
Lecture 8: Identification of Causal Effects Under Treatment Ignorability (ctd)

Outline:

- Identification of ATE under treatment ignorability
 - Methods based on propensity score
- Application: effect of ITQ adoption on the probability of fishery collapse
- Readings: A&P Chapter 3 (especially sections 3.2 and 3.3), I&W Lecture 1
- Also: <http://www.stat.columbia.edu/~gelman/arm/>
- "Data Analysis Using Regression"
- See Ch.9 and 10. Includes R code... Excellent chapters

Propensity score: motivation

- ❑ Linear regression may be unreliable due to extrapolation problem in presence of lack of overlap
- ❑ Exact matching on baseline covariates is very demanding of data in real-world applications, i.e., even a small array of matching variables may lead to a very large numbers of “cells” => small cells, empty cells
- ❑ One way to simplify the issue of matching is to create a scalar (one-number) summary of all the baseline covariates and then use this number to match treatment and control observations

Methods based on the propensity score

- Definition of propensity score:

$$p(X_i) = \Pr(T_i = 1 | X_i) \quad 0 < p(X_i) < 1$$

- This is simply the probability of receiving the treatment conditional on X_i . (Note that $p(X_i)$ is a scalar)
 - So an advantage of propensity score methods is to ‘bypass’ the high-dimensionality of exact matching and related regression estimator
- We need to rule out $p(X_i)=0$ or 1. We can’t learn anything from individuals that get treated (or never treated) with certainty. Also want “overlap” in distributions of $p(X_i)$
 - **Known as overlap / support condition**

Ignorability conditional on propensity score

- Rosenbaum and Rubin (1983) show that ignorability conditional on X_i implies ignorability conditional on $p(X_i)$

$$T_i \perp (Y_{0i}, Y_{1i}) \mid X_i \Rightarrow T_i \perp (Y_{0i}, Y_{1i}) \mid p(X_i)$$

- Seems natural since $P(X_i)$ summarizes the predictive information in X_i for predicting T_i
- This says that two observations, one treated and one controls with the same propensity score are perfect comparisons for each other
 - For example, in an ideal RCT, all observations should theoretically have the same propensity score

Estimating the propensity score

- The propensity score is unknown and must be estimated
- This is typically done with a logistic model (a ML estimator designed for analyzing binary dependent variables):

$$p(X_i) = \Pr(T_i = 1 \mid X_i) = \frac{\exp(h(X_i, \gamma))}{1 + \exp(h(X_i, \gamma))}$$

- Where $h(X_i, \gamma)$ is a function of X_i . Imbens (2014) proposes an algorithm to choose the specification
- The estimated propensity score is simply the predicted value from the model above

Estimating the propensity score: example

- From Costello, Gaines, Lynham (2008):
- “To estimate the propensity scores we estimate the probability that a fishery will be in an ITQ in a given year using four different specifications:
 - (i) a model with a dummy variable for every LME;
 - (ii) a model with a dummy variable for every genus;
 - (iii) a model with a dummy variable for every species;
 - (iv) a model with a dummy variable for every LME, genus and species
- “We use a logit estimator to estimate the four models for each year in the sample”

Balancing property of the propensity score

- Under the treatment ignorability assumption, Rosenbaum and Rubin (1983) show that:

$$\Pr[X_i = x \mid p(x) = p, T_i = 1] = \Pr[X_i = x \mid p(x) = p, T_i = 0]$$

- In words: treated and non-treated observations with the same value of the propensity score have the same distribution of the baseline covariate X_i
 - Suggest something similar to randomization test in RCT
- Approach to test covariate balance: T-tests of equality of means by “blocks” of the p-score distribution
 - Balancing tests can be used to refine the estimating equation for the propensity score (choice of $h(X_i, \gamma)$)

Four approaches to estimate causal effects using the propensity score

- i. Matching on the propensity score
 - I only cover stratification/blocking here. Other p-score matching methods exist
- ii. Re-weighting the data using propensity score
- iii. Weighted least squares estimator
- iv. Linear regression adjustment with the propensity score (shown here for illustration purposes)
- Researchers also use propensity score to “trim” samples to make treatment and control observations more comparable
- ⇒ Estimation of the sampling variance of propensity score based estimators can be tricky. See references at the end

i. Matching on Propensity Score

- Since p-score is continuous random variable, P-score matching is “inexact”, “nearest-neighbor” matching
- Suppose exact p-score matching can be performed for illustration purposes
- Recall exact matching and apply the same method to p-score=p instead of covariate X. Then we would have estimators of the form:

$$= \sum_p w(p) [\bar{Y}_1(p) - \bar{Y}_0(p)]$$

$$\bar{Y}_j(p) = \frac{1}{n} \sum_i Y_i \times 1(T_i = j, p(X_i) = p)$$

“Stratification” (“Subclassification”, “blocking”)

- Define “k” blocks of the propensity score distribution
- (ex: quartiles, so $k=1,2,3,4$)
- In practice, choose #blocks (and model for p-score) so that average p-score is the similar within blocks and distribution of X_i is balanced
- Compute mean difference within block, and re-weight:

$$= \sum_k w(k) [\bar{Y}_1(k) - \bar{Y}_0(k)]$$

- Where $w(k) = N(k)/N$ for ATE and $N(k|T=1)/N(T=1)$ for ATT

Blocking with simulated data

- Consider 4 blocks (quartiles):

