Project Overview	
Original Project Title:	Use of IMV among Asian American compared to Whites
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Funding	R56AG063748
Data Usage Agreement	
Background	The objective of this study is to examine the use of IMV and NIMV between 200-2017

Data Sources	Variables	Link	Years
Hospital RAI and MedPAR	All	www.resdac.org	200-2017
Hospice files	All	www.resdac.org	2000-2017
Master Beneficiary Summary File	Date of Death, MA enrollment on	www.resdac.org	2000-2017

Timeline:

Project Overview	
Data Requested	November 2019
Data Completed	June 2020
Project Folder	"P:\ihicu\shared\CodeforRepository_JAMA2020\imv_nimv_1617-copy-revised.dta"
Unit of Analysis	Medicare decedents age 66 and older
Research Questions	The objective of this study to characterize the time trends in Asian American Compare to Whites in use of invasive mechanical ventilation in a hospitalization in the last 30 days of life.
Working Hypothesis	Our working hypothesis that IMV would differ by Asian Americans compared to whites
Study Retrieval Request	

Study Sample	Fee-for-service Medicare beneficiaries who had an hospitalization in the last 30 days of life. Sensitivity analysis among persons with Medicare Advantage from 2011 to 2017.
Inclusion Criteria	66 years and older, Fee-for-service Medicare beneficiaries who died between 2000-2017
Primary Independent Variable	Race based on Social Security reported data that is part of the Medicare Beneficiary File
Dependent Variables	IMV

Original Statistical Analysis:

Notes:
Stata code used for analyses of file created by programmer.

```
* set up variables / analytic files

* create outcome variables,  2000-2017 / mv_noninv & mv_inv: no data b/t 2000 and 2009
d mvnoninv_30 mvinv_30 mv_noninv mv_inv
tab hkyear mvnoninv_30, m
tab hkyear mvinv_30, m
tab mvnoninv_30 mvinv_30, m


* create a "vent" variable
gen vent = 0
replace vent = 1 if mvnoninv_30==1 & mvinv_30==0
replace vent = 2 if mvnoninv_30==1 & mvinv_30==1
replace vent = 3 if mvnoninv_30==0 & mvinv_30==1

label define ventstat 0 "No MV" 1 "NIMV" 2 "Both" 3 "IMV"
label values vent ventstat

gen imv_only =.
replace imv_only=1 if vent==3
replace imv_only=0 if vent==0

gen mv_both = .
replace mv_both = 1 if vent ==2
replace mv_both = 0 if vent ==0

gen nimv_only = .
```

```
replace nimv_only = 1 if vent ==1
replace nimv_only = 0 if vent ==0

tab nimv_only vent, m
tab imv_only vent, m
tab mv_both vent, m


* delete IDs with any hmo ==1
tab anyhmo
drop if anyhmo==1

* convert a string Provider Number variable to a numeric variable
des hiprovn
gen hospid= real(hiprovn)
encode hiprovn, gen(n_hiprovn)
count if missing(hospid)
count if missing(n_hiprovn)
/* check if there are CCNs representing critical access hospitals,
non-acute hospital etc (if hospid is missing) "gen-real command" changes provider ID involving
characters into missing */

brow hiprovn hospid n_hiprovn if hospid==.

