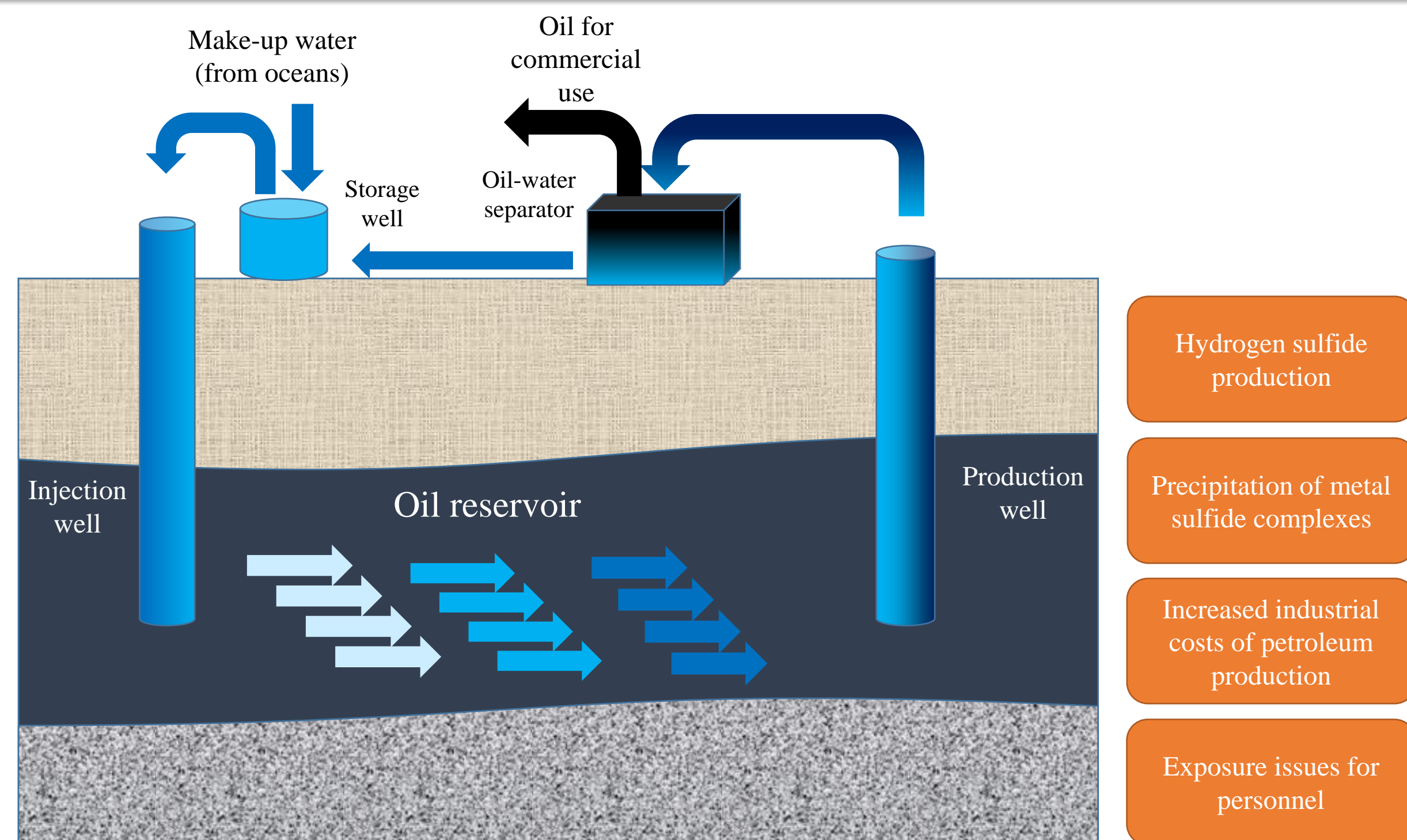


Background

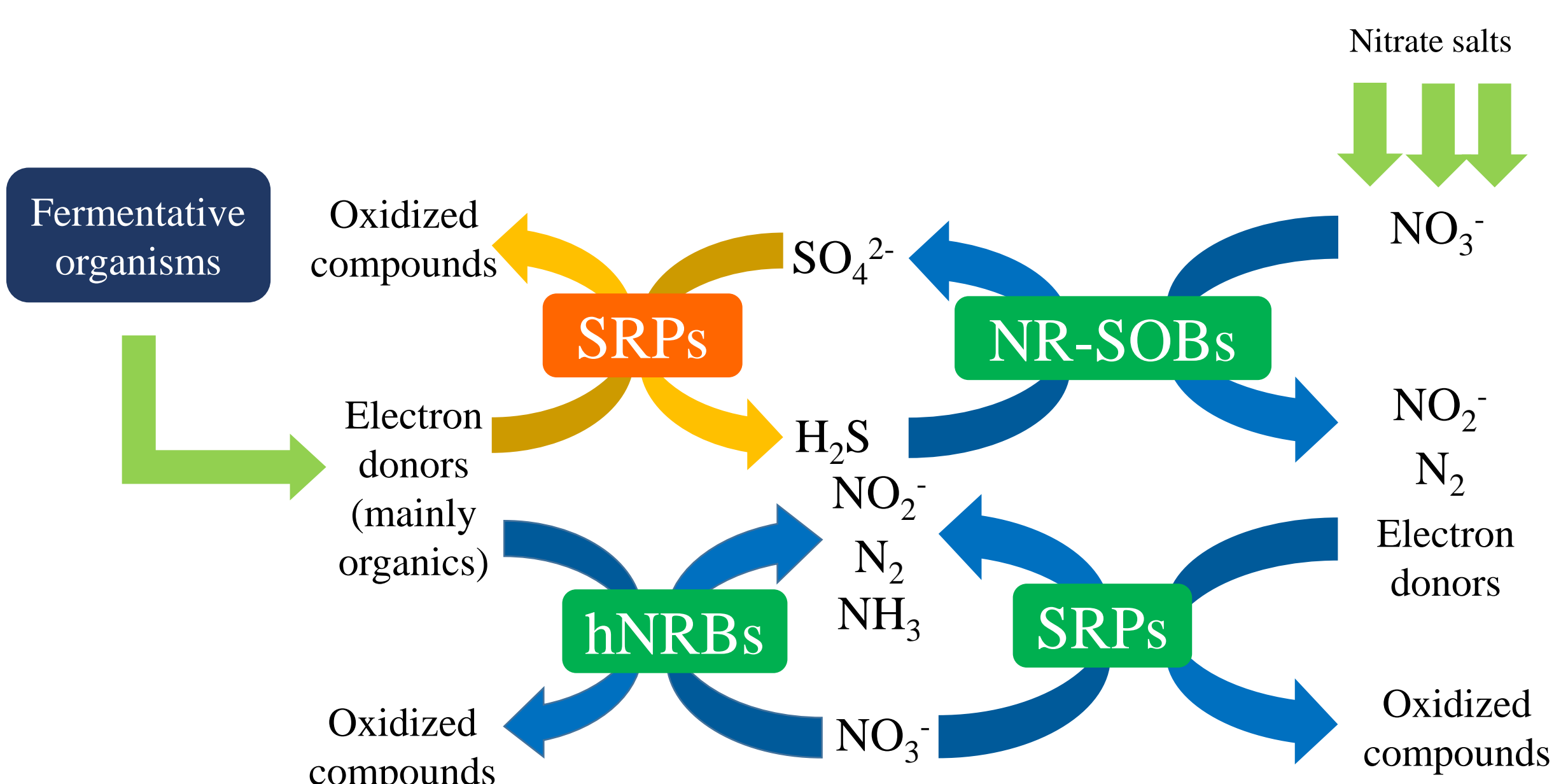
Abstract

Biogenic reservoir souring is a phenomenon in which H₂S is generated in oil reservoirs by sulfate-reducing prokaryotes (SRP). This incurs significant additional operational risk, and associated cost to manage safe production from such reservoirs. As a barrier against reservoir souring, nitrate salts are applied with the aim of limiting SRP activity by promoting nitrate-reducing prokaryotes (NRP), which are able to outcompete SRP for available nutrients. Here we describe results of a long-term (148 days) *ex situ* experiment to assess and predict the microbial community shifts associated with biosouring and mitigation, and impact on H₂S generation. Anaerobic