Quartile	P-value on t-test for X	Mean P-score	N	$\hat{\Delta}(p)$	$w_{ATE}(p)$
1	0.001	0.09	11,367	1.09	0.39
2	0.151	0.50	6,147	1.47	0.21
3	0.804	0.84	6,002	2.04	0.20
4	0.835	0.98	5,984	2.46	0.20

- Implied ATE = 1.62
- Note: X not balanced in 1st strata...

ii. Re-weighting estimator

- Under the treatment treatment ignorability assumption, you can show that:

$$ATE = E \left[\frac{T_i Y_i}{p(X_i)} - \frac{(1-T_i) Y_i}{[1-p(X_i)]} \right] \quad \hat{ATE} = \frac{1}{n} \sum_i \left[\frac{T_i Y_i}{\hat{p}(X_i)} - \frac{(1-T_i) Y_i}{1-\hat{p}(X_i)} \right]$$

- In words: Average of $Y_i / P(X_i)$ among the treated, minus the average of $Y_i / 1 - P(X_i)$ among the controls
- Issues:
 - IPW has trouble when there are probabilities very close to zero or one, as this leads to division by very small numbers
 - Weights will not necessarily sum to 1 in a given sample, so you may need to normalize them to sum to 1
 - Also known as IPW estimator (inverse probability weighting)

Intuition behind re-weighting estimator

- For some intuition for the re-weighting estimator, recall:

$$\bar{Y}_1 - \bar{Y}_0 \xrightarrow{\text{not}} ATE$$

$$\bar{Y}_1(x) - \bar{Y}_0(x) \xrightarrow{p} ATE(x)$$

- The problem is that the distribution of X_i differs in the $T=1$ and $T=0$ groups (i.e. imbalance)
- Weighting the units by the inverse of the probability of receiving the treatment (i.e. $1/P(X_i)$ or $1/1-P(X_i)$) undoes the imbalance
- **Applying this to the simulated data, I get an estimate of ATE of 1.5**

iii. WLS estimator (with p-score weight)

- Estimate ATE using weighted linear regression (WLS) (aweight=w_i in STATA):
- Regress: $Y_i = \beta_0 + \beta_1 T_i + (X_i' \gamma) + u_i$, with weight defined as:

$$w_i = \frac{T_i}{p(X_i)} + \frac{1 - T_i}{1 - p(X_i)}$$

```
. regress Y_soo T_soo X [aweight=w], robust;
(sum of wgt is 6.0000e+04)
```

Linear regression

```
Number of obs = 30000
F( 2, 29997) =23963.90
Prob > F      = 0.0000
R-squared     = 0.5759
Root MSE     = 1.09
```

	Y_soo	Coef.	Robust Std. Err.	t	P> t	[95% Conf. Interval]
	T_soo	1.489764	.0311578	47.81	0.000	1.428693 1.550835
	X	.7172597	.0145206	49.40	0.000	.6887988 .7457207
	_cons	1.516731	.0221433	68.50	0.000	1.473329 1.560133

Weighting by p-score rebalances data:

```
. table X, c(sum T_soo sum C_soo);
```

□ Recall from Lecture 7:

X	sum(T_soo)	sum(C_soo)
1	124	5781
2	898	5064
3	3119	3028
4	5003	999
5	5849	135

□ Now, the same tabulation, using p-score based weight:

```
. gen weight=(T_soo/pscore) + (C_soo/(1-pscore));
```

```
. table X [aw=weight], c(sum T_soo sum C_soo);
```

X	sum(T_soo)	sum(C_soo)
1	2976.5	2976.5
2	2967	2967
3	2924	2924
4	3112	3112
5	3020.498	3020.502

iv. Controlling for propensity score in linear regression (for illustration purpose)

- **Same approach as linear regression before:**

$$E[\varepsilon_{0i}|p(X_i)] = \alpha_0 + \gamma_0 p(X_i)$$

$$E[\varepsilon_{1i}|p(X_i)] = \alpha_1 + \gamma_1 p(X_i)$$

- Implied linear regression function:

$$Y_i = \beta_0 + \beta_1 T_i + (p(X_i) - \bar{p})\gamma_0 + T_i(p(X_i) - \bar{p})(\gamma_1 - \gamma_0) + u_i$$

- \Rightarrow ATE identified by linear regression of outcome on treatment indicator variable, p-score, and interactions between treatment indicator variable and p-score (so only 4 terms in the regression)

Linear regression with p-score with simulated data

```
. regress Y_soo T_soo p Tp, robust;
```

Linear regression

Number of obs = 30000
F(3, 29996) =27387.30
Prob > F = 0.0000
R-squared = 0.7344
Root MSE = 1.0149

		Robust					
Y_soo		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]	

T_soo		1.486425	.0173314	85.76	0.000	1.452455	1.520396
pscore		1.858627	.0331625	56.05	0.000	1.793627	1.923627
Tp		1.92088	.047042	40.83	0.000	1.828676	2.013084
_cons		1.512467	.0122295	123.67	0.000	1.488497	1.536437

- With the simulated data, this linear regression approach does better than linear regression controlling (linearly) for X_i
- I would not think this is a general result...

