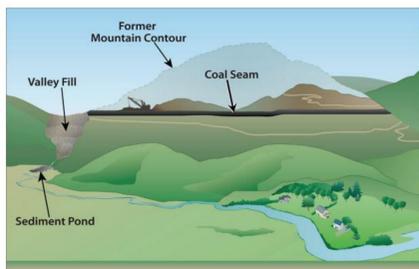


SURFACE COAL MINING IN CENTRAL APPALACHIA: IS BIOACCUMULATION OCCURRING IN THE HEADWATER STREAMS?

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Background

- Strip mining removes the upper layer of soil and rock from a mountaintop to allow access to coal
- Material removed from mountaintop is usually deposited in nearby valley, known as a valley fill
- Headwater streams can be affected by unearthed elements now leaching into headwater streams



<https://www.epa.gov/sc-mining/basic-information-about-surface-coal-mining-appalachia>



https://timeecentric.files.wordpress.com/2011/12/mountaintop_mining.jpg?w=611&h=404&crop=1

Objectives and Methods

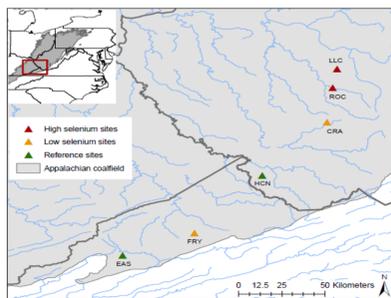


Figure 1
Timpano, A. J. (2017). *Toward improved assessment of freshwater salinization as a benthic macroinvertebrate stressor* (Doctoral dissertation, Virginia Tech).

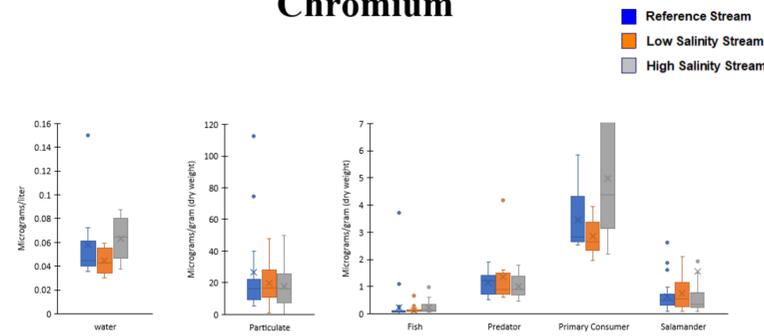


Figure 2

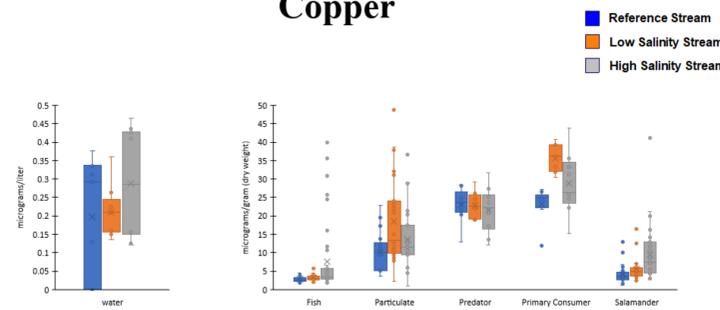
- Figure 1: 6 locations where samples were collected
 - 2 non-mined reference streams
 - 2 low salinity streams
 - 2 high salinity streams
- Figure 2: A stream where data was collected
- Media type collected: water, particulate matter, primary consumers, predators, salamanders, and fish
- Elements tested from media types: arsenic, cadmium, chromium, cobalt, copper, nickel, selenium, strontium, and zinc

