

Evaluation of pharmacist-physician rapid access atrial fibrillation clinic model of care

Protocol

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<https://github.com/cardiopharmnerd/raaf>

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1 Preface

This is the protocol for the paper Evaluation of pharmacist-physician rapid access atrial fibrillation clinic model of care

To generate this document, the Stata package texdoc [?] was used, which is available from: <http://repec.sowi.unibe.ch/stata/texdoc/> (accessed 14 November 2022). The final Stata do file and this pdf are available at: <https://github.com/cardiopharmnerd/raaf>

2 Abbreviations

- AF - Atrial fibrillation
- CHADSVA - Risk score for determining stroke risk in AF
- DCR - Direct current reversion
- ED - Emergency department
- EP - Electrophysiologist
- EQ5D - European Quality of Life survey - 5 dimension version
- GP - General practitioner
- NOAC - Non-vitamin K oral anticoagulant
- NPS - Net promoter score
- RAAF - Rapid Access Atrial Fibrillation Clinic item URN - Unique registrations number
- WebPAS - Web-based Patient Administration System

3 Introduction

People with atrial fibrillation, the most common cardiac arrhythmia worldwide, are at increased risk of hospitalization from both symptoms of atrial fibrillation, as well as higher risk of stroke and heart failure. It is important that when people are diagnosed with atrial fibrillation are risk assessed as soon as possible to ensure appropriate and safe treatment can be provided. This assessment should include stroke risk calculation and provision of anticoagulation, arrhythmia symptom control plans, and comorbidity assessment, in combination with patient education. From 2022 to 2023, Grampians Health Ballarat participated in a Safer Care Victoria funded initiative to establish rapid access atrial fibrillation (RAAF) clinics. This project is a retrospective review of how the RAAF clinic provided care to patients referred to the service, both in quality of service, clinic outcomes, and patient acceptance of service, as well as investigating the costs and benefits of the RAAF clinic as a sustainable model of care.

4 Data source and import

The data for this project was generated via an audit of all individuals seen in the RAAF clinic. Data was extracted from a REDCap collection tool and stata file exported for analysis. [1, 2] A second dataset was used from the outpatient module of the hospital booking system (WebPAS) that listed all medical appointments and referrals to the RAAF clinic.

```
set rmsg on
cd "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output"

*First dataset from REDCap export
clear
import excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\raaf_a
> ds.xlsx", firstrow
ta ref_n
*There are 10 patients where they were referred into the clinic twice, this will be important for co
> llecting appointment statistics.

*Save a local copy of the dataset for checks and cleaning
save pre_ads, replace
*Second dataset from outpatient booking system
clear
import excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\raaf_a
> tt.xlsx", firstrow
rename (UR Attendance Mode) (urn att mode)
drop N
drop if att == .
save pre_appt, replace
```

5 Data cleaning

For a description of the data, we first inspected each variable to ensure there are no unusual pieces of data, and to check missing data to ensure it is intentionally blank or if there is an error in the data entry component of the REDCap tool. We took the following steps:

1. Ensure all individuals accounted for
2. Review date based variables
3. Review categorical variables

5.1 RAAF REDCap data

Although CHADSVA scores are shown as a continuous variable, they are really an ordinal variable, and so were checked and cleaned as part of the categorical variable review. The same approach was considered for NPS scores.

```
*Open pre-cleaned dataset and check variables
use pre_ads, clear
br
de
```

5.1.1 Ensure all individuals accounted for

We wanted to ensure no duplicate entries based on the id numbers generated for each URN entered into the original dataset. We also needed to drop anyone who received no consults as part of this service. These were likely individuals who originally consented to clinic, but changed their mind later.

```
ta id
*No duplicates
keep if either_att == "Yes"
*Twelve people dropped, leaving 275 individuals who attended the service at least once.
bysort urn date_dc : gen nghost = _n
ta nghost
bysort urn appt_pharm : gen nghost1 = _n
ta nghost1
br urn nghost nghost1 if nghost == 2
*Same person entered twice, they will be dropped
drop if nghost == 2
br
drop nghost nghost1
```

5.1.2 Review date based variables

We checked each of the date variables to ensure all appointments occurred after the referral date, and that the first appointment occurred within the implementation phase of 1/4/2022 and 1/11/2023.

```
foreach i in date_dc date_ref appt_pharm appt_phys date_fup {
format `i` %td
}

hist date_dc, color(black) graphregion(color(white)) frequency xtitle("Discharge date")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_discharge.pdf",
> as(pdf) name("Graph") replace

hist date_ref, color(black) graphregion(color(white)) frequency xtitle("Referral date")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_referral.pdf", a
> s(pdf) name("Graph") replace

hist appt_pharm, color(black) graphregion(color(white)) frequency xtitle("Pharmacist appointment d
> ate")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_appt_pharm.pdf",
> as(pdf) name("Graph") replace

hist appt_phys, color(black) graphregion(color(white)) frequency xtitle("Physician appointment dat
> e")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_appt_phys.pdf",
> as(pdf) name("Graph") replace

/**
\color{black}
\begin{figure} [H]
\centering
\includegraphics[width=0.8\textwidth]{hist_discharge.pdf}
\caption{Histogram of discharge date}
\label{hist_discharge}
\end{figure}
\begin{figure} [H]
\centering
\includegraphics[width=0.8\textwidth]{hist_referral.pdf}
\caption{Histogram of referral dates}
\label{hist_referral.pdf}
\end{figure}
\begin{figure} [H]
\centering
```

```

        \includegraphics[width=0.8\textwidth]{hist_appt_pharm.pdf}
        \caption{Histogram of pharmacist appointment dates}
        \label{hist_appt_pharm.pdf}
\end{figure}
\begin{figure} [H]
    \centering
    \includegraphics[width=0.8\textwidth]{hist_appt_phys.pdf}
    \caption{Histogram of physician appointment dates}
    \label{hist_discharge}
\end{figure}

All looks reasonable, now to check time from referral to first appointment.
\color{violet}
***/

gen appt_first = appt_pharm
format appt_first %td
replace appt_first = appt_phys if appt_phys < appt_pharm
gen tts_ref = appt_first - date_ref
gen tts_dc = appt_first - date_dc
gen tts_pharmphys = appt_phys - appt_pharm if pharm_att == "Yes" & phys_att == "Yes"
su tts_ref, detail
su tts_dc, detail
su tts_pharmphys, detail

```

There are no negative numbers when looking at the time difference between referral/dc and first seen, so data makes sense from this perspective.