Sampling variance of estimators

- ❑ Regression: Standard linear regression, “High-dimension” regression, “WLS linear regression estimator” : Use the heteroskedasticity-robust variance estimator (“, robust” in Stata)
- ❑ Matching/Blocking: More complicated. See work of Abadie, Imbens, and others. Cannot use bootstrap due to non-smoothness
- ❑ IPW: use bootstrap
- ❑ Note: The propensity score is unknown, and must be estimated --- so the standard errors in regressions that control for the p-score must adjust for this (“generated regressor bias”)

Papers cited and recommended reading

- ❑ Angrist, Joshua D. (1998): "Estimating the Labor Market Impact of Voluntary Military Service Using Social Security Data on Military Applicants," *Econometrica*, March 1998
- ❑ Dale, S. and A. Krueger (2002): "Estimating the Payoff to Attending a More Selective College: An Application of Selection on Observables and Unobservables," *Quarterly Journal of Economics*
- ❑
Recommend paper and textbook:
- ❑ Guido W. Imbens "Matching Methods in Practice: Three Examples," NBER Working Paper No. 19959 (March 2014)
- ❑ Angrist, J. and S. Pischke (2009): Mostly Harmless Econometrics: An Empiricist's Companion, Princeton University Press
- ❑ Gelman, A. and J. Hill (2006): Data Analysis Using Regression and Multilevel/Hierarchical Models (Chapters 9-10), Cambridge U Press

Application of “treatment ignorability”

Can Catch Shares Prevent Fisheries Collapse?

Christopher Costello,^{1*} Steven D. Gaines,² John Lynham^{3†}

Recent reports suggest that most of the world's commercial fisheries could collapse within decades. Although poor fisheries governance is often implicated, evaluation of solutions remains rare. Bioeconomic theory and case studies suggest that rights-based catch shares can provide individual incentives for sustainable harvest that is less prone to collapse. To test whether catch-share fishery reforms achieve these hypothetical benefits, we have compiled a global database of fisheries institutions and catch statistics in 11,135 fisheries from 1950 to 2003. Implementation of catch shares halts, and even reverses, the global trend toward widespread collapse. Institutional change has the potential for greatly altering the future of global fisheries.

Although the potentially harmful consequences of mismanaged fisheries were forecast over 50 years ago (1, 2), evidence of global declines has only been seen quite recently. Reports show increasing human impacts (3) and global collapses in large predatory fishes

(4) and other trophic levels (5) in all large marine ecosystems (LMEs) (6). It is now widely believed that these collapses are primarily the result of the mismanagement of fisheries.

One explanation for the collapse of fish stocks lies in economics: Perhaps it is economically optimal to capture fish stocks now and invest the large windfall revenues in alternative assets, rather than capturing a much smaller harvest on a regular basis. Although this remains a theoretical possibility for extremely slow-growing species

¹Bren School of Environmental Science and Management, 4410 Bren Hall, University of California, Santa Barbara, CA 93106, USA. ²Marine Science Institute, University of California, Santa Barbara, CA 93106, USA. ³Department of Economics, University of California, Santa Barbara, CA 93106, USA.

*To whom correspondence should be addressed. E-mail: costello@bren.ucsb.edu

†Present address: Department of Economics, University of Hawaii at Manoa, 2424 Maile Way, Honolulu, HI 96822, USA.

19 SEPTEMBER 2008 VOL 321 **SCIENCE** www.sciencemag.org

Background:

- “We tested the hypothetical causal link between the global assignment of catch shares and fisheries sustainability”
 - i.e., goal is to measure the ATE (?or ATT) of ITQ on fishery sustainability
 - They should be clearer about what “causal link” they are interested in measuring...

- “In our analysis, we expanded beyond the characteristics of the ecosystem to consider the characteristics of the regulating fisheries institutions, simultaneously controlling for the ecosystem, genus, and other covariates”

Setup:

- ❑ Treatment variable:
- ❑ “In total, we identified 121 fisheries managed using catch shares—defined as variations on individual transferable quotas (ITQs)—by 2003”
- ❑ Outcome variable:

CGL define a fishery as collapsed in year t if the harvest in year t is $<10\%$ of the maximum recorded harvest up to year t . Using this definition, $\sim 27\%$ of the world's fisheries were collapsed in 2003

 - Note: outcome is a binary variable
- ❑ Covariates:
- ❑ LME (~ 1 -60), genus (~ 1 -600), species (~ 1 -1200)
- ❑ Data from 1950-2003

CGL discussion of identification problem:

- “Demonstrating statistically a causal linkage between rights-based management and fisheries sustainability is complicated by three competing effects: ”
 - i.e. ITQ management not randomly assigned to fisheries
- First, the number of ITQ fisheries is growing, and new ITQ fisheries are drawn from a global pool with an ever-increasing fraction of collapsed fisheries
 - “Simultaneous causality”
- Second, the conversion of fisheries to ITQs may involve a biased selection
 - For example, ITQs may be implemented disproportionately in fisheries that are already less collapsed, possibly giving a misleading perception of benefits from rights-based management (Note: same as the point above, but in reverse)

Identification problem (ctd):

- Finally, there may be temporal benefits of an ITQ (for instance, the longer an ITQ is in place in a given fishery, the less likely that fishery is to collapse)
- All of these mechanisms would lead to differences between ITQ and non-ITQ fisheries, but only the last mechanism implies a benefit from the management change
- Note: CGL never formally states what their identifying assumption (is it treatment ignorability?)

