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Protocol: Evaluating the Effect of ACA Medicaid Expansion on 2015-2018 Mortality Through Matching and Weighting

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Abstract

Starting in 2014, states received the option to expand Medicaid through the Affordable Care Act (ACA). Many states chose to expand Medicaid whereas others opted out. In this protocol, we describe a study to examine the impact of Medicaid expansion on mortality in the continental United States from 2015-2018. We adopt the matching structure of Mann et al. (2021) to estimate causal effects in this study. This protocol outlines both a standard method of analyzing this policy choice along with a method employing a novel weighting scheme to examine the effect of Medicaid expansion on those who stand to benefit most from policy implementation: the individuals newly eligible for Medicaid.

Keywords: Affordable Care Act, weighting, full matching, Medicaid expansion.

1. Introduction

In this article, we outline a pre-analysis plan for a study examining the effect of Medicaid expansion through the Affordable Care Act on 2015-2018 mortality. While initially required by law, the Supreme Court deemed this provision unconstitutional, instead allowing Medicaid expansion to occur at each state's discretion. Twenty-five states intially chose to expand Medicaid in 2014 with many more states adopting the expansion over the following years. As the signature piece of legislation from the Obama Era and the most significant healthcare reform in decades, there is a growing body of literature examining the effect of Medicaid expansion on insurance coverage and mortality (Black et al., 2019; Borgschulte & Vogler, 2020; Miller et al., 2019; Swaminathan et al., 2018). Researchers have arrived at a consensus that Medicaid expansion broadly increased insurance coverage nationwide (Kaestner et al., 2017; Garrett & Gangopadhyaya, 2016; Miller et al., 2019) but much debate remains as to the extent of the effect of the policy on mortality.

For example, Black et al. (2019) found no effect of Medicaid expansion on mortality and conducted power analyses suggesting that studies examining this at the county level tend to be underpowered. On the other hand, Borgschulte & Vogler (2020) found a mortality benefit to expansion from 2014-2017 through an analysis centered around propensity score pair matching. Studies analyzing particular subgroups found benefits to mortality as well. For example, Miller et al. (2019) examined older adults newly eligible for Medicaid as a result of the ACA and discovered decreased mortality and Swaminathan et al. (2018) found reductions in mortality among individuals with end-stage renal disease.

Nonetheless, one gap in the literature is examining the overall effect of Medicaid expansion among individuals who stand to benefit most from policy implementation: those individuals who are newly eligible for Medicaid. In states which expand, all adults with incomes beneath 138% of the federal poverty limit are eligible for Medicaid whereas in states that fail to adopt the expansion, eligibility depends on multiple factors —age, assets, disability status, income, etc. A wide swath of the American public stood to benefit, as no state with the exception of Massachusetts universally offered Medicaid to adults with incomes above the federal poverty limit prior to Medicaid expansion. Consequently, we look to put greater emphasis on this group of adults with incomes beneath 138% of the federal poverty limit who were previously ineligible for Medicaid in our outcome analysis.

In this study, we intend to estimate the effect of ACA Medicaid expansion on mortality for adults aged 20-64 across the continental United States from 2015-2018. This is similar to the work of Borgschulte & Vogler (2020) who evaluated aggregate effects of Medicaid expansion for adults from 2014-2017. Outcome analysis begins in 2015 rather than 2014, the first year of expansion, because we believe the year in which an intervention commences should not be regarded as an outcome year, similar to how Sommers et al. (2014) handle the outcome when examining the effects of the 2006 healthcare reform in Massachusetts. We then intend to conduct the same analysis but with application of a novel weighting scheme constructed around the proportion of adults newly eligible for Medicaid. This is similar to the work of Miller et al. (2019) but deviates in two substantial manners. First, we examine all working-age adults, not merely adults aged 55-64. Then, more importantly, we intend to weight for newly eligible individuals but not solely conduct our analysis on this subgroup. Instead, we look at the entire population, attaching greater emphasis to areas where we expect Medicaid expansion to have a larger effect. We follow the matching structure of Mann et al. (2021) who in turn followed the methods of Sommers et al. (2014), Borgschulte & Vogler (2020), and Black et al. (2019) for matching counties.