sand-filled up-flow bioreactors were used to mimic the overall processes of biosouring, followed by mitigation (via nitrate treatment) and rebound (resumption of sulfide generation when nitrate amendment was stopped). Bacterial populations from 44 time-points covering 57 sessile samples and 674 planktonic samples were analyzed using deep amplicon sequencing of the V4 region of the 16S rRNA gene to assess community structure and its contribution to biosouring and response to nitrate addition. Random forest models were successfully applied to predict biosouring and mitigation phases based on microbial community structure with high accuracies (> 90 %). Regression-based random forest models were used to predict H₂S concentrations based on taxa abundance, cell abundances, and metabolic profiles, and high prediction accuracies were achieved for all the sets of predictor variables (R² > 0.75). A random forest algorithm was further successfully applied to differentiate effluent and sessile microbial communities (accuracy = 100 %). The results from this study suggest that microbial community structure can be a reliable indicator for the detection of phases, H₂S concentration, and source of the microbial communities during operations of an oil field aquifer.

Oil recovery processes and biosouring



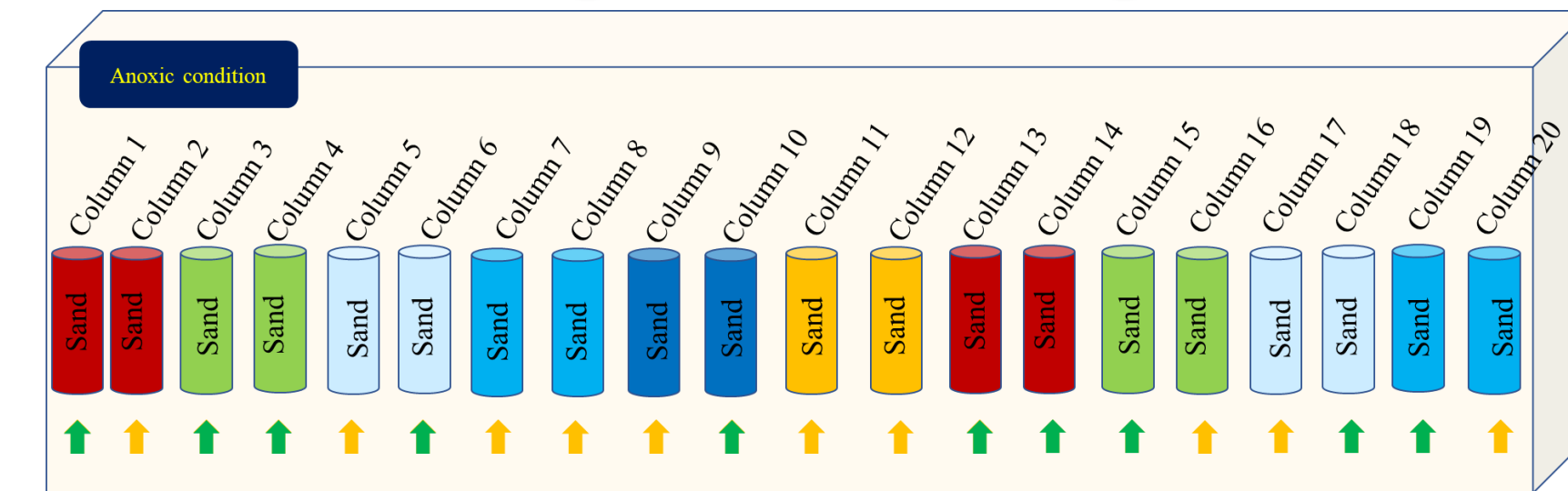
Microbiology behind oil souring and mitigation



SRPs- sulfate-reducing prokaryotes
hNRB- heterotrophic nitrate-reducing bacteria
NR-SOBs- nitrate-reducing sulfur-oxidizing bacteria