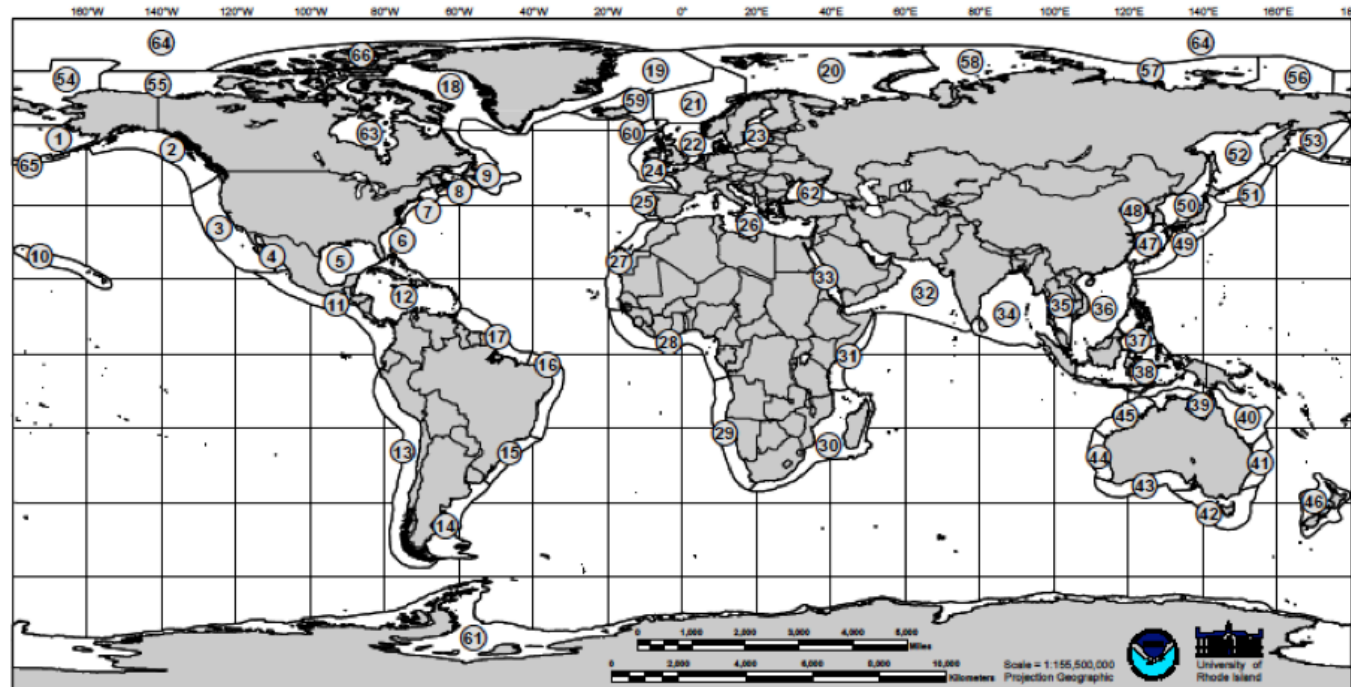
Overview of Findings:

- An initial regression of the data in Fig. 1 suggests that implementing an ITQ reduces the probability of collapse by 13.7 percentage points
- Because ITQs have been disproportionately implemented in a few global ecosystems such as Alaska, Iceland, New Zealand, and Australia, regional or taxonomic biases could generate misleading results
 - Note: difference between ATE and ATT important here, so is external validity?

Findings (ctd):

- ❑ To account for potential selection bias, we used a variety of estimation strategies:
- ❑ (i) We restricted the sample to only those ecosystems or taxa that have experienced ITQ management
 - Control for indicators in LME, genus, species
- ❑ (ii) We used propensity score methods to match ITQ fisheries to appropriate control fisheries
- ❑ (iii) We used fixed-effects estimation to identify the benefit of ITQs within each fishery
- ❑ The results are remarkably similar across all specifications and estimation techniques

Large Marine Ecosystems of the World



- | | | | | |
|-------------------------------------|--|-----------------------------------|-----------------------------------|--|
| 1. East Bering Sea | 15. South Brazil Shelf | 28. Guinea Current | 42. Southeast Australian Shelf | 55. Beaufort Sea |
| 2. Gulf of Alaska | 16. East Brazil Shelf | 29. Benguela Current | 43. Southwest Australian Shelf | 56. East Siberian Sea |
| 3. California Current | 17. North Brazil Shelf | 30. Agulhas Current | 44. West-Central Australian Shelf | 57. Laptev Sea |
| 4. Gulf of California | 18. Canadian Eastern Arctic - West Greenland | 31. Somali Coastal Current | 45. Northwest Australian Shelf | 58. Kara Sea |
| 5. Gulf of Mexico | 19. Greenland Sea | 32. Arabian Sea | 46. New Zealand Shelf | 59. Iceland Shelf and Sea |
| 6. Southeast U.S. Continental Shelf | 20. Barents Sea | 33. Red Sea | 47. East China Sea | 60. Faroe Plateau |
| 7. Northeast U.S. Continental Shelf | 21. Norwegian Sea | 34. Bay of Bengal | 48. Yellow Sea | 61. Antarctic |
| 8. Scotian Shelf | 22. North Sea | 35. Gulf of Thailand | 49. Kuroshio Current | 62. Black Sea |
| 9. Newfoundland-Labrador Shelf | 23. Baltic Sea | 36. South China Sea | 50. Sea of Japan/East Sea | 63. Hudson Bay Complex |
| 10. Insular Pacific-Hawaiian | 24. Celtic-Biscay Shelf | 37. Sulu-Celebes Sea | 51. Oyashio Current | 64. Central Arctic Ocean |
| 11. Pacific Central-American | 25. Iberian Coastal | 38. Indonesian Sea | 52. Sea of Okhotsk | 65. Aleutian Islands |
| 12. Caribbean Sea | 26. Mediterranean | 39. North Australian Shelf | 53. West Bering Sea | 66. Canadian High Arctic - North Greenland |
| 13. Humboldt Current | 27. Canary Current | 40. Northeast Australian Shelf | 54. Northern Bering-Chukchi Seas | |
| 14. Patagonian Shelf | | 41. East-Central Australian Shelf | | |

