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Application of genomics to develop a monitoring tool for stormwater treatment wetlands

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Applying Genomics to Monitor the Performance of Urban Stormwater Treatment Wetlands

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STANLEY PARK ECOLOGY SOCIETY

NSERC CRSNG

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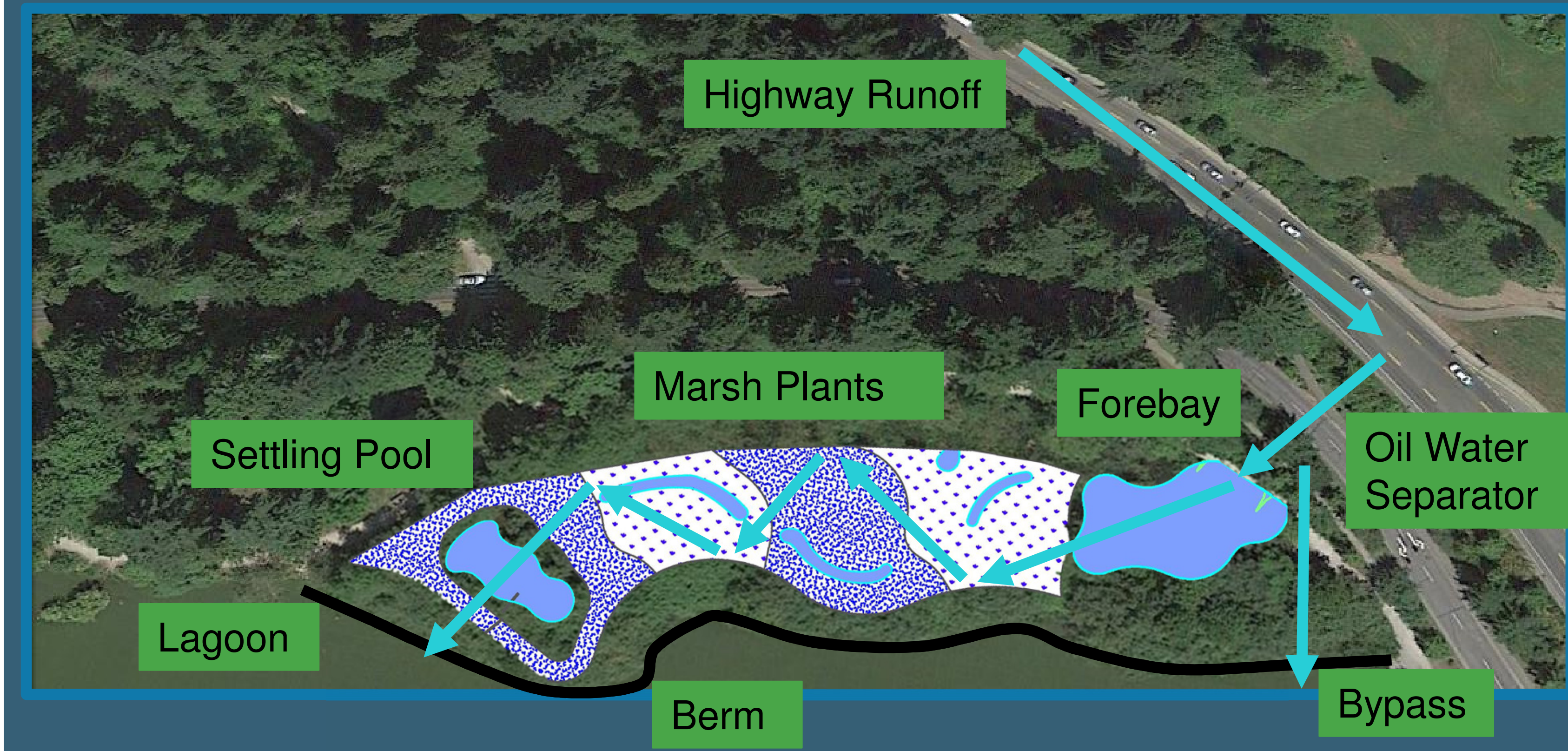
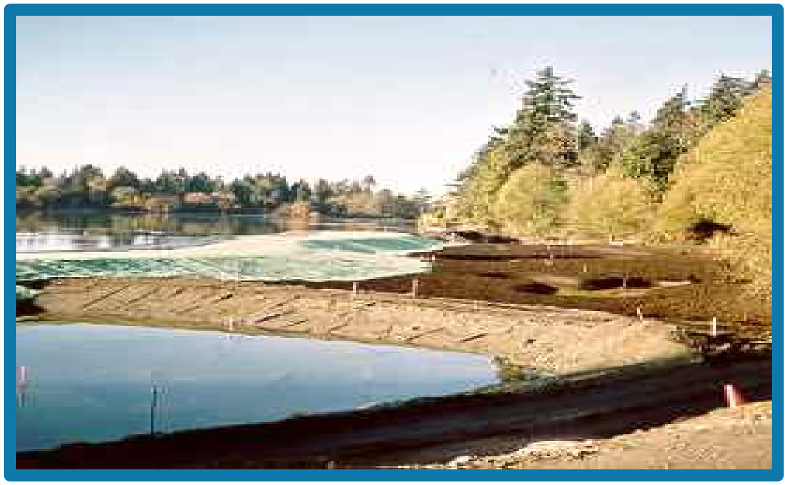
Wetlands for stormwater treatment

+ How do wetlands treat stormwater and what makes a `good` wetland ?