5.2 Review categorical variables

The majority of variables in this dataset are categorical, so we inspected each one to ensure responses were complete and made sense for the question being asked. We also created labels and encoded ordinal variables such as age group to make creating and merging tables easier down the track.

```

label define order 1 "Under 50" 2 "50-59" 3 "60-69" 4 "70-79" 5 "80-89" 6 "Over 90"
encode age_group, gen(age) label(order)
drop age_group
ta age
ta sex
ta refsource
ta refgen
ta pharm_att
ta phys_att
ta either_att
ta careset
ta tte
ta chadsva_done
ta hasbled
ta oac_prior_binary
ta oac_prior

*There are some missing, need to ensure they are intentionally blank and if so, mark them as blank
count if oac_prior == "" & oac_prior_binary != "No"
*All good intentionally blank, so will change to "None"
replace oac_prior = "none" if oac_prior == ""
replace oac_prior = "none" if oac_prior == "None"
ta oac_prior

ta oac_post
br if oac_post == ""

*All appear to be intentionally blank , so will replace with "None"
replace oac_post = "none" if oac_post == ""
replace oac_post = "none" if oac_post == "None"
br
ta oac_post

```


This next section required some recoding due to "0" and "No" being used as values of "None", we will check all the medication data and ensure it either lists the drug or none if no drug present. This was done both pre and post RAAF attendance for the following anti-arrhythmic drug classes:

- Beta blockers
- Calcium channel blockers (non-dihydropyridine)
- Flecainide
- Amiodarone
- Digoxin

We also created a variable to group individuals into CHADSVa of 0, 1 and greater than 2, which are stratifications often use to dictate whether anticoagulation is required [3].

```
*Beta blockers prior to RAAF
ta bb_prior
replace bb_prior = "none" if bb_prior == "0"
replace bb_prior = lower(bb_prior)
ta bb_prior

gen bb_prior_sot = "No"
replace bb_prior_sot = "Yes" if bb_prior == "sotalol"

*Calcium channels blockers prior to RAAF
ta cc_prior
replace cc_prior = "none" if cc_prior == "0"
replace cc_prior = lower(cc_prior)
ta cc_prior

*flecainide prior to RAAF
ta flec_prior
replace flec_prior = "none" if flec_prior == "0"
replace flec_prior = lower(flec_prior)
ta flec_prior

*Amiodarone prior to RAAF
ta amio_prior
replace amio_prior = "none" if amio_prior == "0"
replace amio_prior = lower(amio_prior)
ta amio_prior

*Digoxin prior to RAAF
ta dig_prior /// nil issues

*Beta blockers post RAAF
ta bb_post
replace bb_post = "none" if bb_post == "0"
replace bb_post = "none" if bb_post == "ceased"
replace bb_post = lower(bb_post)
ta bb_post

gen bb_post_sot = "No"
replace bb_post_sot = "Yes" if bb_post == "sotalol"

*Calcium channels blockers post RAAF
ta cc_post
replace cc_post = "none" if cc_post == "0"
replace cc_post = lower(cc_post)
ta cc_post

*flecainide post RAAF
ta flec_post
replace flec_post = "none" if flec_post == "0"
replace flec_post = lower(flec_post)
ta flec_post
```

```

*Amiodarone post RAAF
ta amio_post
replace amio_post = "none" if amio_post == "0"
replace amio_post = lower(amio_post)
ta amio_post

*Digoxin post RAAF
ta dig_post
replace dig_post = "yes" if dig_post == "Yes"
replace dig_post = "none" if dig_post == "0" | dig_post == "ceased"
ta dig_post

*DCR
ta dcr_ref
replace dcr_ref = "yes" if dcr_ref == "Yes" | dcr_ref == "1"
replace dcr_ref = "no" if dcr_ref == "0"
ta dcr_ref

```

The next variables are post RAAF follow up data such as discharge management plans for symptoms, who the individual was discharged to (GP, specialist, etc) as well as hospital outcomes at 30 days such as unplanned ED and hospital admission presentations.

```

ta control_plan
ta next_appt
ta dc_clinic
ta dc_mxplan
ta ed_30
ta adm_30
ta dead_30
ta chadsva, missing
gen oac_indicated = 0
replace oac_indicated = 1 if chadsva == 1
replace oac_indicated = 2 if chadsva > 1

```

We created some tags to indicate changes made in medication pre and post RAAF clinic attendance.

```

*Create a binary tag for post RAAF clinic anticoagulation as not present in the dataset
gen oac_post_binary = "No"
replace oac_post_binary = "Yes" if oac_post != "none"

*Create variable that lists the anticoagulant without dosing
gen oac_prior_drug = "none"
ta oac_prior
replace oac_prior_drug = "apixaban" if oac_prior == "Apixaban 5mg bd" | oac_prior == "Apixaban 2.5mg bd"
> bd"
replace oac_prior_drug = "rivaroxaban" if oac_prior == "Rivaroxaban 15mg d" | oac_prior == "Rivaroxa
> ban 20mg d"
replace oac_prior_drug = "dabigatran" if oac_prior == "Dabigatran 150mg bd" | oac_prior == "Dabigatr
> an 110mg bd"
replace oac_prior_drug = "warfarin" if oac_prior == "warfarin"
ta oac_prior_drug oac_prior

gen oac_post_drug = "none"
ta oac_post
replace oac_post_drug = "apixaban" if oac_post == "Apixaban 5mg bd" | oac_post == "Apixaban 2.5mg bd"
> "
replace oac_post_drug = "rivaroxaban" if oac_post == "Rivaroxaban 15mg d" | oac_post == "Rivaroxaban
> 20mg d"
replace oac_post_drug = "dabigatran" if oac_post == "Dabigatran 150mg bd" | oac_post == "Dabigatran
> 110mg bd"
replace oac_post_drug = "warfarin" if oac_post == "warfarin"
ta oac_post_drug oac_post

*Create a tag to state if anticoagulation required changing following RAAF clinic attendance
gen oac_change = "No"
replace oac_change = "Dose/drug change" if oac_prior != oac_post
replace oac_change = "Ceased" if oac_prior != "none" & oac_post == "none"
replace oac_change = "Added" if oac_prior == "none" & oac_post != "none"