Wikipedia: The system of LMEs has been developed by the US [National Oceanic and Atmospheric Administration](#) (NOAA) to identify areas of the oceans for conservation purposes. The objective is to use the LME concept as a tool for enabling [ecosystem-based management](#) to provide a collaborative approach to management of resources within ecologically-bounded transnational areas

Applying tools (“identification under treatment ignorability”) to CGL (2008) data:

- Outline:
- Overlap in covariates?
- I ignore exact matching methods due to large number of cells (~ 42,000,000!)
- Linear regression approaches
- Propensity score methods
- Disclaimer: This is not my area of expertise ... Results here are only for illustration purposes
- To ease calculations, I am only using the data from 2003 (the last year of data in the sample. N=7784). I use OLS instead of logit for the outcome (Pr collapse) model

Summary statistics

```
. summ collapse DAPever LME genus species;
```

Variable	Obs	Mean	Std. Dev.	Min	Max
collapse	7784	.2687564	.4433415	0	1
DAPever	7784	.0149024	.12117	0	1
DAPimp	7784	.0149024	.12117	0	1
LME	7784	33.55434	18.59308	1	64
genus	7784	372.0847	198.3625	1	687
species	7784	628.906	348.2992	1	1179

```
. normdiff LME genus species, over(DAPever) tstat;
```

	Mean:	Mean:	Difference:	Difference:
	DAPever==0	DAPever==1	Normalized	t-stat
LME	33.473787	38.87931	.24101923	4.6076114
genus	371.8392	388.31034	.06219298	1.0034613
species	628.48344	656.83621	.0607387	.97527797
N	7668	116	.	.

Overlap on LME
not great

Simple linear regression:

- Basic “difference” regression:

$$Y_i = \beta_0 + \beta_1 T_i + u_i$$

```
. xi: regress collapse DAPever, robust;
```

Linear regression

```
Number of obs =      7784
F(   1,   7782) =      20.11
Prob > F        =      0.0000
R-squared       =      0.0015
Root MSE       =      .44304
```

		Robust				
collapse		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
-----+-----						
DAPever		-.1415556	.0315691	-4.48	0.000	-.2034395 -.0796717
_cons		.2708659	.0050757	53.37	0.000	.2609162 .2808157

Linear regressions (adding covariates):

- Variants of model:

$$Y_i = \beta_0 + \beta_1 T_i + X_i' \gamma + u_i$$

The command `i.varname` in Stata asks Stata to create an include indicator variables for all values of LME

```
> quiet xi: regress collapse DAPever i.LME, robust;
```

```
. lincom DAPever;
```

```
( 1)  DAPever = 0
```

collapse		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
-----+-----						
(1)		-.1014672	.0396549	-2.56	0.011	-.1792016 -.0237327

- Note: I am only reporting the coefficient on the treatment variable DAPever (fishery ever in an ITQ) to save on space...


```
. quiet xi: regress collapse DAPever i.LME i.genus, robust;
```

```
. lincom DAPever;
```

```
( 1)  DAPever = 0
```

```
-----  
collapse |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]  
-----+-----  
      (1) |   -.0950564   .0424562    -2.24   0.025    - .1782833    - .0118295  
-----
```

```
. quiet xi: regress collapse DAPever i.LME i.genus i.species, robust;
```

```
. lincom DAPever;
```

```
( 1)  DAPever = 0
```

```
-----  
collapse |      Coef.   Std. Err.      t    P>|t|     [95% Conf. Interval]  
-----+-----  
      (1) |   -.110643   .0426878    -2.59   0.010    - .1943248    - .0269612  
-----
```

- ❑ Overall, this method suggest ITQs reduced probability of collapse by about 10 percentage points

Propensity score based methods (CGL):

- “To estimate the propensity scores we estimate the probability that a fishery will be in an ITQ in a given year using four different specifications:
- (i) a model with a dummy variable for every LME;
- (ii) a model with a dummy variable for every genus;
- (iii) a model with a dummy variable for every species;
- (iv) a model with a dummy variable for every LME, genus and species. We use a logit estimator to estimate the four models for each year in the sample”

Findings: Basic Propensity Score Model

- logit DAPever LME genus species, robust;
 - Control linearly for LME, genus and species. A simple propensity score equation specification (and you will see it seems to work well)
 - I choose this because logit DAPever i.LME did not converge...

Logistic regression	Number of obs	=	7784
	Wald chi2(3)	=	25.35
	Prob > chi2	=	0.0000
Log pseudolikelihood = -597.59669	Pseudo R2	=	0.0091

		Robust					
DA	Pever	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	

	LME	.0159994	.0032516	4.92	0.000	.0096264	.0223724
	genus	.0106171	.0160227	0.66	0.508	-.0207868	.042021
	species	-.0058063	.0091617	-0.63	0.526	-.0237629	.0121504
	_cons	-5.074471	.305704	-16.60	0.000	-5.673639	-4.475302

```
. summ pscore if DAPever==1, d;
```

Pr(DAPever)

	Percentiles	Smallest		
1%	.0100646	.0090331		
5%	.0117896	.0100646		
10%	.0123103	.0104572	Obs	116
25%	.0138282	.01145	Sum of Wgt.	116
50%	.0153624		Mean	.0159223
		Largest	Std. Dev.	.0032067
75%	.0176951	.0224436		
90%	.0208636	.0236199	Variance	.0000103
95%	.0213781	.0237311	Skewness	.6155083
99%	.0237311	.0245315	Kurtosis	2.804617