Background

Motivation - Lost Lagoon Wetland



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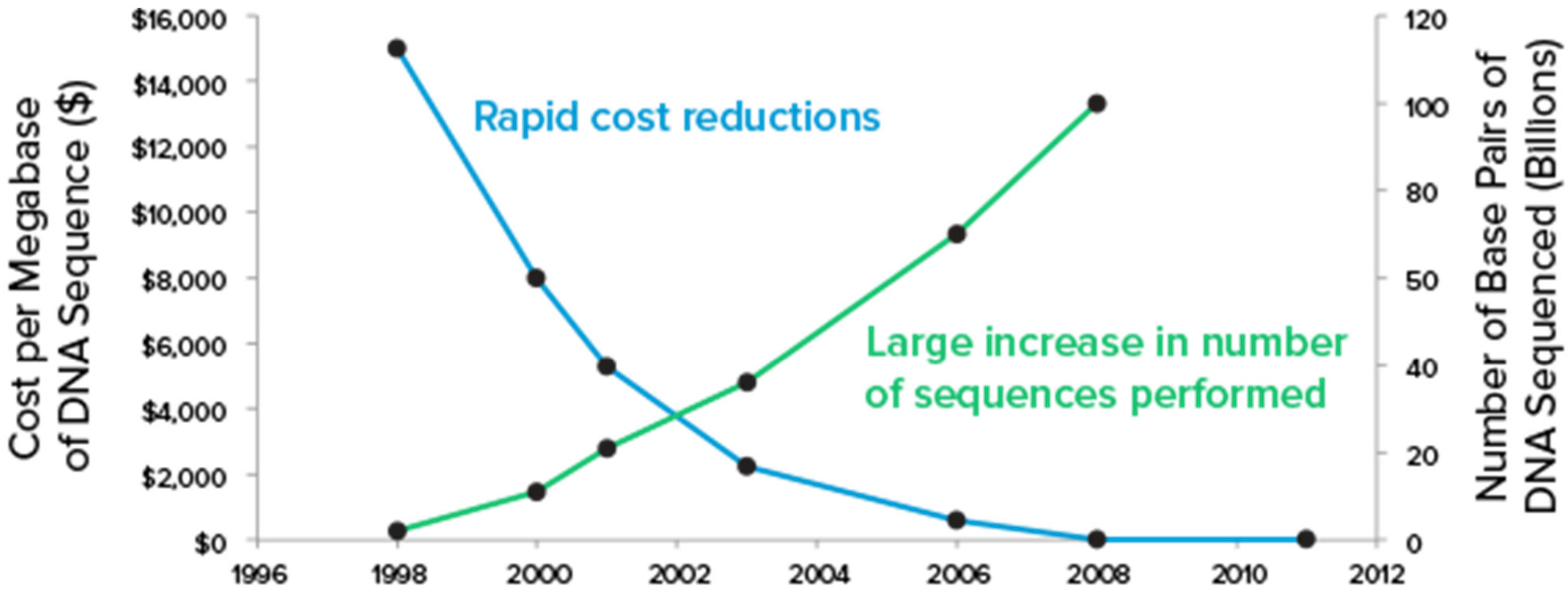
Background
Monitoring Challenges

- Wetlands are challenging to monitor
  - Two-year sampling plan. (Erickson et al 2013)
- Municipalities unlikely to prioritize extensive monitoring

+ Background

Genomics and DNA

"The branch of molecular biology that is concerned with the structure, function, evolution, and mapping of genomes, or the complete set of DNA within a single cell of an organism." (Oxford University Press 2016)

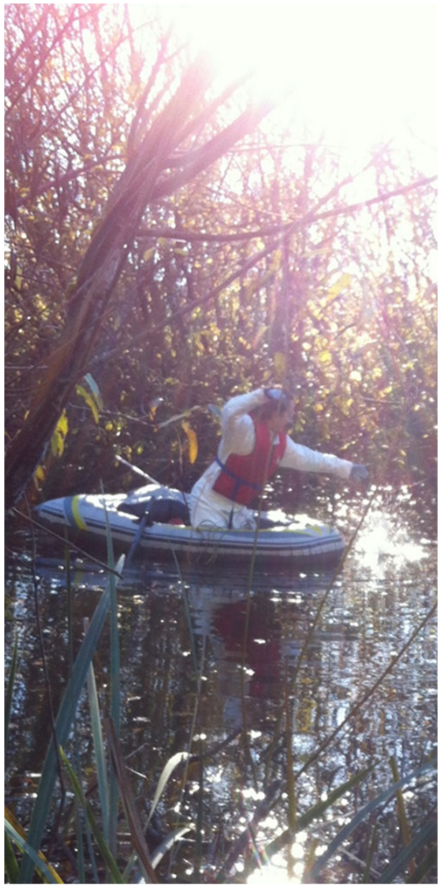


Data from the National Human Genome Institute, Data from the National Center for Biotech Information