```

```

ta oac_change
*Create tag to state anticoagulation was appropriate
gen oac_app = 0
replace oac_app = 1 if oac_change == "No"
ta oac_app oac_change
*Create tag for all beta blockers and calcium channel blockers
gen bb_prior_class = 0
replace bb_prior_class = 1 if bb_prior != "none"
ta bb_prior_class bb_prior
gen bb_post_class = 0
replace bb_post_class = 1 if bb_post != "none"
ta bb_post_class bb_post
gen cc_prior_class = 0
replace cc_prior_class = 1 if cc_prior != "none"
ta cc_prior_class cc_prior
gen cc_post_class = 0
replace cc_post_class = 1 if cc_post != "none"
ta cc_post_class cc_post
*Create a tag for changes made to anti-arrythmic medications
gen bb_change = "No"
replace bb_change = "Ceased" if bb_prior != "none" & bb_post == "none"
replace bb_change = "Added" if bb_prior == "none" & bb_post != "none"
replace bb_change = "Drug change" if bb_prior != "none" & bb_post != bb_prior & bb_post != "none"
replace bb_change = "Switched to sotalol" if bb_prior != "sotalol" & bb_post == "sotalol"
ta bb_change, sort
gen cc_change = "No"
replace cc_change = "Ceased" if cc_prior != "none" & cc_post == "none"
replace cc_change = "Added" if cc_prior == "none" & cc_post != "none"
replace cc_change = "Drug change" if cc_prior != "none" & cc_post != cc_prior & cc_post != "none"
ta cc_change, sort
gen flec_change = "No"
replace flec_change = "Ceased" if flec_prior != "none" & flec_post == "none"
replace flec_change = "Added" if flec_prior == "none" & flec_post != "none"
replace flec_change = "Drug change" if flec_prior != "none" & flec_post != flec_prior & flec_post !=
> "none"
ta flec_change, sort
gen amio_change = "No"
replace amio_change = "Ceased" if amio_prior != "none" & amio_post == "none"
replace amio_change = "Added" if amio_prior == "none" & amio_post != "none"
replace amio_change = "Drug change" if amio_prior != "none" & amio_post != amio_prior & amio_post !=
> "none"
ta amio_change, sort
gen dig_change = "No"
replace dig_change = "Ceased" if dig_prior != "none" & dig_post == "none"
replace dig_change = "Added" if dig_prior == "none" & dig_post != "none"
replace dig_change = "Drug change" if dig_prior != "none" & dig_post != dig_prior & dig_post != "non
> e"
ta dig_change, sort
*Create tag of any change in anti-arrythmic therapy
gen aa_change = "No"
replace aa_change = "Yes" if bb_change != "No" | cc_change != "No" | flec_change != "No" | amio_chan
> ge != "No" | dig_change != "No"
ta aa_change
*create tag for any anti-arrythmic present
foreach i in prior post {
gen aa_`i' = 0
replace aa_`i' = 1 if bb_`i' != "none" | cc_`i' != "none" | flec_`i' != "none" | amio_`i' != "none"
> | dig_`i' != "none"
}
ta aa_prior
ta aa_post
/***

```

```

\color{black}
We checked QoL and and NPS score completion, whhich are both ordinal variables. The EQ5D variable is
> presented here as a 5-digit number, but it is actually the scores of 1-5 from the 5 dimensions of
> the EQ5D survey. We will generate a separate dataset of EQ5D scores in order to calculate utility
> scores across the dataset. \\
The NPS scores range from 1 to 10, and we created a variable to define individuals as promoter (score
> d 9-10), detractors (scored 1-6), and neutral (scored 7-8). However for the paper we opted for ana
> lysis as mean score with 95% confidence intervals to avoid categorising the data further.
\color{violet}
***/
*EQ5D scores
count if eq5d_prior == ""
*24 missing
count if eq5d_post == ""
*110 missing
count if eq5d_prior != "" & eq5d_post != ""
*Follow up avaiable on 165 referrals

*NPS Scores
ta nps, missing
*Follow up on 165 scores available, now to break them up into promoter, detractor and neutral
count if nps == 9 | nps == 10
count if nps < 7
gen nps_group = 3
replace nps_group = 2 if nps < 9
replace nps_group = 1 if nps < 6
replace nps_group = 0 if nps > 10
ta nps_group

save ads, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\raaf_a
> ds_clean.xlsx", firstrow(var) replace

```

5.3 Merge in GARFIELD and HASBLED scores

Following completion of the study and preparation of the dataset, we made a decision to go back into the the records where the dataset was constructed and calculate risk scores for HASBLED and GARFIELD. This was used for the cost effectiveness analysis paper that followed this protocol, with the analysis available at <https://github.com/cardiopharmnerd/raaf> .

```

use ads, clear
br
keep urn appt_pharm
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\garfbl
> ed.xlsx", firstrow(var) replace

```

5.4 Merge in booking system data

We needed to merge in attendance data to confirm attendance of individuals to physician clincs and those who declined the service all together. It also lists some people who were seen as an adhoc appointment by the physician, but were misclassified as being part of the RAAF clinic. Lastly, we needed to reclassify attendance for people who saw the pharmacist but not the physician. This was for people who were already managed by an external specialist, so were seen by pharmacist and an external physician.

```

use ads, clear
bysort urn : keep if _n == 1
keep urn pharm_att phys_att
save urn_att_master, replace
use pre_appt, clear

```

```

merge m:1 urn using urn_att_master

*Remove referred appointments that are not service declines, as these are ad hoc removes not part of
> the RAAF clinic analysis.
count if _merge == 1 & att == 1
drop if _merge == 1 & att == 1
count if _merge == 1 & att == 0
drop if _merge == 1 & att == 0
*Reclassify attendance of those who only saw the pharmacist, as this dataset only contains physician
> appointments.
replace att = 2 if att == .

*We created a table of people who were referred and who declined service and who attended service
bysort urn : gen nghost = _n
gen decline = 1 if att == 999
gen nocontact = 1 if att == 99
ta pharm_att if nghost == 1

ta nghost if nghost == 1, matcell(A1)
ta decline, matcell(A2)
ta nocontact, matcell(A3)
ta att if att == 1, matcell(A4)
ta att if att == 0, matcell(A5)
ta pharm_att if nghost == 1, matcell(A6)
ta att if att == 2, matcell(A7)

matrix A = (A1\A2\A3\A4\A5\A6\A7)
mat li A
clear
svmat A

gen demo = ""
replace demo = "Total number of people referred" if _n == 1
replace demo = "Number of people seeing external specialist" if _n == 2
replace demo = "Number of people unable to be contacted" if _n == 3
replace demo = "Number of physician attendances" if _n == 4
replace demo = "Number of physician non-attendances" if _n == 5
replace demo = "Number of pharmacist non-attendances" if _n == 6
replace demo = "Number of pharmacist attendances" if _n == 7
replace demo = "Number of pharmacist only consults" if _n == 8

*Need to remember there were 10 repeat pharmacist consults not accounted for here:
replace A1 = A1 + 10 if demo == "Number of pharmacist attendances"

order demo
rename A1 n

save table_att, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> attendance.xlsx", firstrow(var) replace

