

# Using R Studio in matched cohort analysis for evaluation of personal health budgets

Irene Ebyarimpa –Waltham Forest and East London (WEL) CCGs  
NHS-R Community Conference 2020

# Overview/Context

- Personal health budgets (PHBs) are an innovative way of empowering people with long-term conditions to plan their own care.
- Implemented in Tower Hamlets in 2018.
- Personalisation strategy team wanted to evaluate programme to determine impact on health care spend and activity.
- Utilised R Studio to perform evaluation.

## Tower Hamlets leads the way on personal health budgets

04 September 2018



The number of people with a personal health budget (PHB) in Tower Hamlets has risen to 375, the highest in London and 169 more than the next highest performing borough.

# The Problem

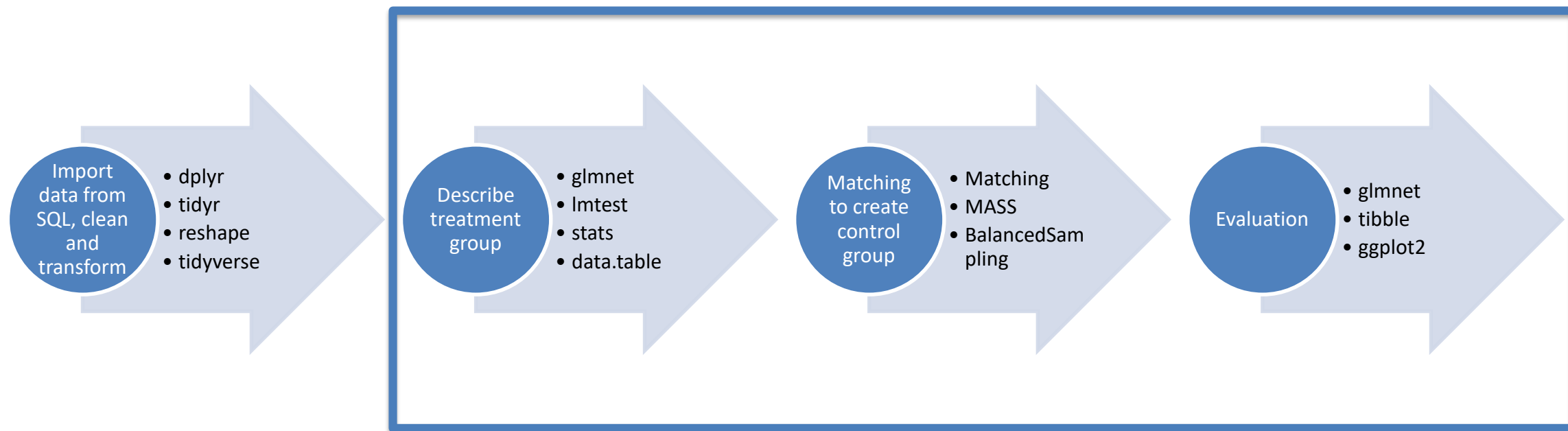
- Received data for a small cohort of individuals that have received PHBs.
  - 68 patients referred to PHB programme with learning disabilities, long term conditions or mental health conditions.
- To determine effectiveness of programme implementation we want to create a control group that have same characteristics as “treatment” group (those receiving PHBs).
  - Allows to control for other programmes or change in health and care system that coincide with personalisation programme.

68  
Control  
Patients

68  
Treatment  
Patients

There are no significant  
differences between treatment  
and control groups

# Using R Studio



# Treatment Group

- Linked patient demographics and characteristics from primary care data to acute datasets.
- Regression analysis to determine significant characteristics of treatment group compared to entire population.
  - Factors identified then used to create control group with same characteristics.

```
## Matching with all long term conditions before refining to those with importance

match_model <- glm(PHB ~ Age + Gender + AdmissionAvoidanceFlag + AFFlag + AnxietyFlag + AsthmaFlag +
  ActiveAsthmaFlag + CancerFlag + CHDFlag + CKDFlag + CoordinatedCareFlag + COPDFlag + COPDPoorMRCFlag
  + DementiaFlag + DepressionFlag + DiabetesFlag + DiabVisImpAmpFlag + DiscretionaryFlag + EpilepsyFlag +
  FallsFlag + FrailtyFlag + HFFlag + HouseboundFlag + HypertensionFlag + LearningDisabilityFlag +
  LiverDiseaseFlag + LowMoodFlag + LTCFlag + MentalHealthFlag + NursingHomeFlag + ObesityFlag +
  OsteoporosisFlag + PADFlag + PalliativeCareFlag + RheumatoidArthritisFlag + RenalFailureFlag +
  ResidentialHomeFlag + SmokingFlag + SmokingCessationFlag + SMIFlag + StrokeFlag +
  SupportedAccommodationFlag + T1DMFlag + T2DMFlag + LifeCourseGroup, Whole_cohort, family =
  binomial())

summary(match_model)

## re-run model with variables that have significance
match_model <- glm(PHB ~ Age + Gender + AsthmaFlag + COPDFlag + DepressionFlag + DiabetesFlag + EpilepsyFlag +
  FallsFlag + LearningDisabilityFlag + LiverDiseaseFlag + LowMoodFlag + HasLTC + MentalHealthFlag +
  ObesityFlag + SmokingFlag + SmokingCessationFlag + SMIFlag + StrokeFlag, Whole_cohort, family =
  binomial())
```