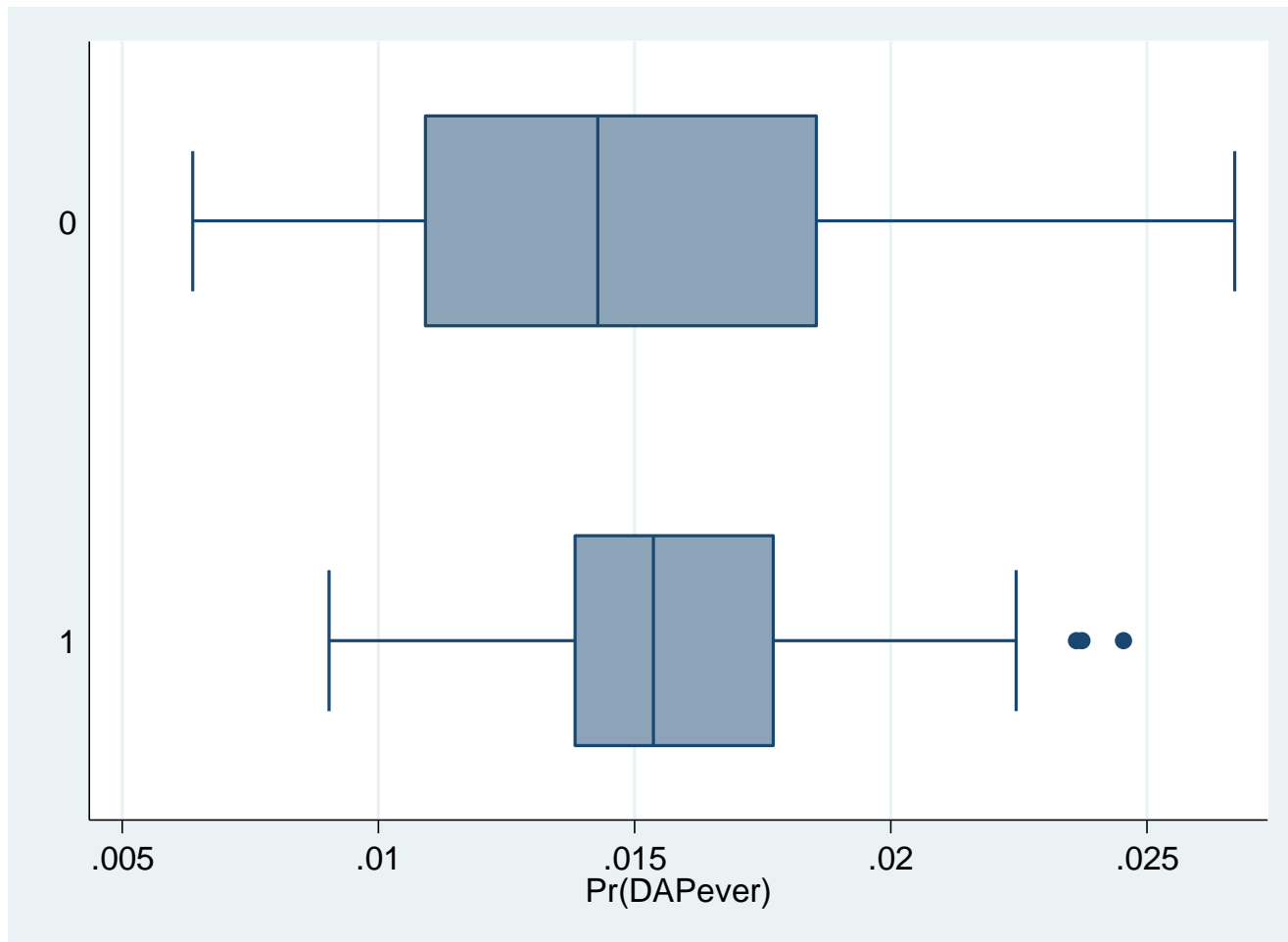
```
. summ pscore if DAPever==0, d;
```

Pr(DAPever)

	Percentiles	Smallest		
1%	.007523	.0063632		
5%	.0087201	.0063758		
10%	.0093896	.0064381	Obs	7668
25%	.0109188	.0064412	Sum of Wgt.	7668
50%	.0142727		Mean	.0148869
		Largest	Std. Dev.	.0045652
75%	.0185458	.0265571		
90%	.0214722	.0265933	Variance	.0000208
95%	.022787	.0267009	Skewness	.3507482
99%	.0244839	.0267076	Kurtosis	2.053998

Findings: Basic Propensity Score Model

Box-plot of estimated propensity score, overlap seems good



Findings: Basic Propensity Score Model

WLS regression, with p-score weights

```
. gen pscore_wgt=(DAPever/pscore) + ((1-DAPever)/(1-pscore));
```

```
. xi: regress collapse DAPever [aw=pscore_wgt], robust;
```

```
(sum of wgt is 1.5356e+04)
```

Linear regression

Number of obs = 7784

F(1, 7782) = 22.00

Prob > F = 0.0000

R-squared = 0.0337

Root MSE = .39225

		Robust				
collapse		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
-----+-----						
DAPever		-.1464205	.0312141	-4.69	0.000	-.2076084 -.0852325
_cons		.2708324	.0050754	53.36	0.000	.2608834 .2807815

Findings: CGL Propensity Score Model (iv)

- quiet xi: logit DAPever i.LME i.genus i.species, robust;
- Control for indicators in LME, genus and species. Many empty cells
- In my application I see this model creating some problems with lack of overlap
- The results that will come highlight the danger of applying a research method without completely understanding the study context and the technical aspect of the method

Stata output (...)