```

5.5 EQ5D data

We used an existing Austrian population derived value set to attribute EQ5D scores to utility scores [4]

```

use ads, clear
keep urn ref_n eq5d_prior eq5d_post
drop if eq5d_post == ""
count if eq5d_prior == ""

bysort urn : gen nghost = _n
ta nghost
keep if nghost == 1
drop nghost

foreach i in prior post {
gen mo_`i'_og = substr(eq5d_`i', 1,1)
gen sc_`i'_og = substr(eq5d_`i', 2,1)
}

```

```

gen ua_`i`_og = substr(eq5d_`i`, 3,1)
gen pd_`i`_og = substr(eq5d_`i`, 4,1)
gen ad_`i`_og = substr(eq5d_`i`, 5,1)

gen mo_`i` = 0
replace mo_`i` = -0.039 if mo_`i`_og == "2"
replace mo_`i` = -0.067 if mo_`i`_og == "3"
replace mo_`i` = -0.237 if mo_`i`_og == "4"
replace mo_`i` = -0.242 if mo_`i`_og == "5"
gen sc_`i` = 0
replace sc_`i` = -0.030 if sc_`i`_og == "2"
replace sc_`i` = -0.058 if sc_`i`_og == "3"
replace sc_`i` = -0.213 if sc_`i`_og == "4"
replace sc_`i` = -0.221 if sc_`i`_og == "5"
gen ua_`i` = 0
replace ua_`i` = -0.055 if ua_`i`_og == "3"
replace ua_`i` = -0.162 if ua_`i`_og == "4" | ua_`i`_og == "5"
gen pd_`i` = 0
replace pd_`i` = -0.044 if pd_`i`_og == "2"
replace pd_`i` = -0.081 if pd_`i`_og == "3"
replace pd_`i` = -0.276 if pd_`i`_og == "4"
replace pd_`i` = -0.285 if pd_`i`_og == "5"
gen ad_`i` = 0
replace ad_`i` = -0.032 if ad_`i`_og == "2"
replace ad_`i` = -0.066 if ad_`i`_og == "3"
replace ad_`i` = -0.238 if ad_`i`_og == "4" | ad_`i`_og == "5"
gen n5_`i` = 0
replace n5_`i` = -0.153 if mo_`i`_og == "5" | sc_`i`_og == "5" | ua_`i`_og == "5" | pd_`i`_og == "5"
> | ad_`i`_og == "5"
gen utility_`i` = 1 + mo_`i` + sc_`i` + ua_`i` + pd_`i` + ad_`i` + n5_`i`
}

foreach i in mo sc ua pd ad {
gen diff_`i` = `i`_post - `i`_prior
}

hist utility_prior, width(0.05) color(black) graphregion(color(white)) frequency xtitle("EQ5D utilit
> y score")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_utility_prior.pdf
> f", as(pdf) name("Graph") replace

hist utility_post, width(0.05) color(black) graphregion(color(white)) xtitle("EQ5D utility score")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_utility_post.pdf
> ", as(pdf) name("Graph") replace

gen utility_diff = utility_post - utility_prior

su utility_diff, detail

hist utility_diff, width(0.05) color(black) graphregion(color(white)) frequency xtitle("Difference i
> n utility scores")
graph export "\\ad.monash.edu\home\User007\acliv1\Documents\GitHub\raaf\output\hist_utility_diff.pdf
> ", as(pdf) name("Graph") replace

gen utility_group = "no change"
replace utility_group = "improved" if utility_diff > 0
replace utility_group = "decreased" if utility_diff < 0
ta utility_group

foreach i in mo sc ua pd ad {
destring `i`_prior_og, replace
destring `i`_post_og, replace
gen diff_`i`_og = `i`_post_og - `i`_prior_og
}

su diff_mo_og, detail
su diff_sc_og, detail
su diff_ua_og, detail
su diff_pd_og, detail
su diff_ad_og, detail

*Paired t-test
su utility_prior, detail
su utility_post, detail

```

```

ttest utility_post == utility_prior

save utility_scores, replace
/**
\color{black}
\begin{figure} [H]
    \centering
    \includegraphics[width=0.8\textwidth]{hist_utility_prior.pdf}
    \caption{Histogram of EQ5D utility scores prior to RAAF clinic}
    \label{hist_utility_prior.pdf}
\end{figure}
\begin{figure} [H]
    \centering
    \includegraphics[width=0.8\textwidth]{hist_utility_post.pdf}
    \caption{Histogram of EQ5D utility scores post RAAF clinic}
    \label{hist_utility_post.pdf}
\end{figure}
\begin{figure} [H]
    \centering
    \includegraphics[width=0.8\textwidth]{hist_utility_diff.pdf}
    \caption{Histogram of difference in utility scores}
    \label{hist_utility_diff.pdf}
\end{figure}
\color{violet}
***/

```

6 Generate result tables

6.1 Model of care evaluation

6.1.1 RAAF clinic cohort description

```

use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta sex if sex == "Female", matcell(A11)
ta age, matcell(A2)
ta reftype, sort matcell(A3)
ta pharm_att if pharm_att == "Yes", matcell(A4)
ta phys_att if phys_att == "Yes", matcell(A5)
ta careset if careset == "Yes", matcell(A6)
ta tte if tte == "Yes", matcell(A7)
ta chadsva_done if chadsva_done == "Yes", matcell(A8)
ta chadsva, matcell(A9)
ta hasbled if hasbled == "Yes", matcell(A10)
matrix A = (A1\A11\A2\A3\A4\A5\A6\A7\A8\A9\A10)
matrix list A
clear
svmat A
egen total = max(A)
gen A2 = string((100 * A1 / total), "%3.1f")+ "%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1
gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "Female" if _n == 2
replace demo = "Under 50" if _n == 3
replace demo = "50-59" if _n == 4
replace demo = "60-69" if _n == 5
replace demo = "70-79" if _n == 6