We organize this article as follows: We begin by describing data and variables used in the study, including how treatment status is assigned across years. We then describe matching methodology along with diagnostics of the resulting matches. We end by discussing the methodology we intend to use to estimate the effect of Medicaid expansion on mortality.

2. Baseline Data

There is disagreement in the literature about which states should be included in studies of Medicaid expansion. For example, Borgschulte & Vogler (2020) excludes states that expand Medicaid after June of 2014 whereas Miller et al. (2019) allows states to enter the treatment group in later years[1]. For matching purposes, we adopt the strategy of Mann et al. (2021) that melds these two ideas. More specifically, we match based on treatment status in June, 2014 but rather than entirely discarding states that expand after that date, we place them in the control with states that have yet to expand. To identify when states expanded Medicaid, we use the Kaiser Family Foundation (KFF) report from August 4, 2020. For the purposes of this study, we again adopt the strategy of Borgschulte & Vogler (2020) and include Wisconsin in the treatment group, despite the fact they did not expand Medicaid through the ACA; instead they expanded coverage to all adults with incomes below 100% of the federal poverty limit, providing greater access to Medicaid than other states that did not expand. We entirely exclude Alaska and Hawaii because this analysis looks at the effect of Medicaid expansion on the continental United States.

Unlike Borgschulte & Vogler (2020), we do not exclude states that expand after June, 2014. Instead, they enter the treatment group during the year they expand. This allows us to incorporate five states that otherwise would have been discarded. Note that since matching occurs based on 2014 treatment status, there will be matches in later years where each county in the matched set belongs to the treatment group.

We obtain mortality counts through the National Center for Health Statistics (NCHS) restricted use, detailed morality data, housed at the Center for Disease Control and Prevention (CDC). For baseline mortality in matching, we use all-cause mortality and healthcare amenable mortality, both for adults aged 20-64 aggregated across 2009-2013. We aggregate these mortality counts for all crosstabs of race (and Hispanic origin), gender, and age using population values from Census Bureau data. Healthcare amenable deaths are defined in the manner of Sommers et al. (2014) and identified through ICD-10 codes.

We then merge these county-level crosstabs of mortality counts with standard demographic and health covariates for each county obtained through the 2019 Area Health Resources File (AHRF) and the Institute for Health Metrics and Evaluation (IHME) respectively. In addition to these factors, we incorporate political leaning of a county through the percentage of votes obtained by Governor Mitt Romney in the 2012 presidential election as calculated by the CQ Press Voting and Elections Collection. The proportion of multigenerational households in a county is included as well and obtained through the American Community Survey (ACS). For each pre-treatment covariate used in matching, 2013 data is used when available. When 2013 data is unavailable, we use data from the most recent available year.

3. Matching

This section describes the method by which we match counties in states that expanded Medicaid through the ACA by June, 2014 with counties that had not expanded at that point. The matching structure described here follows the same approach outlined in Mann et al. (2021) where it is discussed in greater detail. Matching for this analysis uses three techniques: optimal full matching with propensity scores, propensity score calipers, and penalties on pairings that are not well-matched. The combination of these three methods allows us to match as many counties as possible while also maintaining covariate balance.

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[1] It should be noted that Miller et al. (2019) does not employ matching in their analysis

We define "well-matched" to be a matched set where the Mahalanobis distance between members is below a specific threshold where the threshold is determined through Mahalanobis distances within matched sets of adjacent counties (Rosenbaum, 2010).

3.1 Propensity Score Calculation

Propensity scores are widely used in order to create matched sets (Stuart & Green, 2008; Caliendo & Kopeinig, 2008). The full list of covariates used to calculate the propensity score can be found in Table 1.