Note: 42 failures and 6 successes completely determined.

```
. predict pscore;  
(option pr assumed; Pr(DAPever))  
(7560 missing values generated)
```

This occurs when some combination of covariates are only associated with one outcome (either y always 1 or always 0 for some Xs...)
Recall previous map...

```
. summ pscore if DAPever==1, d;
```

Pr(DAPever)

	Percentiles	Smallest		
1%	.0172354	.0172354		
5%	.1373617	.0172356		
10%	.1649775	.0666717	Obs	79
25%	.8048311	.1373617	Sum of Wgt.	79
50%	.8204182		Mean	.7765604
		Largest	Std. Dev.	.258929
75%	.9333286	1		
90%	.9999998	1	Variance	.0670442
95%	1	1	Skewness	-1.821807
99%	1	1	Kurtosis	5.278382

```
. summ pscore if DAPever==0, d;
```

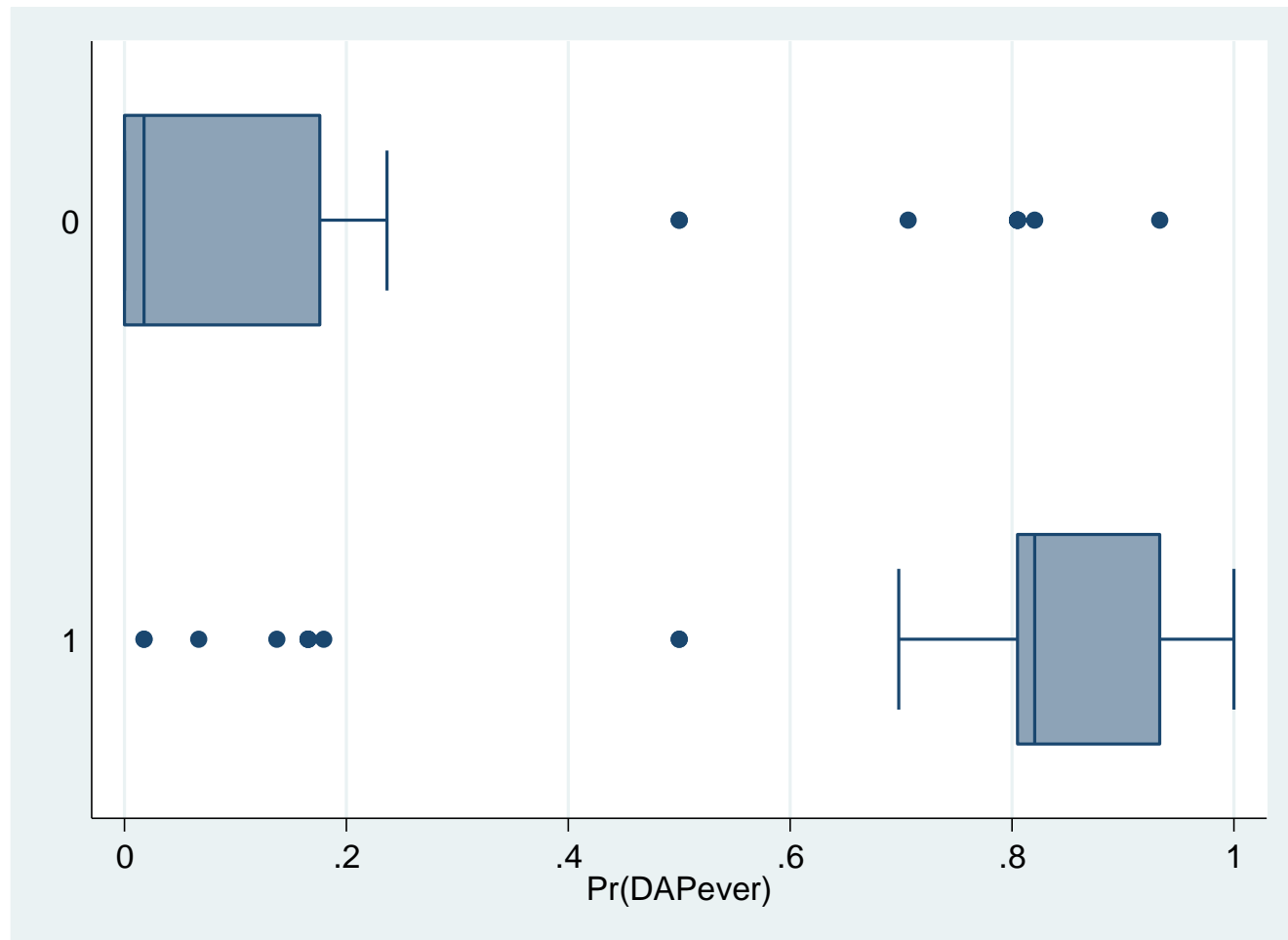
Pr(DAPever)

	Percentiles	Smallest		
1%	8.43e-29	8.43e-29		
5%	5.99e-23	8.43e-29		
10%	6.63e-23	9.33e-29	Obs	145
25%	1.92e-09	9.34e-29	Sum of Wgt.	145
50%	.0172362		Mean	.1217285
		Largest	Std. Dev.	.2002589
75%	.1759221	.8048463		
90%	.1795634	.8048486	Variance	.0401036
95%	.8048333	.8204182	Skewness	2.591087
99%	.8204182	.9333286	Kurtosis	9.353891