* CCN including characters will be deleted later = critical access hospitals, non-acute..etc

tab hospital_30
* Make sure the dataset has a value of 1 for "hospital_30"


**********************************************************************************
**
* Create a flag variable for sample                                    *
* Exclusion criteria                                                   *
* (a) admitting diagnosis of cardiac arrest; (b) admitting dx of tracheostomy  *
* NO missing(hospid) & missing(hksex) & missing(hidiag0)               *
**********************************************************************************
**
*** check missing values for all the vars that will be included in regression models
count if missing(hidiag0)
count if missing(charlson)
count if missing(hksex)
count if missing(charlson) & !missing(hidiag0)

* identify cardiac arrest as primary dx
gen primary_cardiacarrest = 0
```

```
replace primary_cardiacarrest= 1 if hidiag0=="4275"
replace primary_cardiacarrest =1 if hidiag0=="I462" | hidiag0=="I468" | hidiag0=="I469"

* identify tracheostomy as primary dx
gen primary_trach = 0
replace primary_trach=1 if hidiag0=="V440"
replace primary_trach=1 if hidiag0=="V550"
replace primary_trach=1 if inrange(substr(hidiag0, 1, 5), "51900", "51909")
replace primary_trach=1 if hidiag0=="Z430"
replace primary_trach=1 if inrange(substr(hidiag0, 1, 5), "J9501", "J9509")

tab primary_cardiacarrest primary_trach, row col

tab hkyear primary_cardiacarrest, row col

* create f_sample variable
gen f_sample = 0
replace f_sample= 1 if hospid !=. & primary_cardiacarrest!=1 & primary_trach !=1 &
!missing(hksex) & !missing(hidiag0)
tab f_sample

* count the number of hospitalizations per CCN
bysort hkyear hiprovn: egen count_persons_year = total(f_sample)
count if count_persons_year >=5 & f_sample==1

* OR instead of 'egen-total' command, you may run:
* drop if sample==0
* bysort hiprovn hkyear: gen count_persons_year = _N
* If I run the following command (bysort hiprovn hkyear: gen count_persons_year = _N)
* without first dropping cases of f_sample==0
* those who are going to be excluded from the final sample are counted per CCN

drop if f_sample==0
drop if count_persons_year <5

* Save a file that includes the final sample only (FFS without cardiac arrest & tracheostomy from
CCN >=5 )

save "P:\ihicu\shared\CodeforRepository_JAMA2020\imv_nimv_0017_v2.dta", replace
* this dataset only includes the final sample

************************
* creates dx variables *
************************
* Note: YR 2016-17 would have icd10 code instead of icd9
```

```
* create dx9 variable that includes the first 3 digits from ICD9 codes
icd9 generate dx9 = hidiag0 if hkyear <2016, category
gen n_dx9 = real(dx9)
icd9 generate dx9_des = hidiag0 if hkyear <2016, description

browse hidiag0 if hkyear > 2015
icd10 generate dx10 =hidiag0 if hkyear > 2015, category
*icd10 generate dx10_des =hidiag0 if hkyear >2015, description


* Creating flags for key diagnosis groups of interests
*** Update these dx with ICD-10 for 2016-2017 ***

* Cancer
gen cancer =0
replace cancer =1 if n_dx9 >=140 & n_dx9 <=209
replace cancer =1 if n_dx9 >=235 & n_dx9 <=239
replace cancer =1 if hidiag0=="3383"

replace cancer=1 if inrange(substr(dx10,1,3), "C00", "C96")
replace cancer=1 if inrange(substr(dx10,1,3), "D37", "D49")
replace cancer=1 if dx10=="D3A"
replace cancer=1 if hidiag0=="G893"

tab hkyear cancer, col row

* Pneumonia
gen pneumonia = 0
replace pneumonia =1 if n_dx9 >=480 & n_dx9 <=486
replace pneumonia = 1 if n_dx9 ==507

replace pneumonia = 1 if inrange(substr(dx10, 1, 3), "J12", "J18")
replace pneumonia = 1 if hidiag0=="J690"

tab hkyear pneumonia, col row

* Sepsis
gen sepsis = 0
replace sepsis = 1 if n_dx9 ==38

replace sepsis = 1 if inrange(substr(dx10, 1,3), "A40", "A41")
replace sepsis = 1 if hidiag0=="A427"