Demographic Factor	Number of Patients
Median Age	49 years
Female	39 (57.4%)
Ethnicity	
White British or Mixed British	31 (45.6%)
Bangladeshi	13 (19.2%)
Other ethnic groups with < 5	24 (35.3%)
Patient cohort	
Learning Disabilities	22 (32.4%)
Mental Health	22 (32.4%)
Long Term Conditions	19 (27.9%)
Other cohort with < 5	5 (7.4%)

# Matching

- P scores from previous regression model used for propensity score matching using “Match” function.
- Each treatment patient is matched to a control with closest propensity score.
- “MatchBalance” function used to evaluate covariate balance before and after matching.

```
## Calculates PScore for matching
Whole_cohort$logitPScores<-log(fitted(match_model)/(1-fitted(match_model)))

Tr=Whole_cohort$PHB
X=Whole_cohort$logitPScores

## Look up match function
## matching
rr<-Match(Tr=Tr,X=X,M=1,ties=FALSE, caliper=0.1, replace=FALSE)
```

Match

*Multivariate and Propensity Score Matching Estimator for Causal Inference*

## Description

Match implements a variety of algorithms for multivariate matching including propensity score, Mahalanobis and inverse variance matching. The function is intended to be used in conjunction with the MatchBalance function which determines the extent to which Match has been able to achieve covariate balance. In order to do propensity score matching, one should estimate the propensity model before calling Match, and then send Match the propensity score to use. Match enables a wide variety of matching options including matching with or without replacement, bias adjustment, different methods for handling ties, exact and caliper matching, and a method for the user to fine tune the matches via a general restriction matrix. Variance estimators include the usual Neyman standard errors, Abadie-Imbens standard errors, and robust variances which do not assume a homogeneous causal effect. The [GenMatch](#) function can be used to *automatically find balance* via a genetic search algorithm which determines the optimal weight to give each covariate.

## Usage

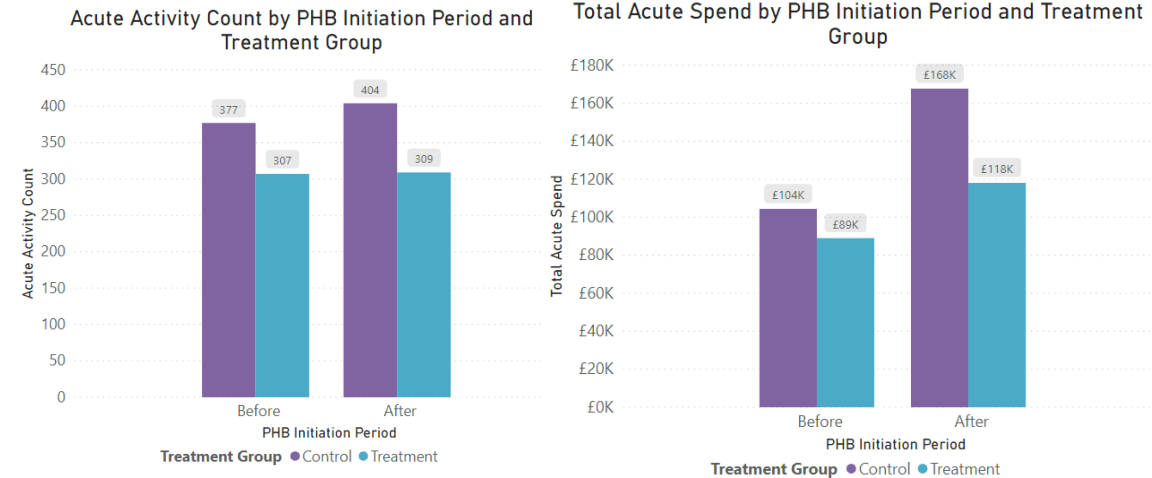
```
Match(Y=NULL, Tr, X, Z = X, V = rep(1, length(Y)), estimand = "ATT", M = 1,
      BiasAdjust = FALSE, exact = NULL, caliper = NULL, replace=TRUE, ties=TRUE,
      CommonSupport=FALSE, Weight = 1, Weight.matrix = NULL, weights = NULL,
      Var.calc = 0, sample = FALSE, restrict=NULL, match.out = NULL,
      distance.tolerance = 1e-05, tolerance=sqrt(.Machine$double.eps),
      version="standard")
```

# Evaluation

- To determine the impact of the personalisation programme, we compare treatment versus control groups and acute activity 12 months before PHBs were initiated to 12 months after PHBs were initiated.
- Negative binomial generalised linear models used to determine difference between treatment and control before and after intervention.

## Results:

- A non-significant increase in acute activity for those with personal health budgets.
- A significant reduction in acute spend for those with personal health budgets compared to a similar cohort of patients without personal health budgets.



```
## Differences in differences
## Difference in spend before and after
TotalAcute[4,4]-TotalAcute[3,4]
TotalAcute[2,4]-TotalAcute[1,4]

## Difference in activity before and after
TotalAcute[4,3]-TotalAcute[2,3]
TotalAcute[3,3]-TotalAcute[1,3]
```

# Thank You

irene.ebyarimpa@nhs.net