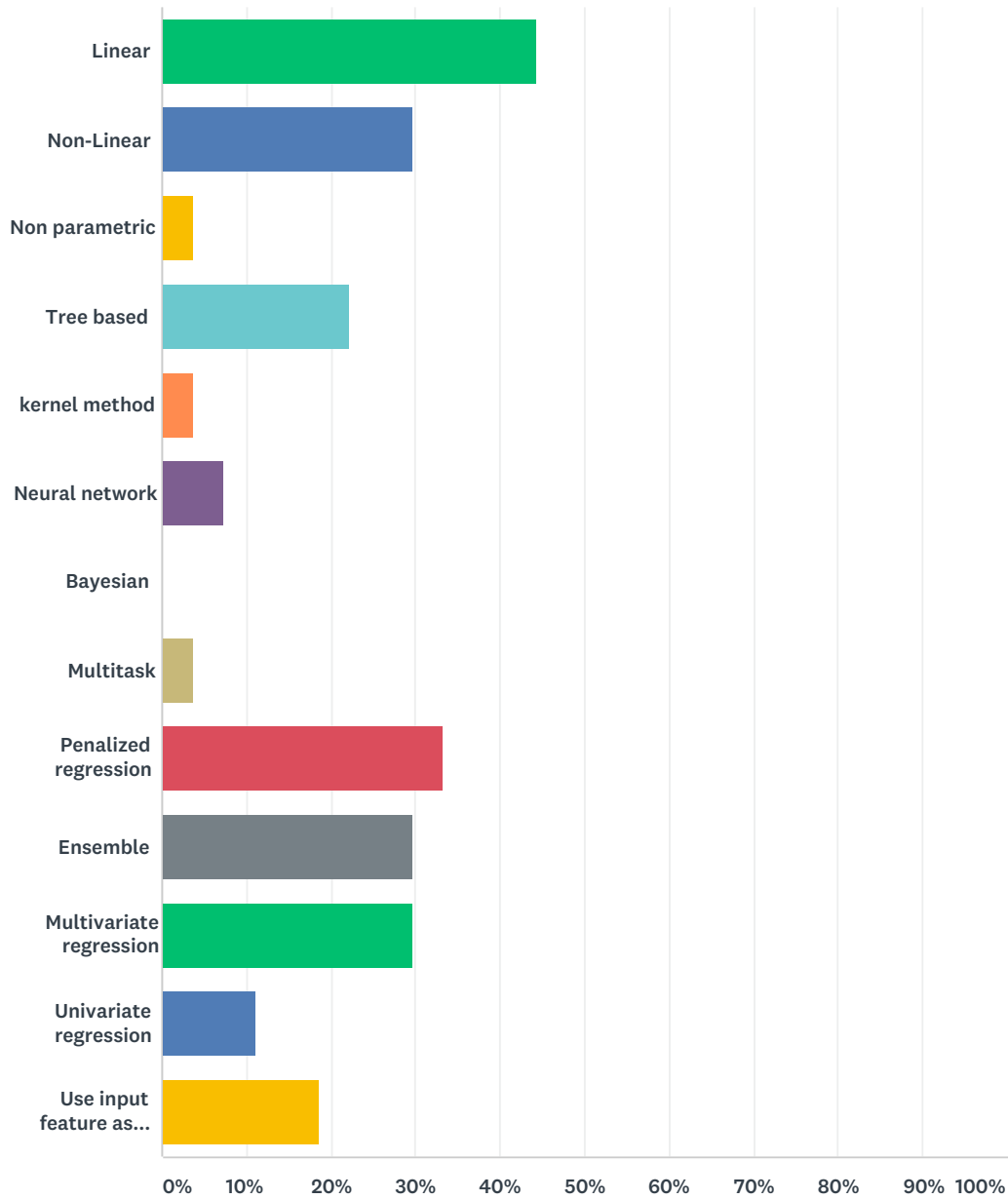
Answered: 27 Skipped: 12



ANSWER CHOICES		RESPONSES	
No		55.56%	15
If Yes, please specify, (for instance, Pathways: KEGG; GO; Reactome. Interaction Networks: Biogrid; String.)		44.44%	12
TOTAL			27