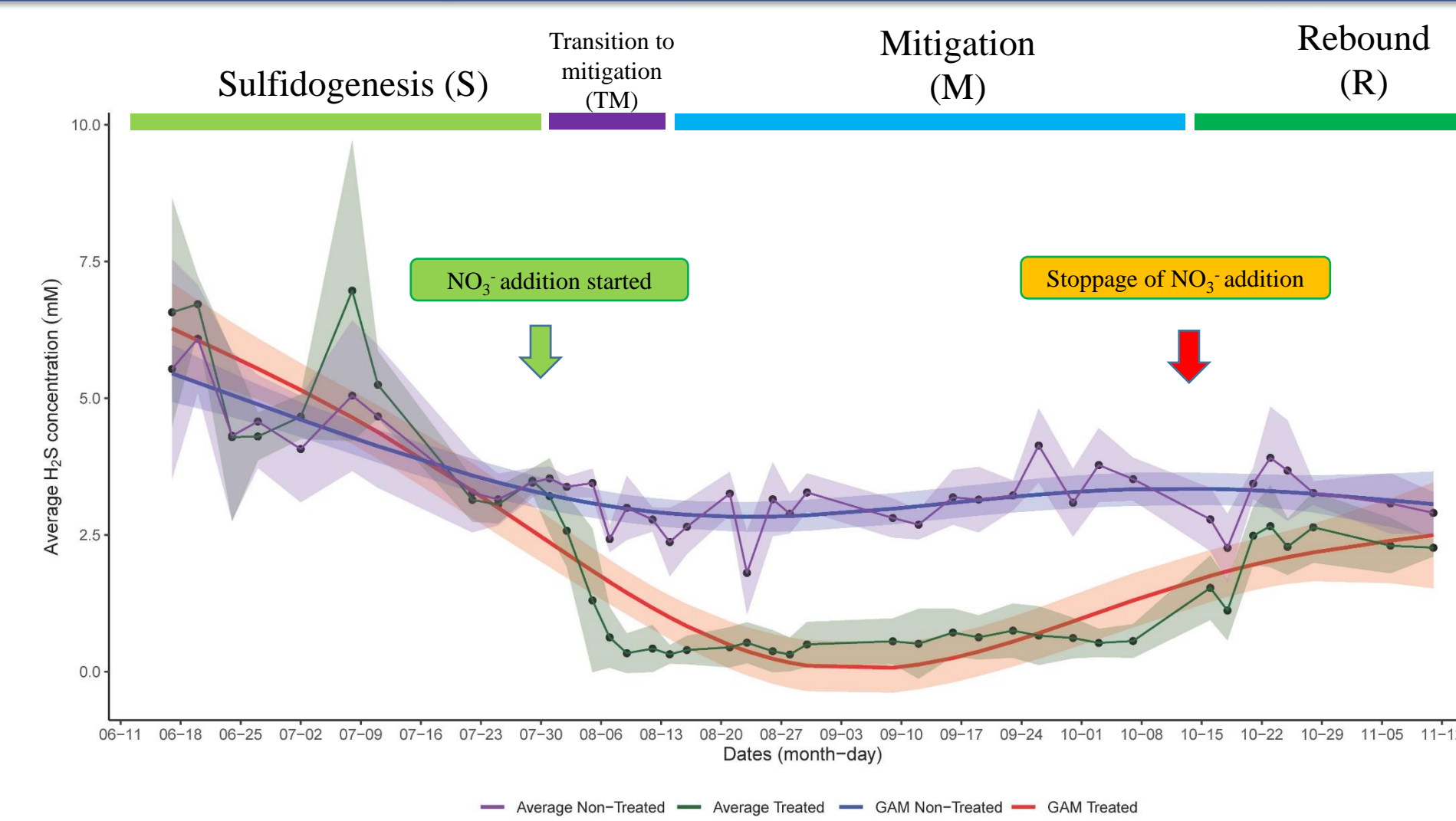
Methods

Experimental setups

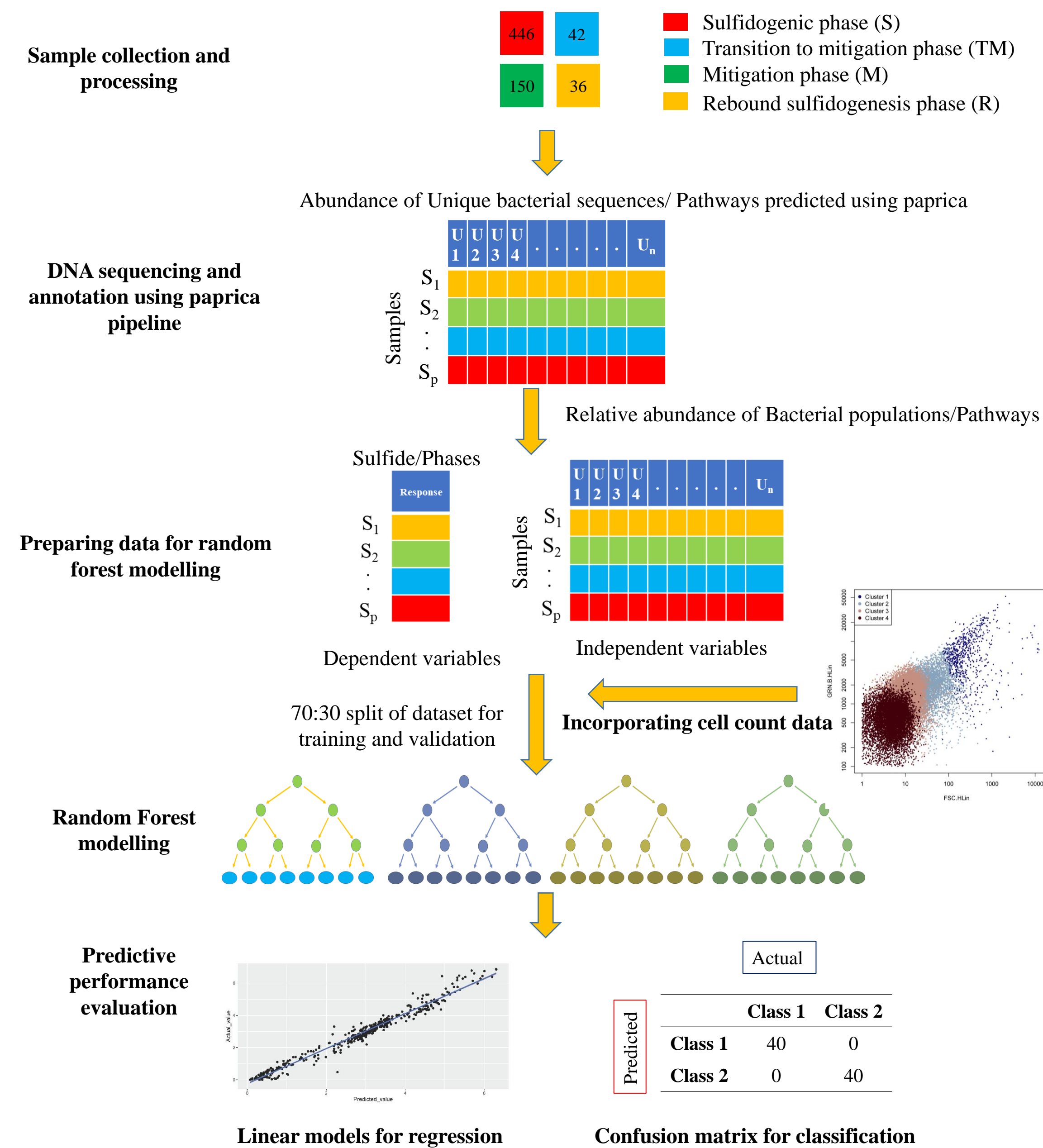


A 148-day experiment covering 20 columns (10 treated columns and 10 non-treated columns) was conducted to observe the microbial community shifts across different phases of oil biosouring and mitigation. Here treated columns refer to columns where nitrate salts were added to suppress sulfidogenesis.