Note: this lack of overlap would make an estimator like the blocking estimator very unreliable

Lack of overlap in p-score model (iv)

Box-plot of estimated propensity score, overlap seems good



WLS estimator in p-score model (iv)

WLS regression, with p-score weights

```
. gen pscore_wgt=(DAPEver/pscore) + ((1-DAPEver)/(1-pscore));
```

(7566 missing values generated)

```
. xi: regress collapse DAPEver [aw=pscore_wgt], robust;
```

```
(sum of wgt is 4.4888e+02)
```

Linear regression

Number of obs = 218

F(1, 216) = 4.53

Prob > F = 0.0344

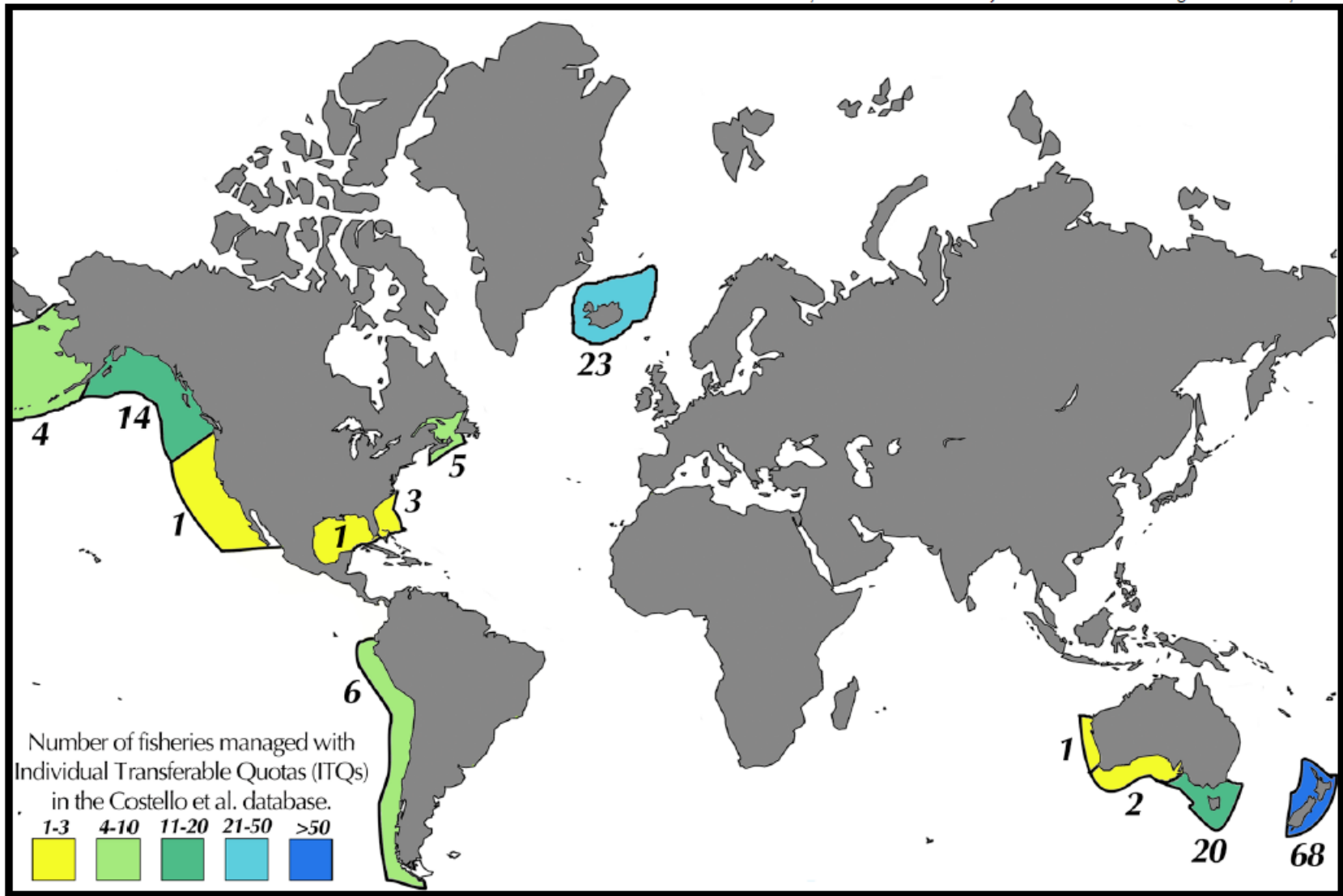
R-squared = 0.0287

Root MSE = .33124

		Robust				
collapse		Coef.	Std. Err.	t	P> t	[95% Conf. Interval]
-----+-----						
DAPEver		-.1139051	.0534992	-2.13	0.034	-.2193525 -.0084577
_cons		.1905855	.034182	5.58	0.000	.1232124 .2579585

Extra Slides

Fisheries are as defined by the Sea Around Us Project 2007 database on large marine ecosystems.



Globally, there are 148 fisheries that are managed under variations on a management scheme called Individual Transferable Quotas (ITQs). ITQs work by allocating a dedicated percentage of a fishery's total allowable catch to individual fishermen, communities, or cooperatives. The value of shares increases when a fishery is well-managed and the fish population is abundant. ITQs are common in New Zealand, Australia, and Iceland, where this form of 'catch shares' dates back to the 1980s. Many fisheries in the Gulf of Alaska transitioned to ITQs in the 1990s with successful results. [Please note: Costello et al. only analyzed the 121 fisheries that transitioned before 2003]