Variable	Source	Years
Population	CDC	2009-2013
Age distribution	CDC	2009-2013
All mortality crosstabs	CDC	2009-2013
Population density	AHRF	2010
% Urban	AHRF	2010
Veteran Population	AHRF	2013
Median household income	AHRF	2013
% persons in poverty	AHRF	2013
Food stamps / SNAP	AHRF	2013
18-64 below 138% of FPL	AHRF	2010
20-64 Medicaid eligible	AHRF	2010
% 18-64 without health insurance	AHRF	2013
Unemployment Rate (16+)	AHRF	2013
PM2.5	AHRF	2013
Total Smoking	IHME	2012
Heavy Drinking prevalence	IHME	2012
Diabetes prevalence	IHME	2012
Hypertension prevalence	IHME	2009
Obesity prevalence	IHME	2011
Sufficient physical activity	IHME	2011
% Voting Republican	CQ Press	2012
% Multigenerational household	ACS	2009-2013

Table 1: Covariates used in modeling and matching and their sources as well as years available. When ranges of years are given, the variable used is the average across those years.

We incorporate covariates believed to be correlated with both general mortality and a state's decision to adopt Medicaid expansions to ensure there is balance between treatment and control groups. We fit a logistic regression of Medicaid expansion status in June, 2014 on these covariates, and then refit the model with outlier counties from the first regression excluded. Predictions from this refitted model are used as our final propensity score in matching.

3.2 Full Matching

We match counties using a full matching procedure (Hansen, 2004; Rosenbaum, 1991) which differs from pair matching in that it allows for matched sets with unequal numbers of treatment or control counties rather than one of each[2]. This procedure is implemented in `R` using the `optmatch` package (Hansen & Klopfer, 2006b).

Counties are matched on the refitted propensity score within calipers of width one-quarter of the weighted pooled standard deviation (Rosenbaum & Rubin, 1985) with further penalties added for pairings that are not well-matched. 106 counties are trimmed due to this caliper and 6 additional counties are trimmed due to outlying baseline mortalities, which leaves us with an effective sample size of 828.1. The weighted average values for each variable along with the standardized differences before and after matching can be found in Table 2. The overall test of balance indicates reasonable balance between treatment and control groups. While some covariates do possess standardized differences outside the desired range, we will further control for this imperfect balance in outcome analysis.

Rather than readjust matches each year based on states adopting Medicaid expansion between July, 2014 and 2018, we keep these same matches because the matching structure remains well balanced when using treatment and control groups at the end of this period (see Mann et al. (2021) for standardized differences in 2020).