```

```

replace demo = "80-89" if _n == 7
replace demo = "Over 90" if _n == 8
replace demo = "Inpatient ward" if _n == 9
replace demo = "Emergency department" if _n == 10
replace demo = "General Practitioner" if _n == 11
replace demo = "External hospital" if _n == 12
replace demo = "At least one pharmacist appointment" if _n == 13
replace demo = "At least one physician appointment" if _n == 14
replace demo = "Care-set completed" if _n == 15
replace demo = "Echocardiogram completed" if _n == 16
replace demo = "CHADSVA Assessment completed" if _n == 17
replace demo = "CHADSVA = 0" if _n == 18
replace demo = "CHADSVA = 1" if _n == 19
replace demo = "CHADSVA = 2" if _n == 20
replace demo = "CHADSVA = 3" if _n == 21
replace demo = "CHADSVA = 4" if _n == 22
replace demo = "CHADSVA = 5" if _n == 23
replace demo = "CHADSVA = 6" if _n == 24
replace demo = "CHADSVA = 7" if _n == 25
replace demo = "CHADSVA = 8" if _n == 26
replace demo = "HASBLED assessment completed" if _n == 27

keep demo A

save table_demo1, replace

*Create row for median CHADSVA
use ads, clear
su chadsva, de
ret li
matrix A = r(p50), r(p25), r(p75)
mat li A
clear
svmat A
gen demo = "Median CHADSVA score (IQR)"
forval i = 1/3 {
  gen A`i`s = string(A`i`)
}
gen A = A1s + " (" + A2s + "-" + A3s + ")"
keep demo A

save table_demo2, replace

*Bring tables together and finalise formatting
append using table_demo1

gen id = _n
replace id = 27.5 if id == 1
sort id
drop id

gen cat = ""
replace cat = "Age ranges" if _n == 3
replace cat = "Referral source " if _n == 9
replace cat = "Attendance" if _n == 13
replace cat = "Risk assessments" if _n == 15
order cat demo A

save table_demo, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> demo.xlsx", firstrow(var) replace

```

6.1.2 Timely access

```

*Create table of median times for appointments
use ads, clear
su tts_ref, de
return li
mat A = (r(p50),r(p25),r(p75))
su tts_dc, de

```



```

mat A = (A\r(p50),r(p25),r(p75)))
su tts_pharmphys, detail
mat A = (A\r(p50),r(p25),r(p75)))
su pharmatt_total, de
mat A = (A\r(p50),r(p25),r(p75)))
su physatt_total, de
mat A = (A\r(p50),r(p25),r(p75)))

mat li A

clear
svmat A

gen demo = ""
replace demo = "Median time from referral to first appointment (IQR)" if _n == 1
replace demo = "Median time from discharge to first appointment (IQR)" if _n == 2
replace demo = "Median time between pharmacist and physician appointment* (IQR)" if _n == 3
replace demo = "Median number of pharmacist attendances per referral (IQR)" if _n == 4
replace demo = "Median number of physician attendances per referral (IQR)" if _n == 5
forval i = 1/3 {
gen A`i`s = string(A`i`)
}
gen A = A1s + " (" + A2s + "-" + A3s + ")"
keep demo A
save table_att1, replace

*Create table for attendance and discharge outcomes statistics
use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta pharm_att if pharm_att == "Yes", matcell(A2)
ta phys_att if phys_att == "Yes", matcell(A3)
ta dc_mxplan if dc_mxplan == "Yes", matcell(A4)
ta control_plan, sort matcell(A5)
ta dc_clinic, sort matcell(A6)
ta ed_30 if ed_30 == "Yes", matcell(A7)
ta adm_30 if adm_30 == "Yes", matcell(A8)
matrix A = (A1\A2\A3\A4\A5\A6\A7\A8)
matrix list A
clear
svmat A

egen total = max(A)
gen A2 = string((100 * A1 / total), "%3.1f")+ "%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "At least one pharmacist appointment" if _n == 2
replace demo = "At least one physician appointment" if _n == 3
replace demo = "Management plan present on discharge from clinic" if _n == 4
replace demo = "Rhythm control plan documented on discharge from clinic" if _n == 5
replace demo = "Rate control plan documented on discharge from clinic" if _n == 6
replace demo = "No rate/rhythm control plan documented on discharge from clinic" if _n == 7
replace demo = "General practitioner" if _n == 8
replace demo = "Public regional cardiology clinic" if _n == 9
replace demo = "Private cardiologist clinic" if _n == 10
replace demo = "Public electrophysiology clinic" if _n == 11
replace demo = "Public regional heart failure clinic" if _n == 12
replace demo = "Metropolitan cardiologist clinic" if _n == 13
replace demo = "Unplanned presentation to emergency department" if _n == 14
replace demo = "Unplanned admission to hospital" if _n == 15

keep demo A
save table_att2, replace

*Merge tables together
append using table_att1
gen id = _n

```

```

replace id = 3.5 if id > 15
sort id
drop id

gen cat = ""
replace cat = "Attendance statistics" if _n == 2
replace cat = "Discharge documentation" if _n == 9
replace cat = "Discharge from RAAF clinic to" if _n == 13
replace cat = "Representation outcomes at 30 days post discharge" if _n == 19
order cat demo A

save table_att, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> attdc.xlsx", firstrow(var) replace

```

6.1.3 Anticoagulant use before and after RAAF clinic

```

*OAC use pre and post as one column table
use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta oac_indicated, matcell(A2)
ta oac_prior_binary if oac_indicated == 1 & oac_prior_binary == "Yes", matcell(A3)
ta oac_prior_binary if oac_indicated == 2 & oac_prior_binary == "Yes", matcell(A4)
ta oac_prior_drug if oac_prior != "none", sort matcell(A5)
ta oac_post_binary if oac_indicated == 1 & oac_post_binary == "Yes", matcell(A6)
ta oac_post_binary if oac_indicated == 2 & oac_post_binary == "Yes", matcell(A7)
ta oac_post_drug if oac_post != "none", sort matcell(A8)
ta oac_change, sort matcell(A9)

matrix A = (A1\A2\A3\A4\A5\A6\A7\A8\A9)
matrix list A
clear
svmat A

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "CHADSVA = 0" if _n == 2
replace demo = "CHADSVA = 1" if _n == 3
replace demo = "CHADSVA > 1" if _n == 4
replace demo = "OAC prescribed with CHADSVA of 1" if _n == 5
replace demo = "OAC prescribed with CHADSVA > 1" if _n == 6
replace demo = "Apixaban" if _n == 7
replace demo = "Rivaroxaban" if _n == 8
replace demo = "Dabigatran" if _n == 9
replace demo = "Warfarin" if _n == 10
replace demo = "OAC prescribed with CHADSVA of 1" if _n == 11
replace demo = "OAC prescribed with CHADSVA > 1" if _n == 12
replace demo = "Apixaban" if _n == 13
replace demo = "Rivaroxaban" if _n == 14
replace demo = "Dabigatran" if _n == 15
replace demo = "Warfarin" if _n == 16
replace demo = "No changes made to anticoagulation" if _n == 17
replace demo = "OAC commenced" if _n == 18
replace demo = "OAC ceased" if _n == 19
replace demo = "OAC dose/drug correction made" if _n == 20

save oactab, replace

gen total = A1
replace total = A1[3] if _n == 5 | _n == 7
replace total = A1[4] if _n == 6 | _n == 8
replace total = A1[1] if _n > 8

gen A2 = string((100 * A1 / total), "%3.1f")+ "%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1