+ Project Overview

Purpose

Begin to develop DNA-based monitoring tool for engineered stormwater treatment wetlands



Project Overview Objective 1 – Opportunities

- Demonstrate that the wetland is meeting water quality treatment guidelines

- Identify knowledge gaps and opportunities for complimentary data analyses using genomics

+ Project Overview Objective 2 – Design

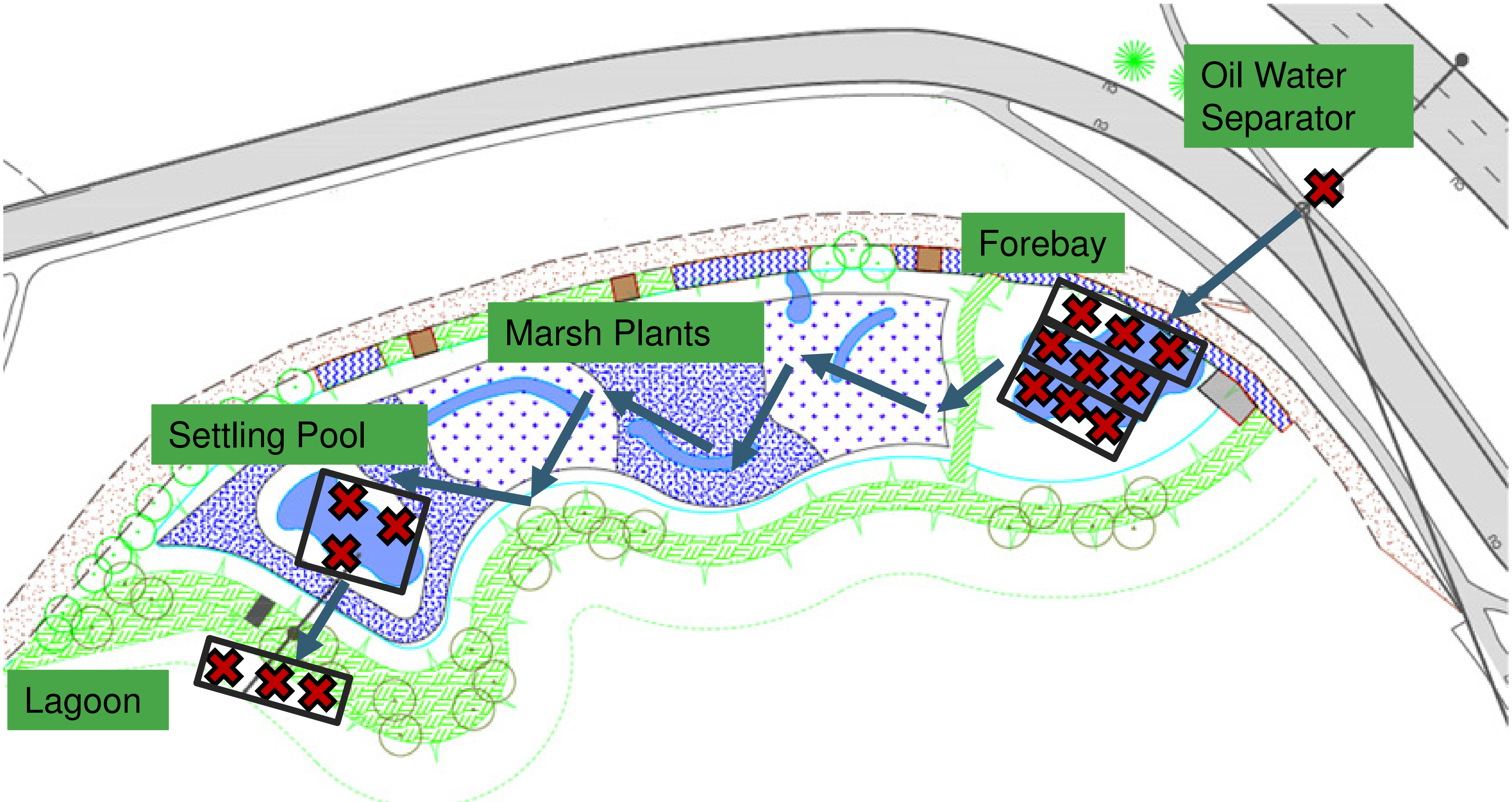
- Shifts in the bacteria and genes
- Correlations between the contaminant levels and the bacteria and genes observed
- Opportunities to expand and pursue DNA-based analyses at other sites

+
Research Activities
Field Study - Overview

- "Textbook example" stormwater treatment wetland

- 8 sampling days between July and December 2015
- 90 core sediment samples, 12 grab sediment samples, and 105 water samples