Elemental Data Graphs

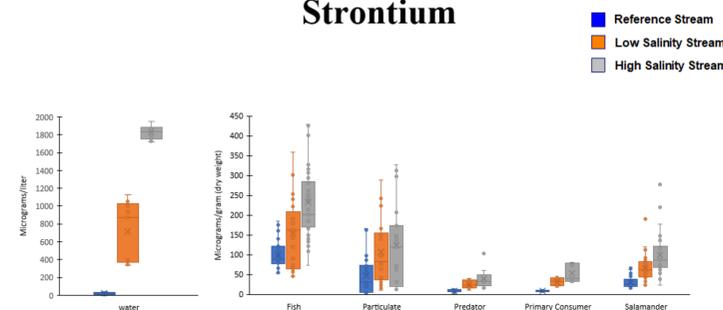
Chromium



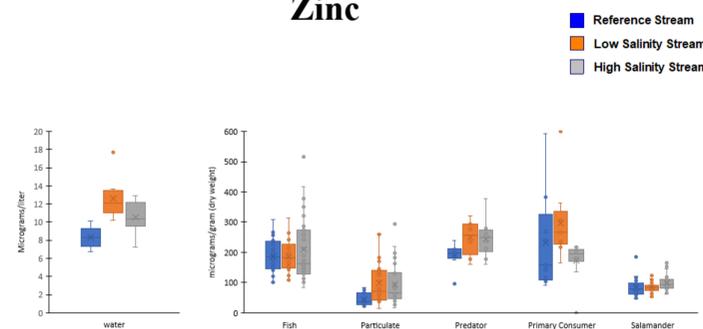
Copper



Strontium



Zinc



Statistical Analysis

Before being able to test for bioaccumulation, it must be determined if each of the three categories (reference, low salinity, high salinity) are normally distributed. If so, then a one-way ANOVA is run to determine if there is a significant difference between the three. If the three are not normally distributed, then a Kruskal Wallis H Test is used.

Strontium Fish - Reference		Strontium Fish - Low Salinity		Strontium Fish - High Salinity	
Mean	160.36	Mean	358.49	Mean	191.2415758
Standard Error	97.71363636	Standard Error	147.8346875	Standard Error	234.3531714
Median	5.773482498	Median	14.24866728	Median	14.68836788
Mode	88.39	Mode	152.63	Mode	207.73
Standard Deviation	#N/A	Standard Deviation	#N/A	Standard Deviation	#N/A
Sample Variance	33.1661319	Sample Variance	80.60263403	Sample Variance	95.19150351
Kurtosis	1099.992305	Kurtosis	6496.784613	Kurtosis	9061.422341
Skewness	0.612220604	Skewness	-1.009623035	Skewness	1.7611793
Range	0.977856548	Range	0.295808042	Range	1.177692655
Minimum	131.39	Minimum	263.49	Minimum	469.9156377
Maximum	53.46	Maximum	45.78	Maximum	73.46436231
Sum	184.85	Sum	309.27	Sum	543.38
Count	3224.55	Count	4730.71	Count	9842.8332
Count	33	Count	32	Count	42

Excel - Testing for normal distribution

HO	All populations are distributed the same way			
HA	At least one of the populations is distributed differently			
Rank	=RANK(AO3, \$AO3:\$AQ12,1)	=RANK(AP3, \$AP3:\$AQ12,1)	=RANK(AQ3, \$AQ3:\$AQ12,1)	
	=RANK(AO4, \$AO3:\$AQ12,1)	=RANK(AP4, \$AP3:\$AQ12,1)	=RANK(AQ4, \$AQ3:\$AQ12,1)	
	=RANK(AO5, \$AO3:\$AQ12,1)	=RANK(AP5, \$AP3:\$AQ12,1)	=RANK(AQ5, \$AQ3:\$AQ12,1)	
	=RANK(AO6, \$AO3:\$AQ12,1)	=RANK(AP6, \$AP3:\$AQ12,1)	=RANK(AQ6, \$AQ3:\$AQ12,1)	
	=RANK(AO7, \$AO3:\$AQ12,1)	=RANK(AP7, \$AP3:\$AQ12,1)	=RANK(AQ7, \$AQ3:\$AQ12,1)	
	=RANK(AO8, \$AO3:\$AQ12,1)	=RANK(AP8, \$AP3:\$AQ12,1)	=RANK(AQ8, \$AQ3:\$AQ12,1)	
	=RANK(AO9, \$AO3:\$AQ12,1)	=RANK(AP9, \$AP3:\$AQ12,1)	=RANK(AQ9, \$AQ3:\$AQ12,1)	
	=RANK(AO10, \$AO3:\$AQ12,1)	=RANK(AP10, \$AP3:\$AQ12,1)	=RANK(AQ10, \$AQ3:\$AQ12,1)	
	=RANK(AO11, \$AO3:\$AQ12,1)	=RANK(AP11, \$AP3:\$AQ12,1)	=RANK(AQ11, \$AQ3:\$AQ12,1)	
			=RANK(AQ12, \$AQ3:\$AQ12,1)	
Sum of ranks	=SUM(AO17:AO25)	=SUM(AP17:AP25)	=SUM(AQ17:AQ25)	
Count	=COUNT(AO17:AO26)	=COUNT(AP17:AP26)	=COUNT(AQ17:AQ26)	=SUM(AO28:AQ28)
sum of squares*2/count	=AO27*2/AO28	=AP27*2/AP28	=AQ27*2/AQ28	=SUM(AO29:AQ29) <<<sum
K	=(12/(AR28*(AR28+1)))*AR29-3*(AR28+1)			
Critical Value	=CHINV(0.05,2)			
P-value	=CHDIST(AO31,2)			

Excel - Formulas created to run a Kruskal Wallis H Test

Conclusions and Future Work

Excel was used to analyze data and help determine one-way Analysis of Variance and Kruskal Wallis H tests, but a more powerful program such as R should be used to finish comparing data relationships to look for bioaccumulation.

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