```

```

keep demo A
gen cat = ""
replace cat = "Stroke risk assessment" if _n == 2
replace cat = "Prior to RAAF clinic" if _n == 5
replace cat = "Following RAAF clinic" if _n == 11
replace cat = "Summary of changes" if _n == 17
order cat demo A

save table_drugtotaloac1C, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> drugtotaloac1C.xlsx", firstrow(var) replace

*OAC use pre and post as two column table
use ads, clear

ta oac_indicated oac_prior_drug, matcell(A1)
ta oac_indicated oac_post_drug, matcell(A2)

matrix A = (A1,A2)
matrix list A
clear
svmat A

gen A0 = A1 + A2 + A3 + A4 + A5
gen A11 = A1 + A2 + A4 + A5
gen A12 = A6 + A7 + A9 + A10
forval i = 1/12 {
gen A`i`p = string((100 * A`i` / A0), "%3.1f")+ "%"
}
forval i = 1/12 {
gen A`i`s = string(A`i`)
replace A`i`s = A`i`s + " (" + A`i`p + ")"
}
gen A0s = string(A0)
order A0s A11s A1s A2s A4s A5s A3s A12s A6s A7s A9s A10s A8s
keep A0s A11s A1s A2s A4s A5s A3s A12s A6s A7s A9s A10s A8s

gen demo = ""
replace demo = "CHADSVA = 0" if _n == 1
replace demo = "CHADSVA = 1" if _n == 2
replace demo = "CHADSVA > 1" if _n == 3
order demo
set obs 4
replace demo = "CHADSVA score" if demo == ""
replace A0s = "Total" if A0s == ""
replace A11s = "Anticoagulated" if A11s == ""
replace A12s = "Anticoagulated" if A12s == ""
replace A1s = "Apixaban" if A1s == ""
replace A6s = "Apixaban" if A6s == ""
replace A2s = "Rivaroxaban" if A2s == ""
replace A7s = "Rivaroxaban" if A7s == ""
replace A3s = "None" if A3s == ""
replace A8s = "None" if A8s == ""
replace A4s = "Dabigatran" if A4s == ""
replace A9s = "Dabigatran" if A9s == ""
replace A5s = "Warfarin" if A5s == ""
replace A10s = "Warfarin" if A10s == ""
gen id = _n
replace id = 0 if id == 4
sort id
drop id

save table_drugtotaloac2C, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> drugtotaloac2C.xlsx", replace

*Indiviudal OAC use graph
foreach ii in prior post{
forval i = 1/2 {
use ads, clear
ta oac_`ii`_drug if oac_indicated == `i`, matcell(A1)

```

```

matrix A = (A1)
matrix list A
clear
svmat A

gen drug = _n
label define drug 1 "Apixaban" 2 "Dabigatran" 3 "None" 4 "Rivaroxaban" 5 "Warfarin"
label values drug drug
gen ind = "`ii'"
order drug
save oacgraph_`i'_`ii', replace
}
}

foreach ii in prior post{
use ads, clear
ta oac_`ii'_drug oac_indicated if oac_indicated == 0 , matcell(A1)

matrix A = (A1)
matrix list A
clear
svmat A

set obs 5
gen drug = _n
label define drug 1 "Apixaban" 2 "None" 3 "Dabigatran" 4 "Rivaroxaban" 5 "Warfarin"
label values drug drug
gen ind = "`ii'"
replace A1 = 0 if A1 ==.
order drug
save oacgraph_0_`ii', replace
}

forval i = 0/2 {
use oacgraph_`i'_prior, clear
append using oacgraph_`i'_post
append using oacgraph_`i'_prior
sort drug ind
gen drugind = _n
drop if drugind == 3 | drugind == 6 | drugind == 9 | drugind == 12 | drugind == 15
if `i' == 0 | `i' == 1 {

twayway ///
(bar A1 drugind if ind == "prior" , barw(0.8) col(dknavy%90)) ///
(bar A1 drugind if ind == "post", barw(0.8) col(red%90)), ///
graphregion(color(white)) ///
yscale(range(0,150)) ylabel(0 "0" 20 "20" 40 "40" 60 "60" 80 "80" 100 "100" 120 "120" 140 "140"
> 160 "160") ytitle("Number of people using anticoagulants") ///
xtitle("") xlabel(1.5 "Apixaban" 4.5 "None" 7.5 "Rivaroxaban" 10.5 "Dabigatran" 13.5 "Warfarin") //
> /
legend(order(2 "Pre-RAAF" 1 "Post-RAAF") ring(0) position(12) region(lcolor(white) color(none))) tit
> le("CHADSVA score of `i'")

graph save "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\fig_oac_
> `i'.gph", replace
}

else {

twayway ///
(bar A1 drugind if ind == "prior" , barw(0.8) col(dknavy%90)) ///
(bar A1 drugind if ind == "post", barw(0.8) col(red%90)), ///
graphregion(color(white)) ///
yscale(range(0,150)) ylabel(0 "0" 20 "20" 40 "40" 60 "60" 80 "80" 100 "100" 120 "120" 140 "140"
> 160 "160") ytitle("Number of people using anticoagulants") ///
xtitle("") xlabel(1.5 "Apixaban" 4.5 "None" 7.5 "Rivaroxaban" 10.5 "Dabigatran" 13.5 "Warfarin") //
> /
legend(order(2 "Pre-RAAF" 1 "Post-RAAF") ring(0) position(12) region(lcolor(white) color(none))) tit
> le("CHADSVA score of 2 or greater")

graph save "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\fig_oac_
> `i'.gph", replace
}
}