	No Adjustment			After Matching			Dispersion	
	Control	Treat.	Dif.	Control	Treat.	Dif.	Overall	Adjacent
% White	80.0	80.8	0.8	84.2	80.8	-3.4	14.1	8.3
% Black	15.9	10.5	-5.4	10.3	10.8	0.5	12.4	6.4
% Hispanic	12.9	15.9	2.9	8.5	15.3	6.8	15.3	5.2
% Male	48.4	48.5	0.2	48.3	48.5	0.2	1.6	2.4
% 20-34	28.2	28.1	-0.1	26.1	28.1	2.0	5.4	5.1
% 35-44	17.9	18.0	0.0	17.4	17.9	0.5	2.2	1.7
% 45-54	19.3	19.6	0.3	19.9	19.6	-0.3	1.8	1.5
% 55-64	16.3	16.4	0.1	17.1	16.4	-0.7	1.9	1.9
All Mortality	373.6	314.5	-59.1	354.8	316.5	-38.3	101.5	90.0
20-34 Mortality	111.5	91.0	-20.5	107.3	91.5	-15.8	35.3	52.1
35-44 Mortality	194.3	159.9	-34.5	180.5	161.0	-19.5	61.9	80.7
45-54 Mortality	452.5	377.4	-75.1	410.0	379.7	-30.2	122.7	119.5
55-64 Mortality	923.2	791.7	-131.5	842.9	795.4	-47.5	204.4	181.5
White Male Mortality	398.8	345.3	-53.5	373.7	346.1	-27.6	95.4	86.1
White Female Mortality	232.0	198.3	-33.7	218.2	198.7	-19.5	59.8	57.8
Black Male Mortality	517.4	467.0	-50.4	472.6	469.6	-2.9	224.8	550.8
Black Female Mortality	322.2	296.0	-26.2	316.8	297.3	-19.5	229.5	740.4
Other Race Male Mortality	182.2	194.0	11.9	216.7	194.0	-22.8	186.8	562.7
Other Race Female Mortality	111.7	115.6	3.9	108.8	115.2	6.3	114.5	294.2
Healcare Amenable (non-flu) Mortality	195.6	165.0	-30.6	176.9	166.2	-10.7	49.3	49.1
Opioid Mortality	21.8	20.7	-1.1	24.7	20.8	-3.9	10.7	20.1
Flu Mortality	4.7	3.9	-0.8	4.4	3.9	-0.4	3.2	10.3
Population Density	926.6	3267.6	2341.0	1184.3	3430.6	2246.4	6867.4	1085.2
% Urban	76.4	85.2	8.8	77.3	85.1	7.7	23.9	25.6
% Veteran	7.7	6.2	-1.5	7.6	6.2	-1.3	2.5	1.7
Median Income	50579.9	58156.3	7576.4	57560.7	57676.6	115.9	13998.3	7251.3
% Poverty	16.7	15.3	-1.4	14.1	15.3	1.1	5.4	4.3
% SNAP	15.7	14.1	-1.6	13.8	14.2	0.3	6.5	5.0
% No Health Insurance	23.1	18.3	-4.9	17.1	18.4	1.2	6.7	3.3
Unemployment Rate	6.9	7.9	1.0	7.2	7.8	0.7	2.0	1.5
PM2.5	0.1	0.1	-0.0	0.1	0.1	-0.0	1.7	0.2

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[2] We still prioritize matched pairs by including a stability increment to matched distances when constructing matched sets (Hansen & Klopfer, 2006a).

Smoking	21.3	19.0	-2.2	21.4	19.2	-2.2	4.3	2.4
Heavy Drinking	7.6	8.7	1.0	8.0	8.6	0.7	1.8	1.3
Diabetes	15.0	13.8	-1.2	13.7	13.8	0.2	2.1	1.3
Male Hypertension	37.5	35.8	-1.7	36.3	35.9	-0.5	3.2	1.9
Female Hypertension	40.0	38.3	-1.8	38.6	38.4	-0.2	3.4	2.0
Male Obesity	35.4	32.5	-2.9	34.5	32.6	-1.9	4.3	2.2
Female Obesity	37.8	34.6	-3.2	36.0	34.7	-1.3	5.1	3.3
Male Physical Activity	54.2	57.9	3.7	56.3	57.8	1.5	5.2	3.7
Female Physical Activity	49.8	55.0	5.2	52.3	54.7	2.3	6.0	3.4
% Republican	54.3	42.1	-12.2	48.6	42.3	-6.2	14.8	9.1
% Multigenerational Households	0.0	0.0	-0.0	0.0	0.0	-0.0	0.0	0.1
Population	5.2	5.5	0.4	5.2	5.5	0.3	0.6	0.4

Table 2: Standardized differences between control and treatment (ACA Medicaid expansion by June 2014) counties before and after matching. The test of overall balance results in a p-value of .55 which is insignificant, indicating good balance.

4. Outcome Analysis

In this section, we outline two separate estimation strategies we plan to implement: (I) The effect of Medicaid expansion on mortality from 2015-2018 (hereafter referred to as "standard analysis"); and (II) The effect of Medicaid expansion on mortality from 2015-2018, weighted by the proportion of newly eligible residents (hereafter referred to as the "weighted analysis"). Note that since the weighted analysis employs a novel weighting scheme, we include the standard analysis primarily as a check on our results.