Q15 Describe your method. (Choose all that apply)

Answered: 27 Skipped: 12



ANSWER CHOICES	RESPONSES	
Linear	44.44%	12
Non-Linear	29.63%	8
Non parametric	3.70%	1
Tree based	22.22%	6
kernel method	3.70%	1
Neural network	7.41%	2

Bayesian	0.00%	0
Multitask	3.70%	1
Penalized regression	33.33%	9
Ensemble	29.63%	8
Multivariate regression	29.63%	8
Univariate regression	11.11%	3
Use input feature as proxy (e.g use mRNA as protein abundance)	18.52%	5
Total Respondents: 27		

Q16 What is the computational complexity of your method (time and nodes) ?

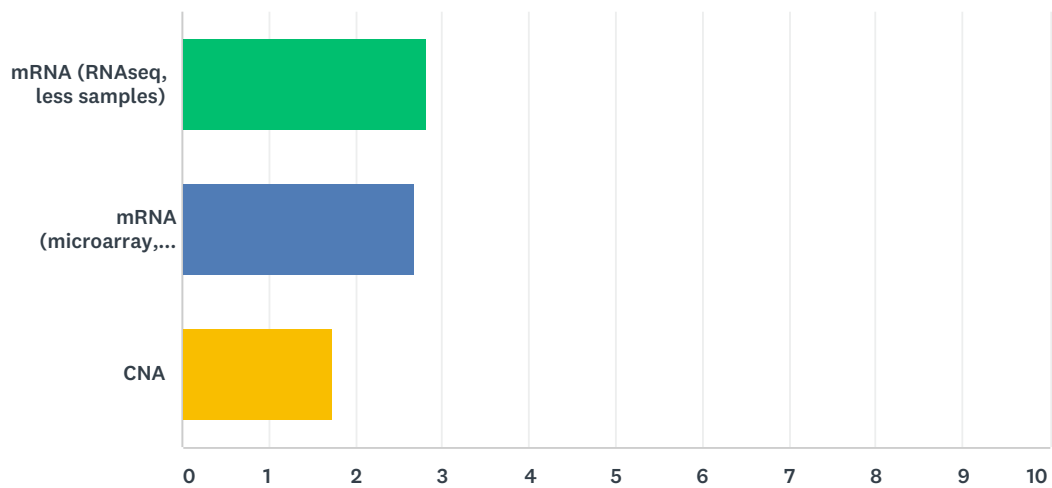
Answered: 24 Skipped: 15

Q17 How did you treat the missing values in the dataset? Please elaborate your effort on predictor variables and response variable respectively.

Answered: 25 Skipped: 14

Q18 Which data types provide most power to your model for prediction ?
(select most important to least (1 being most important). If you do not know, please click N/A for all of them)