Research Activities Field Study - Site



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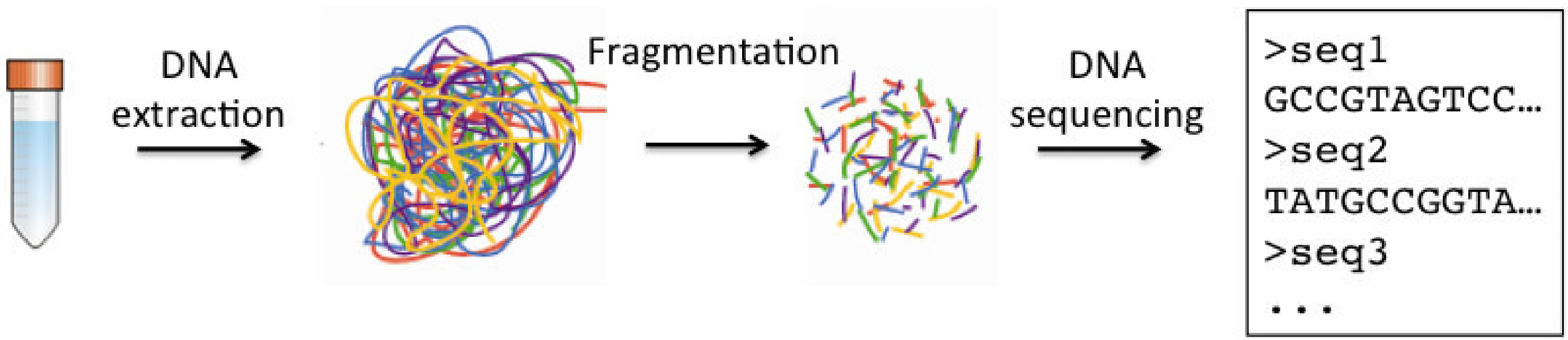
Research Activities
Laboratory Study - Overview

- Apply stormwater to an uncontaminated soil and monitor the response of the microbial community over time
  - 4 gal buckets with 10 kg soil
  - 11 columns fed stormwater and 6 columns fed distilled water
  - 3 columns analyzed each month

+ Research Activities
Analytical Methods - Sequencing

- To compare the composition of bacteria species in each sample:
  - Sequence a specific 'signature gene' fragment of the DNA known as the 16S rRNA gene, which is unique to each species
- To compare the composition of functional genes within the bacteria in each sample
  - Sequence all of the DNA and prepare what are known as metagenomes



+ Research Activities
Analytical Methods – Data Analysis

```
>seq1
GCCGTAGTCC…
>seq2
TATGCCGGTA…
>seq3
...
```

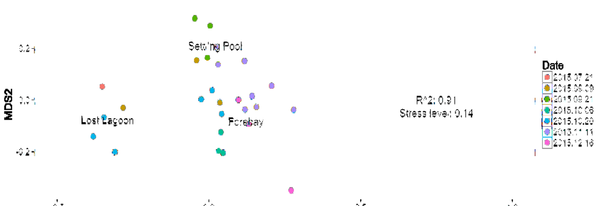
Assemble, bin and compare to a reference library

Sample No.

	1	2	3	4	5	6	7	….
Acidobacteria	15	4947	15	6806	0	0	15	
Actinobacteria	10	5674	10	7141	1	1	20	
AncK6	1	802	1	896	0	0	2	
Bacteroidetes	16	1487	15	1305	3	678	21	
Chlamydiae	0	0	0	0	0	0	0	
Chloroflexi	35	1763	34	1902	1	1	18	
Cyanobacteria	0	0	0	0	0	0	3	
Firmicutes	7	120	1	1	1	1	5	
Gemmatimonadetes	8	879	7	503	0	0	7	
Lentisphaerae	0	0	0	0	0	0	0	
Nitrospirae	2	163	1	272	0	0	2	
OD1	0	0	0	0	0	0	0	
PAUC34f	4	3759	4	2634	0	0	4	
Planctomycetes	5	13	4	15	0	0	8	
Poribacteria	6	3726	5	2137	0	0	5	

Linear algebra and coding software for analysis

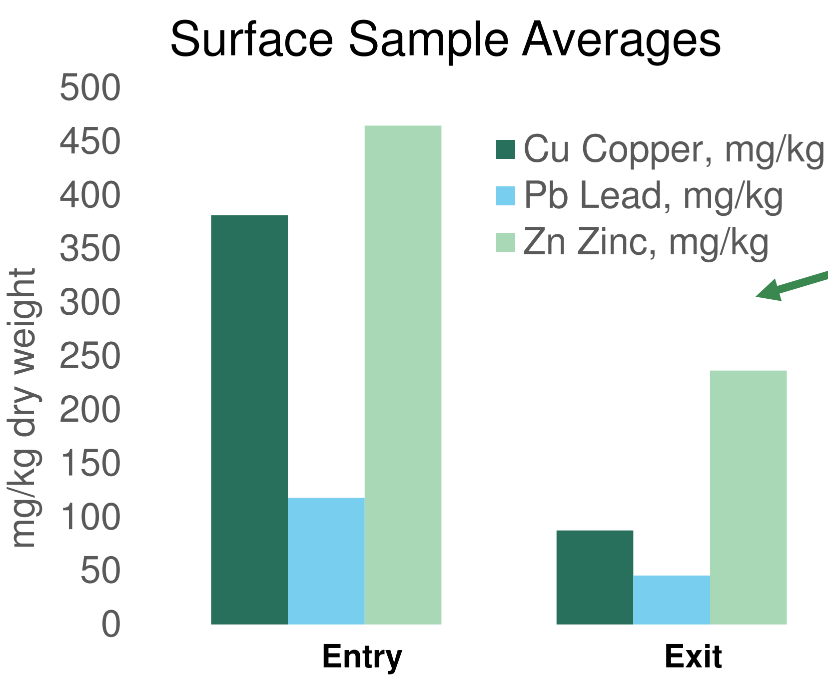
Example – convert to two dimensions using similarity between samples and prepare a plot to visualize the samples