4.1 Mortality Data and the Newly Eligible

For both the standard and the weighted analysis, we use the same restricted use mortality files from the NCHS. This provides us with access to mortality counts by race, ethnicity, gender, and age. For each of these analyses, we consider two outcomes: all cause mortality and healthcare amenable mortality.

More attention must be paid to calculating the proportion of newly eligible. Using the 2018 AHRF, which in turn uses the Census Small Area Health Insurance Estimates (SAHIE), we estimate the number of adults in each county aged 20-64 who are expected to be newly eligible for Medicaid after expansion. To achieve this, we use the 2010 estimates of (1) the number of adults aged 18-64 with incomes beneath 138% of the federal poverty limit and (2) the number of adults aged 20-64 who were eligible for Medicaid. The second allows us to account for varying eligibility requirements by state prior to the ACA. The difference between these two numbers then estimates the total number of adults in a given county who are newly eligible for Medicaid under the expansion, which in turn allows us to estimate the proportion of adults newly eligible in any given county.

Multiple points must be noted. First, this analysis examines mortality for adults aged 20-64, corresponding with (2), but the proportion of newly eligible must be calculated partially using adults aged 18-64 due to lack of data specificity. Next, we are forced to use 2010 data estimates rather than more recent estimates because states report more recent years of Medicaid eligible adults in different fashions; 2010 data on the other hand, was uniform nationwide. Finally, Wisconsin only expanded Medicaid up to 100% of the federal poverty limit. Nonetheless, we keep them in the treatment group for consistency with Borgschulte & Vogler (2020) and Mann et al. (2021) and calculate their newly eligible rate using 2010 estimates of the number of adults aged 18-64 with incomes beneath 100% of the federal poverty limit rather than beneath 138% of the federal poverty limit as described in (1).

4.2 Notation

We have K matched sets with $n_k \geq 2$ counties in each matched set and $\sum_{k=1}^{K} n_k = N$ total counties. We define $Z_{ki(t)} = (Z_{ki2015}, ...Z_{kit})'$, $t = 2015, \ldots, 2018$; to be the binary treatment assignments for county i in matched set k across the four years of our study. In other words, this vector denotes whether the given county belonged to a state that had expanded Medicaid by year t for each year of interest. Under the potential outcomes framework of Neyman (1923), Rubin (1974) and Holland (1986), county $i = 1, \ldots, n_k$ within each matched set $k \in \{1, \ldots, K\}$ has 2^{t-2014} potential outcomes in each of years $t = 2015, \ldots, 2018$: $y_{kit}^{(Z_{(t)}=\mathbf{0})}$,$\ldots$, $y_{kit}^{(Z_{(t)}=\mathbf{1})}$. We can then write the observed outcome in year t as $Y_{kit} = Z_{ki(t)} y_{kit}^{(Z_{(t)}=1)} + (1 - Z_{ki(t)}) y_{kit}^{(Z_{(t)}=0)}$.

4.3 Standard Analysis Estimation Procedure

To estimate the effect of Medicaid expansion on both all cause and healthcare amenable mortality from 2015-2018, we fit the following generalized linear mixed effects model for the negative binomial family with random effects for the matched sets:

$$Y_{kit} = \theta Z_{kit} + X_{kit}\beta + \gamma_k + \epsilon_{kit},$$

$$\gamma_k = \alpha_0 + \omega_k,$$

where X_{kit} denotes the matrix of fixed effects for which we adjust[3]. We then calculate a cluster-robust standard error with clusters at the state level using the bias-reduced linearization adjustment of Bell & McCaffrey (2002) that was further adapted by Pustejovsky & Tipton (2016).

4.4 Weighted Analysis Estimation Procedure

The weighted analysis procedure largely follows the same steps as the standard analysis with a few notable changes. First, each county is assigned to a bracket b_j with $j \in \{1, \ldots, 6\}$ based on the proportion of newly eligible adults in that county in 2010, where b_1 consists of counties with the lowest proportion of newly eligible adults and b_6 consists of counties with the highest proportion of newly eligible adults. Within each bracket, we calculate the county-size weighted average of the proportion of newly eligible $\bar{b}_j$.