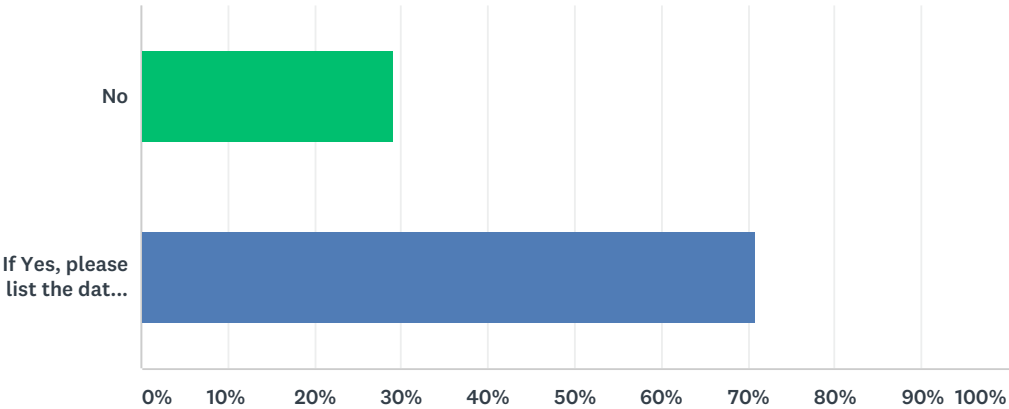
Answered: 26 Skipped: 13



	1	2	3	N/A	TOTAL	SCORE
mRNA (RNAseq, less samples)	57.69% 15	11.54% 3	0.00% 0	30.77% 8	26	2.83
mRNA (microarray, moresamples)	16.00% 4	8.00% 2	0.00% 0	76.00% 19	25	2.67
CNA	0.00% 0	42.31% 11	15.38% 4	42.31% 11	26	1.73

Q19 Did you use multiple data types to make your predictions?

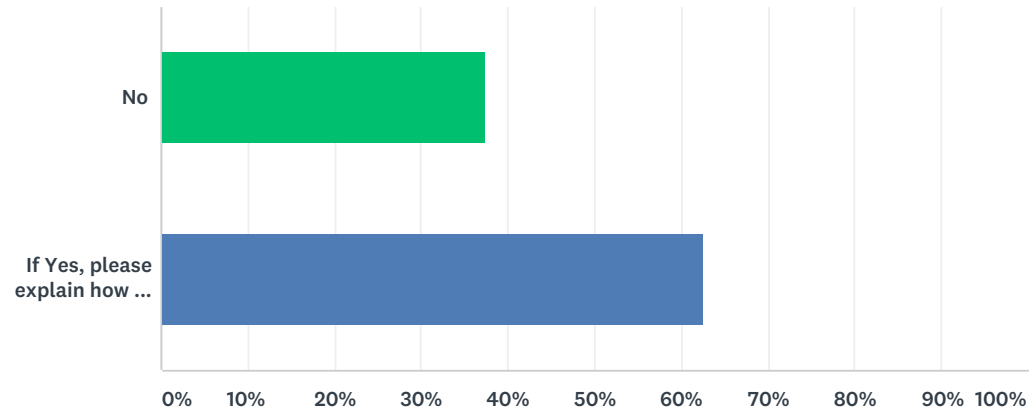
Answered: 24 Skipped: 15



ANSWER CHOICES		RESPONSES	
No		29.17%	7
If Yes, please list the data types:		70.83%	17
TOTAL			24

Q20 Did you normalize or standardize the data before carrying any analysis?

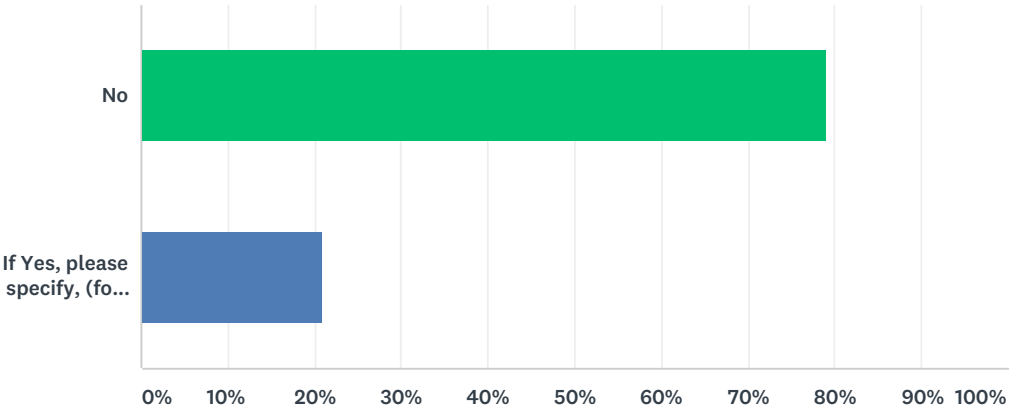
Answered: 24 Skipped: 15



ANSWER CHOICES	RESPONSES	
No	37.50%	9
If Yes, please explain how you normalized each data type.	62.50%	15
TOTAL		24

Q21 Did you use external data / prior knowledge to build your model?
(e.g. pathway databases)