Shift in H₂S concentration across columns



Machine Learning Approach



Acknowledgement

- This study received funding from BP Biosciences Center.
- Lab members of Bowman Lab

Results

Phase prediction

Independent variables:
Relative abundance of unique sequences
(for validation dataset)

Number of independent variables - 12713

Actual \ Predicted	M	R	S	TM
M	45	2	0	0
R	0	15	0	0
S	0	0	131	11
TM	1	0	0	0

Accuracy – 93.17%

Independent variables:
Absolute abundance of unique sequences
(for validation dataset)

Number of independent variables - 10887

Actual \ Predicted	M	R	S	TM
M	34	2	0	0
R	0	7	0	0
S	1	0	99	9
TM	0	0	0	0

Accuracy – 92.11%

Independent variables:
Relative abundance of pathways
(for validation dataset)

Number of independent variables - 809

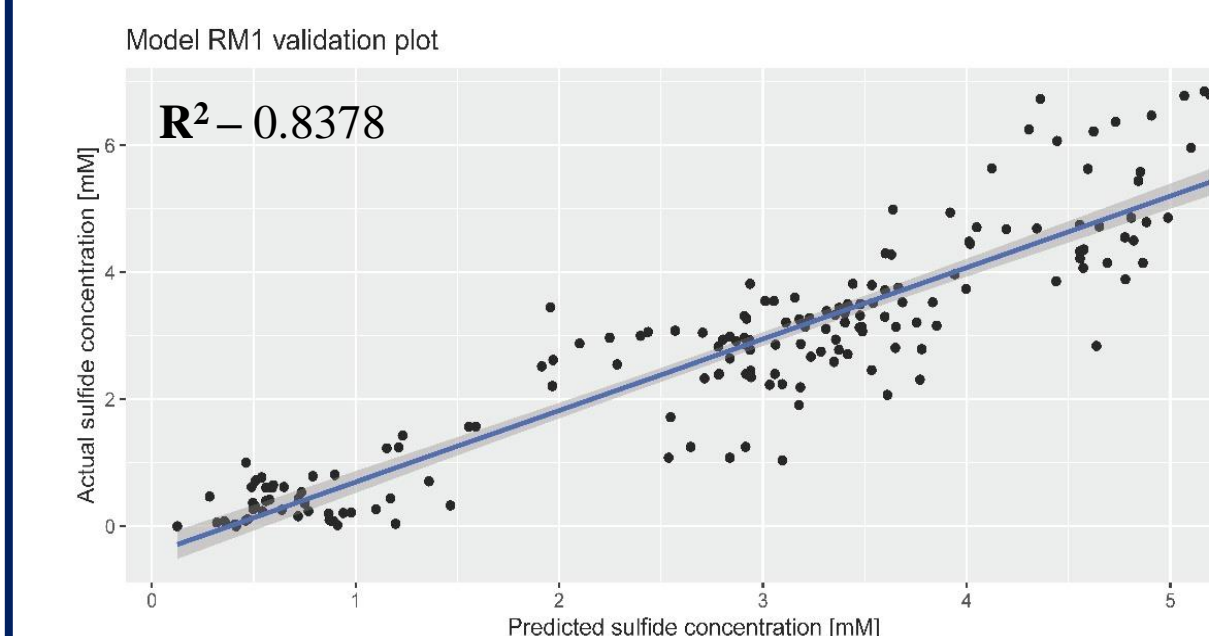
Actual \ Predicted	M	R	S	TM
M	46	1	1	1
R	0	14	0	0
S	0	2	129	10
TM	0	0	1	0