We then fit the following generalized linear mixed effects model for the negative binomial family with random effects for the matched sets and the treatment interacted by the bracket

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[3] This includes widely used demographic covariates like year, gender, race, ethnicity, age, socioeconomic status, county population, etc.

of the county[4]:

$$Y_{kit} = Z_{kit} b_{ki} \vec{\theta} + Z_{kit} \text{Year}_t + X_{kit}\beta + \gamma_k + \epsilon_{kit}, \tag{1}$$

$$\gamma_k = \alpha_0 + \omega_k.$$

This negative binomial regression provides six treatment effect estimates, $\hat{\theta}_b$ with $b \in \{1, \ldots, 6\}$, one for each of the six brackets. The question is then how best to aggregate them into a single overall treatment effect estimate. In other words, what linear combination of parameters will provide the greatest opportunity to reject the null hypothesis of no effect?

We choose to aggregate them by weighting each effect estimate by a term proportional to $\bar{b}_j$, the average proportion of newly eligible adults in that bracket (described in greater detail in Section 4.4.1). We then calculate a cluster-robust standard error for the overall aggregated effect estimate following the same method as in the standard procedure.

4.4.1 Hypothesis Test Inversion to Test Dosage Response

We invert hypothesis tests to assess the belief that the effect of Medicaid expansion is proportional to the dose (i.e. the proportion of newly eligible) versus a null hypothesis of no effect (Rosenbaum, 2010). In other words, we use the duality between hypothesis tests and confidence intervals to test a family of hypotheses through construction of confidence region $A(\theta)$ by testing each hypothesis $H_0 : \theta = \theta_0$ for all $\theta_0 \in \Theta$ and retaining values not rejected by the test at level α. Our confidence region $A(\theta)$ is then the smallest region containing the entire set of values across these tests not rejected at level α.

As we test these hypotheses of no reduction in mortality as a result of Medicaid expansion, we do so in a manner such that we maximize power against the alternative that there is a benefit, but that benefit is propotional to the rate of newly eligible adults in a county $\bar{b}$. This maximizes power against alternative hypotheses centered around statistics of the form $\hat{\theta} = \sum_b \hat{\omega}_b \hat{\theta}_b$. In this representation, $\hat{\theta}$ is the linear combination of individual bracket effect estimates aggregated by weights $\hat{\omega}$, where $\hat{\omega} \propto \bar{b}\hat{\Sigma}$. Here, we let $\hat{\Sigma}$ denote the empirical covariance of estimated coefficients which calibrates the relative precision of the estimates $\hat{\theta}_b$.

By estimating the parameter in this fashion, i.e. by aggregating individual treatment effect estimates, we allow the effect of Medicaid expansion on mortality to take a form that is monotonically increasing with dosage, but not necessarily increasing in a constant or linear fashion. This provides flexibility over other standard methods because it does not require researchers to prespecify how Medicaid expansion interacts with dosage. Instead, it merely requires an assumption that there is an interaction between the two.

4.4.2 Analysis of Secondary Outcomes

The effect of Medicaid expansion on mortality for each year of follow-up (2015-2018) are outcomes of secondary interest. We estimate these effects through the additional interaction terms in Equation 1. To account for multiplicity and ensure proper Type I error rates, we apply a max-t correction to these secondary outcomes (Hothorn et al., 2008). Note that

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[4] We additionally interact the treatment with the year for analysis of secondary outcomes. We further discuss this in Section 4.4.2.

we only control for multiplicity within a given mortality type, i.e. within columns in Table 3, and solely for outcomes designated as secondary. The all-cause mortality analysis will be conducted independently of healthcare amenable mortality analysis and no multiplicity adjustment is performed on primary outcomes.

Subgroup	**All Cause**	**Healthcare Amenable**
All	Primary	Primary
2015	Secondary	Secondary
2016	Secondary	Secondary
2017	Secondary	Secondary
2018	Secondary	Secondary

Table 3: Designation of primary or secondary outcome for mortality outcomes.