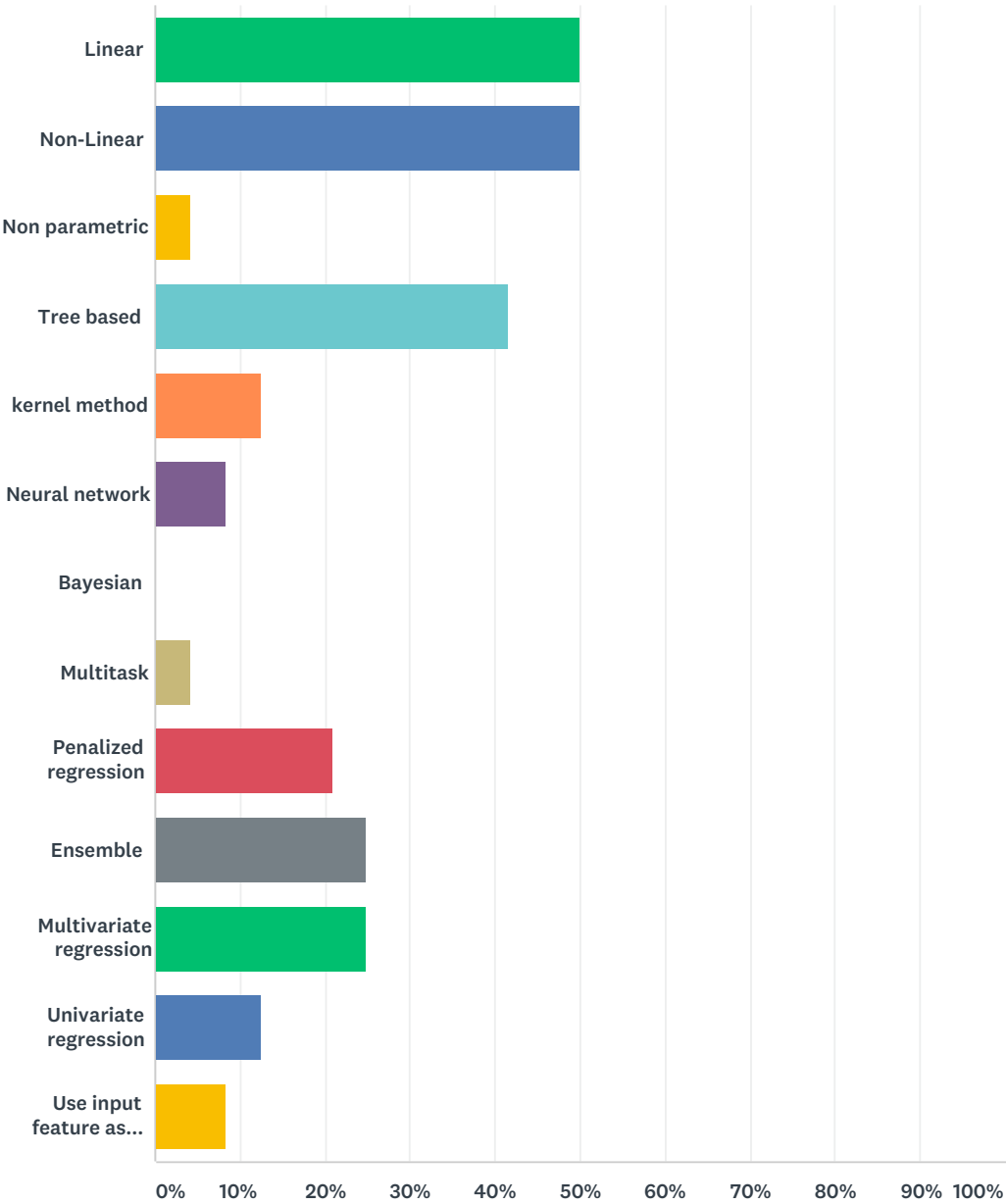
Answered: 24 Skipped: 15



ANSWER CHOICES		RESPONSES	
No		79.17%	19
If Yes, please specify, (for instance, Pathways: KEGG; GO; Reactome. Interaction Networks: Biogrid; String.)		20.83%	5
TOTAL			24