Environmental Analysis Hypothesis 1

1. The wetland removes heavy metals

Environmental Analysis Results



- Stormwater metals show high concentrations at the wetland entry
- Cu, Pb, and Zn had the most significant reductions (p.val <0.05 using Wilcoxon Rank test)
- High variability between sampling dates even at the same location

Hypothesis 1

The concentrations of metals associated with stormwater decrease along the length of the wetland.

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Microbial Analysis Hypothesis 2

2. The bacteria at the entry of the wetland differ from the bacteria at the exit of the wetland

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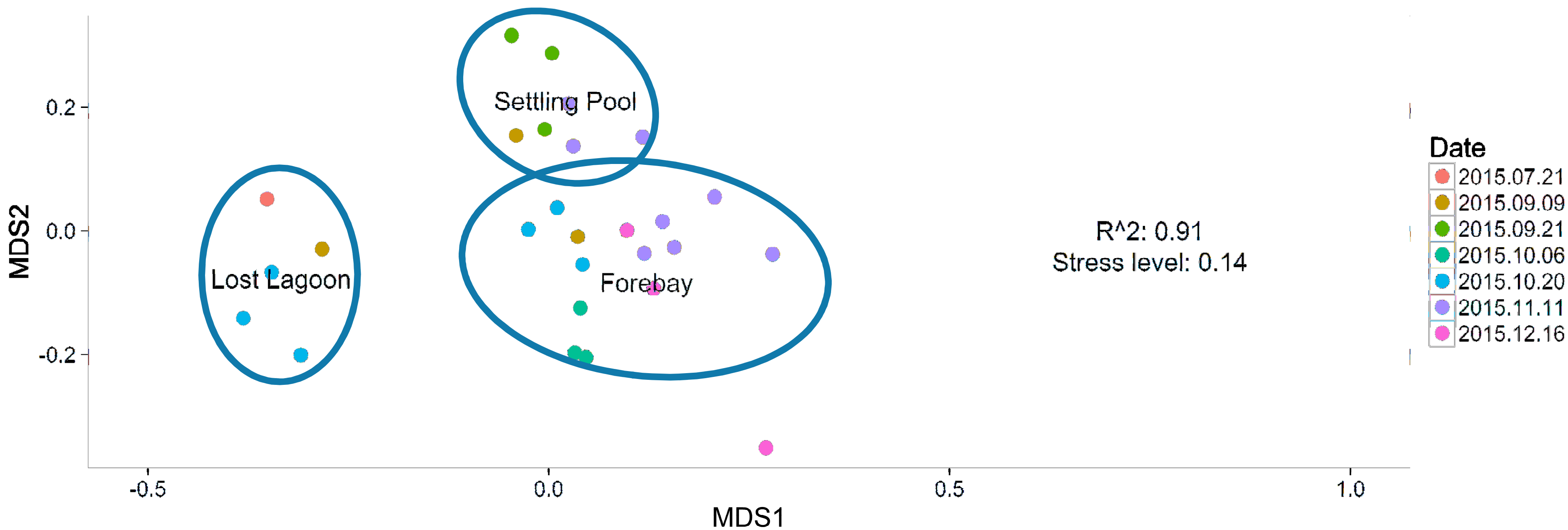
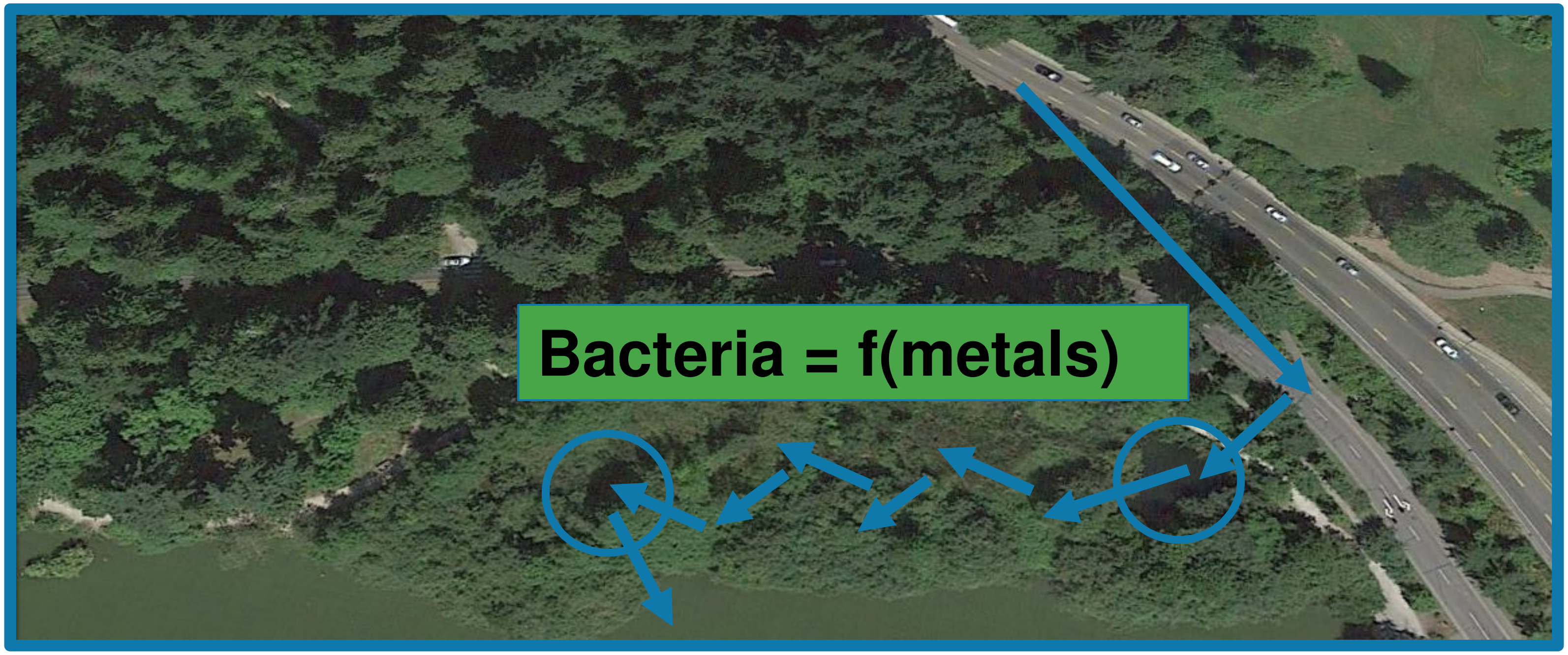
Microbial Analysis Results – Surface Sediment



