HW4

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Spring semester 2023
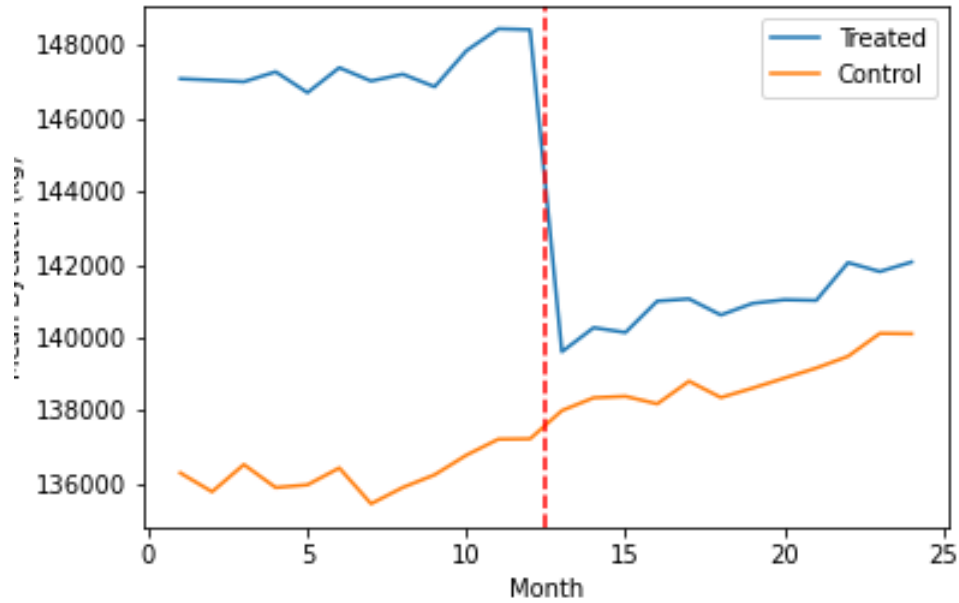
1 Python

1.1

Figure 1: Caption

1.2

- The point estimate for the coefficient of interest is -9591.35. It implies that the treatment reduces bycatch by that amount, in pounds.

1.3

	Dependent variable:		
	(1)	(2)	(3)
const	137228.60***	136154.05***	1547.01***
	(18543.61)	(12035.83)	(346.41)
Firm Size			-2119.71**
			(982.42)
Pre-treatment	773.22		
	(26238.57)		
Salmon			0.60***
			(0.06)
Shrimp			1.06***
			(0.02)
Treated	-9591.35	-8956.78	-8436.28***
	(33094.88)	(9435.06)	(806.64)
Treatment Group	11202.04	11052.45*	-21.90
	(23383.90)	(6624.65)	(94.15)
Month indicators	Y	Y	Y
Observations	100	1,200	1,200
R^2	0.00	0.00	0.99
Adjusted R^2	-0.03	-0.02	0.99
Residual Std. Error	81287.17	80284.53	7537.89
F Statistic	0.11	0.14	12183.47***

Note: *p<0.1; **p<0.05; ***p<0.01

- With the full sample and additional controls, the estimated treatment effect is both smaller and more precise.

2 Stata

2.1

VARIABLES	(1) Firm indicators	(2) Within-transformation
treated	-8,085***	-8,085***
	(2,619)	(2,564)
shrimp	1.552***	1.552***
	(0.178)	(0.175)
salmon	-0.680	-0.680
	(1.125)	(1.101)
firmsize	12,972	
	(16,649)	
Constant	5,029	128,582
	(4,575)	(147,891)
Observations	1,200	1,200
R-squared	0.996	0.428
Number of firm		50

Robust standard errors in parentheses
*** p<0.01, ** p<0.05, * p<0.1

- These two specifications report identical point estimates, but different standard errors. Also of note, the within-transformation in Stata drops the variable $firmisize$ due to collinearity. Compared to the Python results above, we have still smaller point estimates for treatment effect, though we have lost some efficiency compared to the full-sample DiD (spec. 3). This is because the mathematical demeaning of each variable can "absorb" variation in the data, leading to less precise estimates.