```

```

*Total OAC use graph
use ads, clear

ta oac_prior_binary if oac_indicated == 0 & oac_prior_binary == "Yes", matcell(A1)
ta oac_prior_binary if oac_indicated == 1 & oac_prior_binary == "Yes", matcell(A2)
ta oac_prior_binary if oac_indicated == 2 & oac_prior_binary == "Yes", matcell(A3)
ta oac_post_binary if oac_indicated == 0 & oac_post_binary == "Yes", matcell(A4)
ta oac_post_binary if oac_indicated == 1 & oac_post_binary == "Yes", matcell(A5)
ta oac_post_binary if oac_indicated == 2 & oac_post_binary == "Yes", matcell(A6)
ta oac_indicated, matcell(A7)

matrix A = (A1\A2\A3\A4\A5\A6)
matrix B = (A7\A7)
matrix A = (A,B)

matrix list A
clear
svmat A

gen As = A1/A2*100
gen A = round(As, 1)
keep A
gen time = 0
replace time = 1 if _n > 3
gen cv = 3
replace cv = 2 if _n == 2 | _n == 5
replace cv = 1 if _n == 1 | _n == 4
label define cv 1 "0" 2 "1" 3 "2 or greater"
label values cv cv
sort cv time

set obs 8
gen id = _n
replace id = 2.5 if id == 7
replace id = 4.5 if id == 8
sort id
gen timecv = _n
drop if timecv == 3 | timecv == 6
drop id

gen As = string(A)
replace As = As + "%"

twayway ///
(bar A timecv if time == 0 & cv == 1, barw(0.8) col(dknavy%90)) ///
(bar A timecv if time == 1 & cv == 1, barw(0.8) col(red%90)) ///
(bar A timecv if time == 0 & cv == 2, barw(0.8) col(dknavy%90)) ///
(bar A timecv if time == 1 & cv == 2, barw(0.8) col(red%90)) ///
(bar A timecv if time == 0 & cv == 3, barw(0.8) col(dknavy%90)) ///
(bar A timecv if time == 1 & cv == 3, barw(0.8) col(red%90)) ///
(scatter A timecv, m (i) mlabel(As) mlabposition(12) mlabcolor(black)) , ///
graphregion(color(white)) ///
yscale(range(0,100)) ylabel(0 "0" 20 "20" 40 "40" 60 "60" 80 "80" 100 "100" ) ytitle("Percentag
> e of people using anticoagulants") ///
xtitle("") xlabel(1.5 "CHADSVa of 0" 4.5 "CHADSVa of 1" 7.5 "CHADSVa of 2 or greater") ///
legend(order(1 "Pre-RAAF" 2 "Post-RAAF") ring(0) position(12) region(lcolor(white) color(none)))
graph save "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\fig_oac_
> total.gph", replace

```

6.1.4 Anticoagulant appropriateness and risk factors

```

use ads, clear
de
ta oac_indicated
ta oac_app
ta sex
ta age

gen sexbin = 0

```

```

replace sexbin = 1 if sex == "Male"
ta sexbin
ta refsourc
gen refcat = 0
replace refcat = 1 if refsourc == "Emergency Dept"
replace refcat = 2 if refsourc == "External Health Service"
replace refcat = 3 if refsourc == "GP"
replace refcat = 4 if refsourc == "Ward"
ta refcat
logistic oac_app i.sexbin i.age i.refcat

```

6.1.5 Anti-arrythmic use before and after RAAF clinic

```

use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta aa_prior if aa_prior == 1, matcell(A2)
ta bb_prior_class if bb_prior_class == 1, matcell(A3)
ta bb_prior if bb_prior != "none" & bb_prior != "carvedilol", sort matcell(A4)
ta cc_prior_class if cc_prior_class == 1, matcell(A5)
ta cc_prior if cc_prior != "none", sort matcell(A6)
ta flec_prior if flec_prior != "none", matcell(A7)
ta amio_prior if amio_prior != "none", matcell(A8)
ta dig_prior if dig_prior != "none", matcell(A9)

matrix A = (A1\A2\A3\A4\A5\A6\A7\A8\A9)
matrix list A
clear
svmat A

egen total = max(A)
gen A2 = string((100 * A1 / total), "%3.1f")+%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "Any anti-arrythmic medication" if _n == 2
replace demo = "Beta blocker" if _n == 3
replace demo = "Metoprolol" if _n == 4
replace demo = "Sotalol" if _n == 5
replace demo = "Atenolol" if _n == 6
replace demo = "Bisoprolol" if _n == 7
replace demo = "Nebivolol" if _n == 8
replace demo = "Calcium channel blocker" if _n == 9
replace demo = "Diltiazem" if _n == 10
replace demo = "Verapamil" if _n == 11
replace demo = "Flecainide" if _n == 12
replace demo = "Amiodarone" if _n == 13
replace demo = "Digoxin" if _n == 14

order demo A
keep demo A A1
save aadrugprior, replace

use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta aa_post if aa_post == 1, matcell(A2)
ta bb_post_class if bb_post_class == 1, matcell(A3)
ta bb_post if bb_post != "none" & bb_post != "carvedilol", sort matcell(A4)
ta cc_post_class if cc_post_class == 1, matcell(A5)
ta cc_post if cc_post != "none", sort matcell(A6)
ta flec_post if flec_post != "none", matcell(A7)
ta amio_post if amio_post != "none", matcell(A8)

```

```

ta dig_post if dig_post != "none", matcell(A9)
matrix A = (A1\A2\A3\A4\A5\A6\A7\A8\A9)
matrix list A
clear
svmat A
egen total = max(A)
gen A2 = string((100 * A1 / total), "%3.1f")+%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "Any anti-arrythmic medication" if _n ==2
replace demo = "Beta blocker" if _n == 3
replace demo = "Metoprolol" if _n == 4
replace demo = "Sotalol" if _n == 5
replace demo = "Atenolol" if _n == 6
replace demo = "Bisoprolol" if _n == 7
replace demo = "Nebivolol" if _n == 8
replace demo = "Calcium channel blocker" if _n == 9
replace demo = "Diltiazem" if _n == 10
replace demo = "Verapamil" if _n == 11
replace demo = "Flecainide" if _n == 12
replace demo = "Amiodarone" if _n == 13
replace demo = "Digoxin" if _n == 14

*Need to rearrange beta blockers
gen id = _n
replace id = 7.5 if id == 6
sort id
drop id

order demo A
keep demo A A1
rename (A A1) (Apost A1post)
gen id = _n
merge 1:1 demo using aadrugprior
drop _merge
order demo A Apost A1 A1post
replace Apost = "0" if Apost == ""
replace A1post = 0 if A1post ==.

preserve
drop A Apost id
save aatable, replace
restore

drop A1 A1post
sort id
drop id

save table_drugtotalaa, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> drugtotalaa.xlsx", firstrow(var) replace

*Changes in AA use
use ads, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta aa_change if aa_change != "No", matcell(A2)
ta bb_change if bb_change != "No", matcell(A3)
ta cc_change if cc_change != "No", matcell(A4)
ta flec_change if flec_change != "No", matcell(A5)
ta amio_change if amio_change != "No", matcell(A6)
ta dig_change if dig_change != "No", matcell(A7)
ta dcr_ref if dcr_ref == "yes", matcell(A8)

matrix A = (A1\A2\A3\A4\A5\A6\A7\A8)
matrix list A
clear
svmat A