Accuracy – 92.2%

H₂S concentration prediction

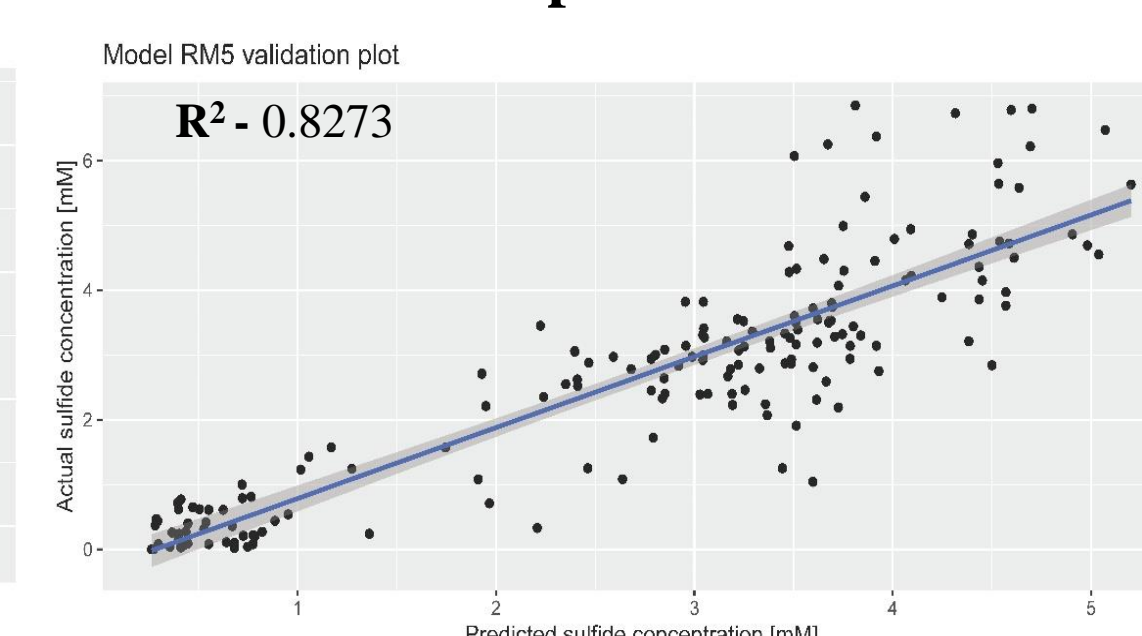
Independent variables:
Relative abundance of unique sequences
(for validation dataset)

Number of independent variables - 11637



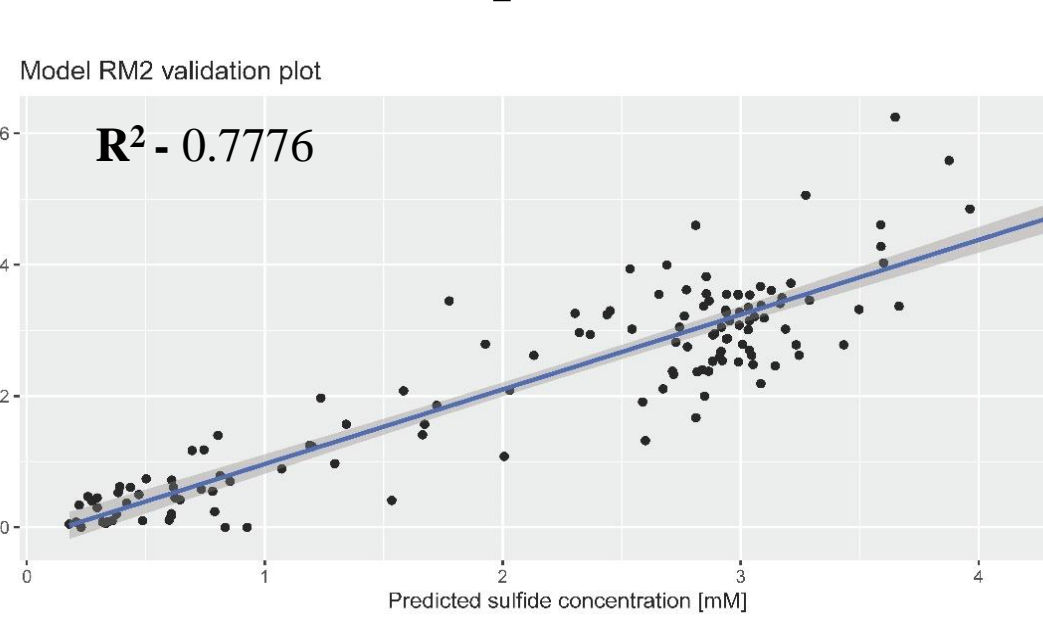
Independent variables:
Absolute abundance of unique sequences
(for validation dataset)