tab hkyear sepsis, col row

* A flag for Pneumonia OR Sepsis
```

```
gen pneu_sepsis = 0
replace pneu_sepsis= 1 if sepsis ==1
replace pneu_sepsis = 1 if pneumonia==1
tab pneu_sepsis

* CHF -- fixed
gen chf=0
replace chf = 1 if n_dx9 ==428
replace chf = 1 if hidiag0=="39891" | hidiag0=="40201" | hidiag0=="40211" | hidiag0=="40291"
replace chf=1 if inrange(substr(hidiag0,1,4), "I501", "I509")
replace chf=1 if hidiag0=="I110" | hidiag0=="I130" | hidiag0=="I132"
replace chf=1 if hidiag0=="I0981"

tab hkyear chf, col row

* COPD
gen copd=0
replace copd = 1 if n_dx9 >=490 & n_dx9 <=494
replace copd = 1 if n_dx9 ==496
replace copd = 1 if inrange(substr(dx10, 1,3), "J40", "J47")

tab hkyear copd, col row

* dementia
gen dementia=0
replace dementia=1 if icd_alz==1 | icd_dem==1

* dementia2 (dementia2 is the one that was identified based on primary
* or the first nine ICD-9 dx codes)
gen dementia2=0
replace dementia2=1 if icd_alz_v2==1 | icd_dem_v2==1

tab hkyear dementia, row col
tab hkyear dementia2, row col


* Create dx variables without the presence of a secondary diagnosis of dementia
* This will be the main variables to use in analyses (Dementia trumping over other diagnoses)

gen cancer2=0
replace cancer2=1 if cancer==1 & dementia2==0

gen pneumonia2=0
replace pneumonia2=1 if pneumonia==1 & dementia2==0

gen sepsis2=0
```

```
replace sepsis2=1 if sepsis==1 & dementia2==0

gen pneu_sepsis2=0
replace pneu_sepsis2=1 if pneu_sepsis==1 & dementia2==0

gen chf2=0
replace chf2=1 if chf==1 & dementia2==0

gen copd2=0
replace copd2=1 if copd==1 & dementia2==0


tab hkyear dementia2, row col
tab hkyear cancer2, row col
tab hkyear pneumonia2, row col
tab hkyear sepsis2, row col
tab hkyear chf2, row col
tab hkyear copd2, row col



*************************************************************************
* Prepare variables to create figures and run regression models         *
*************************************************************************

tab hksex, gen(d)
rename d1 Male
rename d2 Female

tab hkrace, gen(d)
rename d1 R_Unknown
rename d2 R_White
rename d3 R_Black
rename d4 R_Other
rename d5 R_Asian
rename d6 R_Hispanic
rename d7 R_Native

tab lastplace, gen(d)
rename d1 AcuteInpatient
rename d2 ER_OBS
rename d3 Home
rename d4 HomeHealth
rename d5 NH_NonSNF
rename d6 OtherInpt
rename d7 SNF
```

```
tab dod_dual, m
count if inrange(substr(dod_dual, 1, 2), "01", "08")
gen f_dual = 1 if inrange(substr(dod_dual, 1, 2), "01", "08")
tab f_dual if hkyear >2012
tab dod_dual if hkyear >2012


* SINCE we are working on the dataset where f_sample ==0 and count_persons_year <5 were
excluded,
* this code (if count_persons_year >= 5 & f_sample==1) is not necessary -
* but I will just keep the prior code as is - since it doesn't make any change  with or without it

keep if R_Asian==1|R_white==1

* note saved and then used the following file

use "P:\ihicu\shared\July2020 JAMA\GSA work with racial focus\Teno mods to
IMV_white_asian_ffs_Ma_v1.dta"


*************************************************************************
* creates a set of figures/time-series changes in IMV by Asian vs. Whtie    *
*************************************************************************

**Descriptive data analysis

tab vent imv_teno

bysort imv_teno: su age charlson if R_White==1 & anyhmo==0, d

bysort imv_teno: su age charlson if R_Asian==1 & anyhmo==0, d

bysort imv_teno: ci proportions Female chf2 copd2 cancer2 pneu_sepsis2
dementia2 other_dx f_dual if R_White==1 & anyhmo==1

bysort imv_teno: ci proportions Female chf2 copd2 cancer2 pneu_sepsis2
dementia2 other_dx f_dual if R_Asian==1 & anyhmo==1

bysort imv_teno: ci proportions Female chf2 copd2 cancer2 pneu_sepsis2
dementia2 other_dx f_dual if R_White==1 & anyhmo==0

bysort imv_teno: ci proportions Female chf2 copd2 cancer2 pneu_sepsis2