Q22 Describe your method. (Choose all that apply)

Answered: 24 Skipped: 15



ANSWER CHOICES	RESPONSES	
Linear	50.00%	12
Non-Linear	50.00%	12
Non parametric	4.17%	1
Tree based	41.67%	10
kernel method	12.50%	3
Neural network	8.33%	2

Bayesian	0.00%	0
Multitask	4.17%	1
Penalized regression	20.83%	5
Ensemble	25.00%	6
Multivariate regression	25.00%	6
Univariate regression	12.50%	3
Use input feature as proxy (e.g use mRNA as protein abundance)	8.33%	2
Total Respondents: 24		

Q23 How did you treat the missing values in the dataset? Please elaborate your effort on predictor variables and response variable respectively.

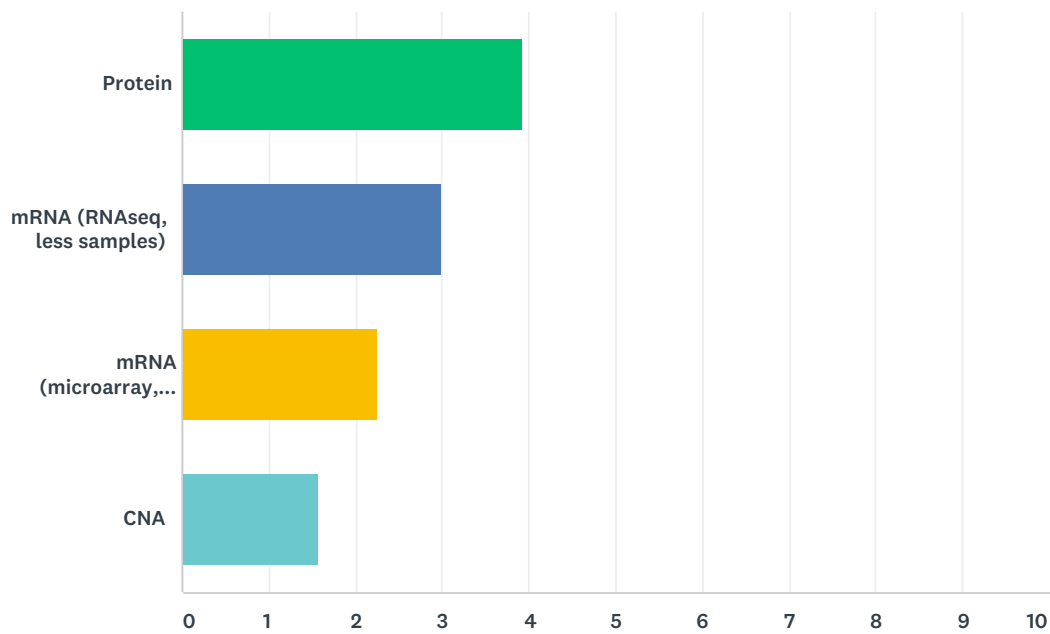
Answered: 22 Skipped: 17

Q24 What is the computational complexity of your method (time and nodes) ?

Answered: 22 Skipped: 17

Q25 Which data types provide most power to your model for prediction ?
(select most important to least (1 being most important). If you do not know, please click N/A for all of them)

Answered: 23 Skipped: 16



	1	2	3	4	N/A	TOTAL	SCORE
Protein	65.22% 15	4.35% 1	0.00% 0	0.00% 0	30.43% 7	23	3.94
mRNA (RNAseq, less samples)	8.70% 2	52.17% 12	8.70% 2	0.00% 0	30.43% 7	23	3.00
mRNA (microarray, moresamples)	0.00% 0	9.09% 2	27.27% 6	0.00% 0	63.64% 14	22	2.25
CNA	0.00% 0	4.35% 1	26.09% 6	30.43% 7	39.13% 9	23	1.57

Q26 How did you predict multiple phosphosites observed for the same protein/peptide?

Answered: 23 Skipped: 16