+ Microbial Analysis Hypothesis 3

3. There is a link between metal removal and bacteria



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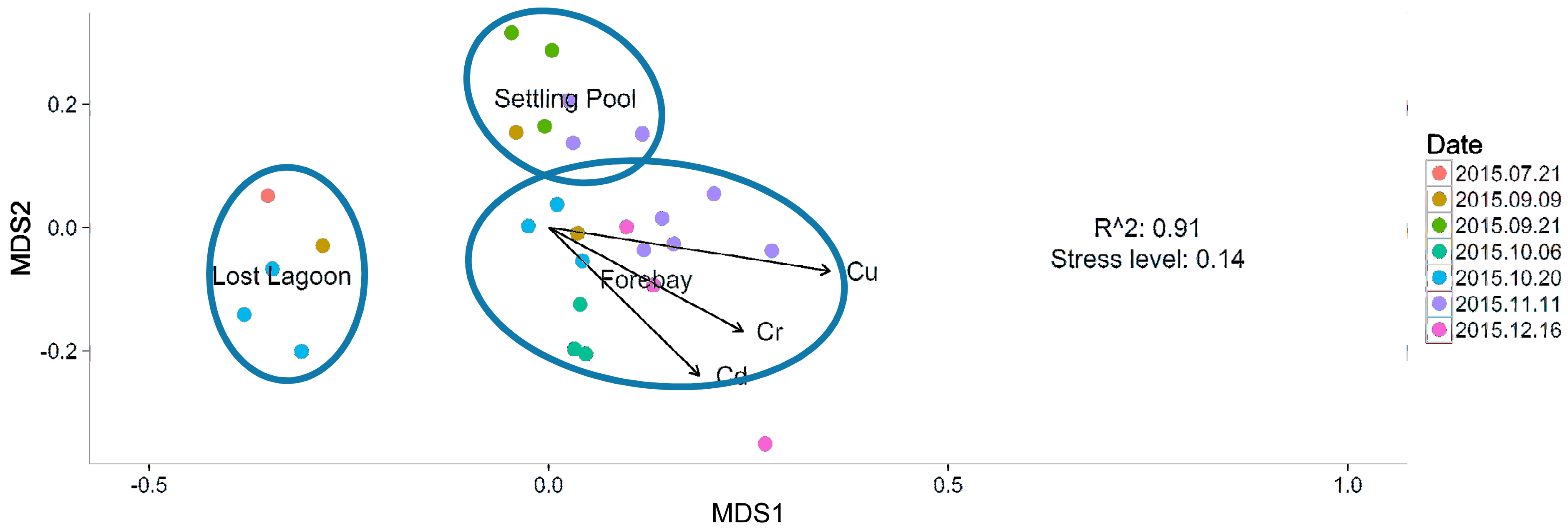
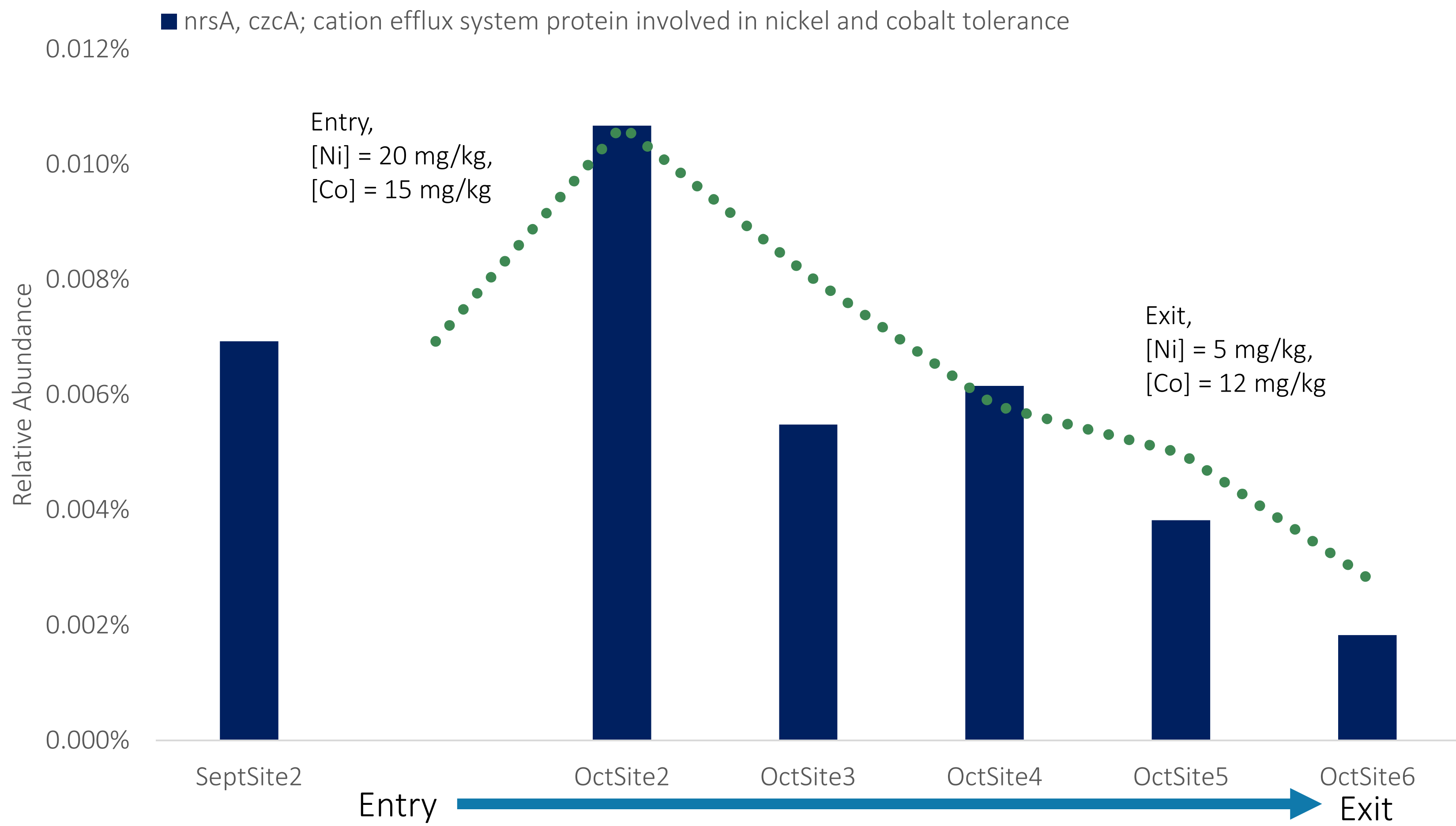
Microbial Analysis Results – Surface Sediment