dementia2 other_dx f_dual if R_Asian==1 & anyhmo==0


** For figures

tab imv_teno hkyear if R_Asian==1 & anyhmo==0, row col chi

tab imv_teno hkyear if R_White==1 & anyhmo==0, row col chi
```

```
tab imv_teno hkyear if R_Asian==1 & anyhmo==1 & hkyear >2010, row col chi

tab imv_teno hkyear if R_White ==1 & anyhmo==1 & hkyear >2010, row col chi

** Multivariate

. xtset hospid
       panel variable:  hospid (unbalanced)

xtlogit imv_teno age Female R_Asian pneu_sepsis2 chf2 copd2 dementia2
other_dx charlson i.hkyear if anyhmo==0, i(hospid) or re

xtlogit imv_teno age Female R_Asian pneu_sepsis2 chf2 copd2 dementia2
other_dx charlson i.hkyear if anyhmo==0, i(hospid) or fe

xtlogit imv_teno age Female R_Asian pneu_sepsis2 chf2 copd2 dementia2
other_dx charlson i.hkyear if hkyear>=2011, i(hospid) or re

xtlogit imv_teno age Female R_Asian pneu_sepsis2 chf2 copd2 dementia2
other_dx charlson i.hkyear if hkyear>=2011, i(hospid) or fe


** diseases limited

xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if anyhmo==0 &
dementia2==1, i(hospid) or

xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if anyhmo==0 &
chf2==1, i(hospid) or

xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if anyhmo==0 &
copd2==1, i(hospid) or

. xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if anyhmo==0 &
cancer2==1, i(hospid) or

MA 2011-2017


Cancer is the reference diagnosis


. ***********

. * MA only *

. ***********

. * Overall, IMV

. xtlogit imv_teno age Female R_Asian pneu_sepsis2 chf2 copd2 dementia2
other_dx charlson f_dual i.hkyear if hkyear>2010 & anyhmo==1, i(hospid) or

. * Dementia, IMV, one of the secondary or primary dx
```

```
.

. xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if hkyear>2010
& dementia2==1 & anyhmo==1, i(hospid) or

.

. * CHF, IMV, primary dx

. xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if hkyear>2010
& chf2==1 & anyhmo==1, i(hospid) or


. * COPD, IMV, primary dx

. xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if hkyear>2010
& copd2==1 & anyhmo==1, i(hospid) or

.

. * Cancer, IMV, primary dx

. xtlogit imv_teno age Female R_Asian charlson f_dual i.hkyear if hkyear>2010
& cancer2==1 & anyhmo==1, i(hospid) or


** Table 2 ****

** merge by hospid - data from Dartmouth Atlas 2017 characterizing hospitals

. gen hospital_teach = 0
. replace hospital_teach = 1 if teachstatus =="Major Teaching"
. replace hospital_teach = 2 if teachstatu =="Other Teaching"
. tab R_Asian hospital_teach, row col chi


. tab hosptype
tab pstate if R_Asian==1, sort

. tab pstate if R_Asian==0, sort


. sum AHAbeds if R_Asian==1, detail


. sum AHAbeds if R_Asian==0, detail

. ttest AHAbeds, by(R_Asian)



. sum died_in_hospital if R_Asian==1 & died_in_hospital != -99999, detail


. sum died_in_hospital if R_Asian==0 & died_in_hospital != -99999, detail
```

```
. ttest died_in_hospital if died_in_hospital!=-99999, by(R_Asian)

. ttest ICU_admission_death if ICU_admission_death !=-99999, by(R_Asian)

. sum ICU_admission_death if R_Asian==1 & ICU_admission_death != -99999,
detail
. sum ICU_admission_death if R_Asian==0 & ICU_admission_death != -99999,
detail

. gen n_percent_hospice = real( Percent_hospice_six)
(18 missing values generated)

. sum n_percent_hospice if R_Asian==1 & n_percent_hospice != -99999, detail


. sum n_percent_hospice if R_Asian==0 & n_percent_hospice != -99999, detail



. ttest n_percent_hospice if n_percent_hospice !=-99999, by(R_Asian)


. gen n_hospice_reibursement= real(hospice_reimbursement)
(18 missing values generated)

. ttest hospice_reimbursement if hospice_reimbursement !=-99999, by(R_Asian)
type mismatch
r(109);

. ttest n_hospice_reimbursement if n_hospice_reimbursement !=-99999,
by(R_Asian)
variable n_hospice_reimbursement not found
r(111);

. ttest n_hospice_reibursement if n_hospice_reibursement !=-99999,
by(R_Asian)
```