Number of independent variables - 10058



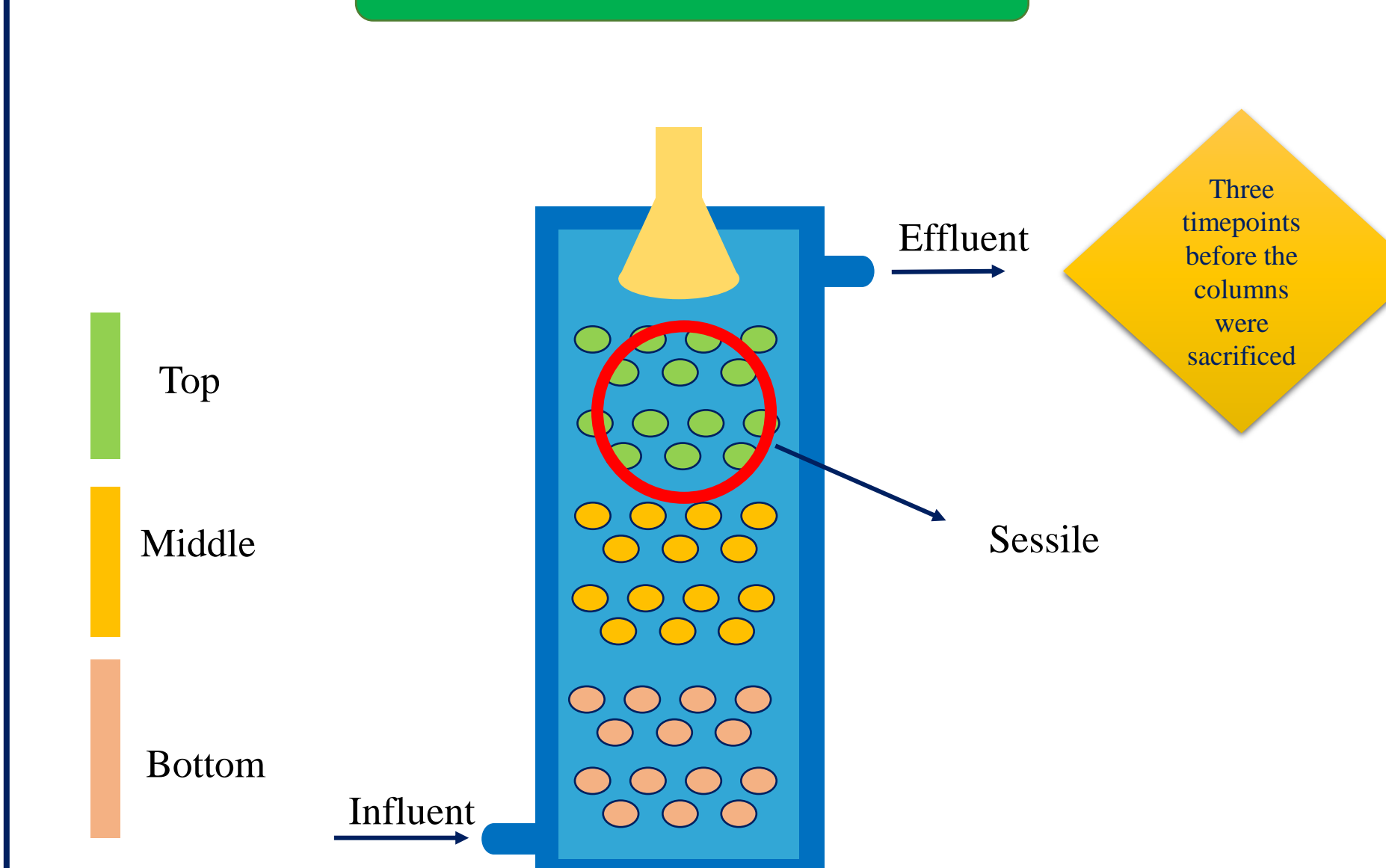
Independent variables:
Relative abundance of pathways
(feature selected)
(for validation dataset)

Number of independent variables - 33



Sessile/effluent prediction

Study Design



Independent variables:
Relative abundance of unique sequences
(for validation dataset)

Number of independent variables - 5300

	Sessile	Effluent
Sessile	17	0
Effluent	0	17

Accuracy – 100%

Observation and Inferences

- Microbial communities can be used as an indicator for successful mitigation of biosouring.
- Random forest models can be used for prediction of biosouring and mitigation phases, sulfide concentrations, and the source of microbial community.
- Predicted pathway abundances can be used as an alternative and generalized training set for predicting phases and H₂S concentrations.
- These models can be modified and developed as a valuable tool for predicting key biogeochemical processes in fields and open environments