+ Functional Analysis Results – Surface Sediment

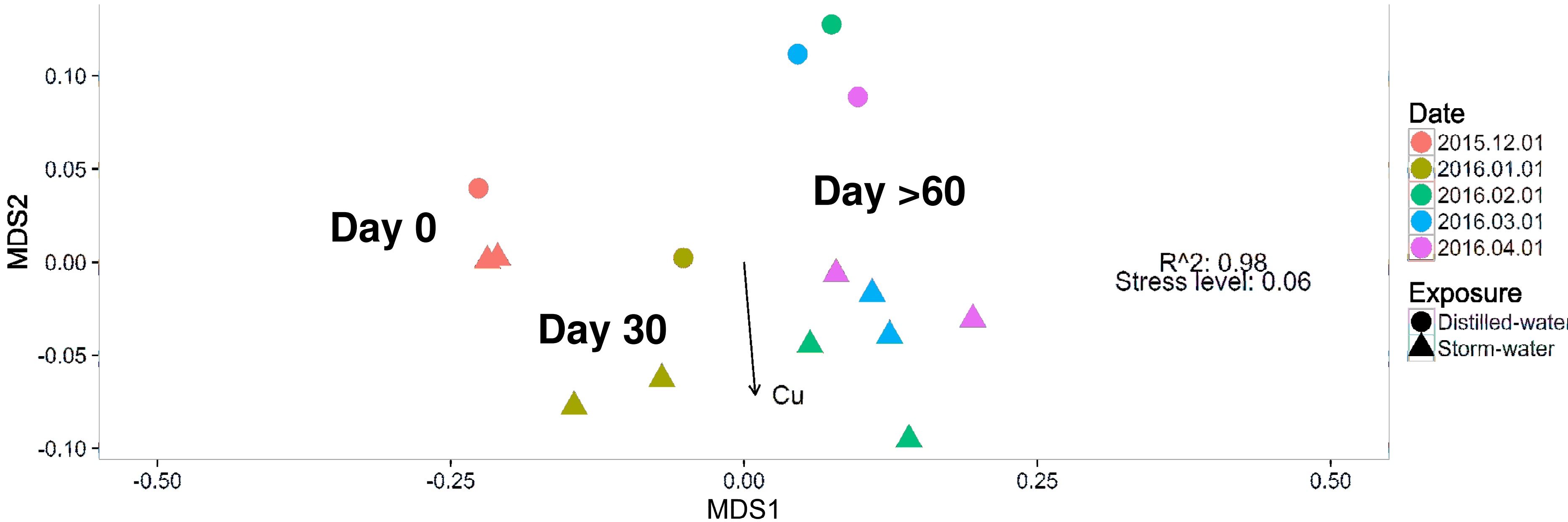


Relative Abundance of Functional Genes Associated with Nickel and Cobalt Measured in Field Samples

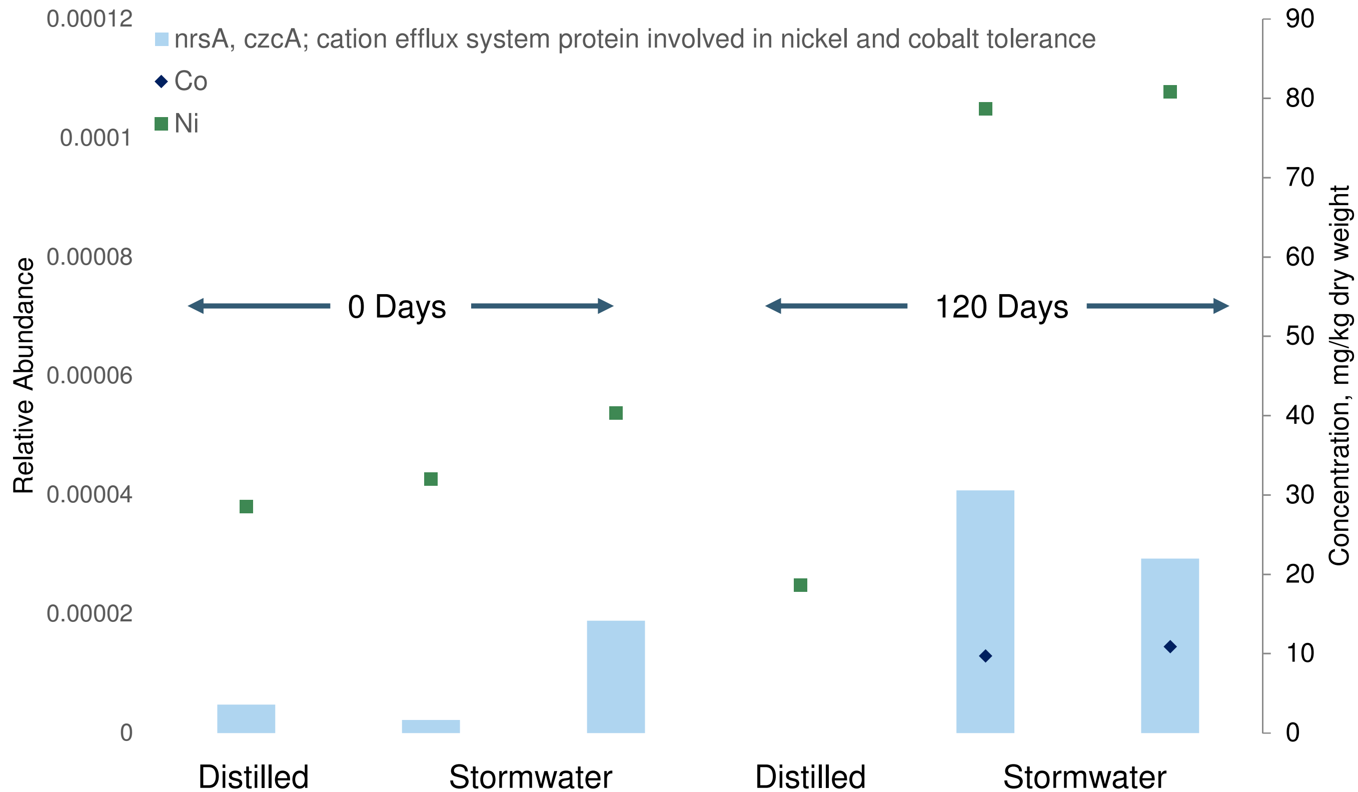
Microbial Analysis Hypothesis 4

4. Stormwater exposure causes bacterial communities to form similar adaptations at other sites

Microbial Analysis Results – Surface Sediment



Functional Analysis Results – Column Surface Sediment



Relative Abundance of Functional Genes Associated with Cobalt and Nickel

+ Final Comments

- Data support hypotheses and interest in microbial results

- Results will support the Lost Lagoon wetlands

- Next step is to repeat this work at other sites

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Acknowledgements
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consulting engineers

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Questions??
Comments!!

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