```

```

egen total = max(A)
gen A2 = string((100 * A1 / total), "%3.1f")+%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1
keep A

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "Any change" if _n == 2
replace demo = "Added" if _n == 3 | _n == 7 | _n == 9 | _n == 10 | _n == 12
replace demo = "Ceased" if _n == 4 | _n == 8 | _n == 11 | _n == 13
replace demo = "Drug change" if _n == 5
replace demo = "Switched to sotalol" if _n == 6
replace demo = "DCR referral" if _n == 14

gen cat = ""
replace cat = "Beta blockers" if _n == 3
replace cat = "Calcium channel blockers" if _n == 7
replace cat = "Flecainide" if _n == 9
replace cat = "Amiodarone" if _n == 10
replace cat = "Digoxin" if _n == 12
replace cat = "Proecdure" if _n == 14
order cat demo A

save table_drugchangeaa, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> drugchangeaa.xlsx", firstrow(var) replace

```

6.1.6 Quality of life outcomes - EQ5D

```

use utility_scores, clear
gen tahelp = 1
ta tahelp, matcell(A1)
ta utility_group, sort matcell(A2)
matrix A = (A1\A2)
matrix li A
clear
svmat A

egen total = max(A1)
gen A2 = string((100 * A1 / total), "%3.1f")+%"
gen A1s = string(A1)
gen A = A1s + " (" + A2 + ")"
replace A = A1s if _n == 1

gen demo = ""
replace demo = "Total with follow up" if _n == 1
replace demo = "Improvement" if _n == 2
replace demo = "Reduction" if _n == 3
replace demo = "No change" if _n == 4

keep demo A
order demo

save table_utilitychange, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> utilitychange.xlsx", firstrow(var) replace

*T-test table for EQ5D change

use utility_scores, clear

ttest utility_post == utility_prior
return li

matrix A = (r(mu_2), r(sd_2), r(mu_1), r(sd_1), r(p), r(t), r(N_1))
clear
svmat A

gen lb1 = (A1 - (A6 * (A2/(sqrt(A7)))))

```



```

gen ub1 = A1 + (A6 * (A2/(sqrt(A7))))
gen lb2 = A3 - (A6 * (A4/(sqrt(A7))))
gen ub2 = A3 + (A6 * (A4/(sqrt(A7))))

foreach i in A1 lb1 ub1 A3 lb2 ub2 A5 {
gen `i`s = string(`i`, "%03.2f")
}

gen prior = A1s + " (" + lb1s + "-" + ub1s + ")"
gen post = A3s + " (" + lb2s + "-" + ub2s + ")"

keep prior post A5s
order prior post A5s

save table_utility_ttest, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> utility_ttest.xlsx", firstrow(var) replace

*Mean difference and 95% CI table

use utility_scores, clear

su utility_diff
return li

matrix A = (r(mean), r(sd), r(N))
clear
svmat A

gen lb = (A1 - (1.96 * (A2/(sqrt(A3)))))
gen ub = (A1 + (1.96 * (A2/(sqrt(A3)))))

foreach i in A1 lb ub {
gen `i`s = string(`i`, "%03.2f")
}

gen diff = A1s + " (" + lbs + "-" + ubs + ")"
keep diff

save table_utility_meandiff, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> utility_meandiff.xlsx", firstrow(var) replace

```

6.1.7 Quality of life outcomes - NPS

```

*NPS table

use ads, clear

bysort urn : keep if _n == 1

gen tahelp = 1

ta tahelp, matcell(A1)
ta tahelp if nps != . , matcell(A2)
ta nps, matcell(A3)

matrix A = (A1\A2\A3)
matrix list A
clear
svmat A
set obs 12
replace A1 = 0 if A1 ==.
gen id = _n
replace id = 3.5 if id == 11
replace id = 4.5 if id == 12
sort id
drop id

egen total = max(A1[2])
gen A2 = A1/total*100
drop total
replace A2 = 100*A1/A1[_n-1] if A2 == 100
gen As = string(A1)
gen Bs = string(A2, "%3.2f")
gen A = As + " (" + Bs + "%)"

```

```

replace A = As if _n == 1 | _n == 2
keep A

gen demo = ""
replace demo = "Total" if _n == 1
replace demo = "Completed NPS follow up" if _n == 2
replace demo = "1" if _n == 3
replace demo = "2" if _n == 4
replace demo = "3" if _n == 5
replace demo = "4" if _n == 6
replace demo = "5" if _n == 7
replace demo = "6" if _n == 8
replace demo = "7" if _n == 9
replace demo = "8" if _n == 10
replace demo = "9" if _n == 11
replace demo = "10" if _n == 12

gen cat = ""
replace cat = "Detractors (scored 1-6)" if _n == 3
replace cat = "Neutral (scored 7-8)" if _n == 9
replace cat = "Promoter (scored 9-10)" if _n == 11
order cat demo A
save table_nps1, replace

use ads, clear
keep if nps != .

bysort urn : keep if _n == 1
su nps, detail
return li

mat A = (r(mean),r(sd))
matrix list A
clear
svmat A
gen As = string(A1, "%3.2f")
gen Bs = string(A2, "%3.2f")
gen A = As + " (" + Bs + ")"
keep A

append using table_nps1
gen id = _n
replace id = 13.5 if _n == 1
sort id
replace demo = "Mean NPS score (standard deviation)" if id == 13.5
order cat demo A
drop id

save table_nps, replace
export excel "C:\Users\acliv1\Dropbox\~ADAM\PhD\4. Project 4 RAAF implementation and ROI\Data\table_
> nps.xlsx", firstrow(var) replace

```

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