5. Discussion

There is a growing body of literature examining the effects of Medicaid expansion through the Affordable Care Act on mortality rates but studies are mixed as to its benefit. We look to contribute to this research by estimating the mortality benefit on 2015-2018 data through full matching with propensity scores and propensity score calipers. Unlike previous studies, we match on 2014 expansion status but do not exclude states that expand between 2015 and 2018, providing us with richer, nationwide data. We additionally apply a novel weighting scheme centered around those who stood to benefit most from policy implementation: the newly eligible. By attaching greater importance to counties with higher proportions of newly eligible adults, we expect to gain power against alternative hypotheses where there is a mortality benefit to Medicaid expansion, but that benefit does not accrue homogenously but rather accrues proportional to dosage.

Appendix A. Supplemental Tables

Condition(s)	ICD-10 Codes
Healthcare amenable	
Tuberculosis	A16-19, B90
Other infections	A35-A37, A40-41, A80, B05
Malignant neoplasm of colon and rectum	C18-C21
Malignant neoplasm of skin	C44
Malignant neoplasm of breast	C50
Malignant neoplasm of cervix or uterus	C53-C55
Malignant neoplasm of testis	C62
Hodgkins disease	C81
Leukemia	C91-C95
Disorders of thyroid gland	E00-E07
Diabetes Mellitus	E10-E14
Epilepsy	G40-G41
Chronic rheumatic heart diseases	I05-I09
Hypertensive diseases	I10-I13, I15
Ischemic heart diseases	I20-I25
Cerebrovascular diseases	I60-I69
All respiratory diseases	J00-J98
Gastric and duodenal ulcers	K25-K27
Diseases of appendix	K35-K38
Hernia	K40-K46
Diseases of gallbladder and biliary tract	K80-K83
Glomerular diseases	N00-N07
Renal failure	N17-N19
Pregnancy, childbirth and the puerperium	O00-O99
Misadventures to patients during surgical and medical care	Y60-Y69, Y83-Y84

Table 4: ICD-10 codes used in defining healthcare amenable mortality.

State	Date Implemented	Treatment Entered
Alabama	-	-
Alaska	9/1/2015	Excluded
Arizona	1/1/2014	2014
Arkansas	1/1/2014	2014
California	1/1/2014	2014
Colorado	1/1/2014	2014
Connecticut	1/1/2014	2014
Delaware	1/1/2014	2014
District of Columbia	1/1/2014	2014
Florida	-	-
Georgia	-	-
Hawaii	1/1/2014	Excluded
Idaho	1/1/2020	-
Illinois	1/1/2014	2014
Indiana	2/1/2015	2015
Iowa	1/1/2014	2014
Kansas	-	-
Kentucky	1/1/2014	2014
Louisiana	7/1/2016	2016
Maine	1/10/2019	-

Maryland	1/1/2014	2014
Massachusetts	1/1/2014	2014
Michigan	4/1/2014	2014
Minnesota	1/1/2014	2014
Mississippi	-	-
Missouri	-	-
Montana	1/1/2016	2016
Nebraska	-	-
Nevada	1/1/2014	2014
New Hampshire	8/15/2014	2014
New Jersey	1/1/2014	2014
New Mexico	1/1/2014	2014
New York	1/1/2014	2014
North Carolina	-	-
North Dakota	1/1/2014	2014
Ohio	1/1/2014	2014
Oklahoma		-
Oregon	1/1/2014	2014
Pennsylvania	1/1/2015	2015
Rhode Island	1/1/2014	2014
South Carolina	-	-
South Dakota	-	-
Tennessee	-	-
Texas	-	-
Utah	1/1/2020	-
Vermont	1/1/2014	2014
Virginia	1/1/2019	-
Washington	1/1/2014	2014
West Virginia	1/1/2014	2014
Wisconsin	-	2014
Wyoming	-	-

Table 5: Date of ACA Medicaid expansion implementation by state and year of entry into the treatment group.

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