NP-complete Problems and Large Datasets: Examples from the `Matching` Package

Jasjeet S. Sekhon

UC Berkeley

The Problem

- The size of datasets is growing fast in the social sciences—e.g., administrative data with millions of observations
- Our methods are becoming computationally intensive: MCMC, genetic optimization, simulating annealing, and **MATCHING**
- These methods are often used for problems whose asymptotic order is exponential: $\mathbf{O}(c^N),\ c > 1$
- We try to turn exponential problems into polynomial time problems:
  - $\mathbf{O}(N^2 log(N))$ for pair matching
  - $\mathbf{O}(N^3 log(N \max(\text{dist})))$ for full matching

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The Limits of Computational Power

- Faster computers will take care of our problems?
- With faster and cheaper computers, it is easier to get more data
- Moore's Law is currently holding because of parallelization–e.g., Core Duo, Cell processor
- Is parallel code worth the effort?
- R was not designed for software development and computationally intensive algorithms—e.g., pass by value
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Example: Matching

- The goal of matching is to make the distribution of observed covariates the same between treatment and control groups
- People measure covariate balance various ways:
  - minimize mean differences of observed confounders across matched treated and control units
  - minimize the discrepancy in QQ-plots across the variables
- The search space of possible matched datasets grows exponentially with N: it's a Traveling Salesman problem

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Propensity Score (pscore)

- The propensity score is:

$$Pr(T_i = 1|X_i) = E(T_i|X_i)$$

- Almost always estimated by logistic regression
- It greatly helps to reduces the difficulty of the matching problem.
- If one matches on and balances the propensity score, one balances the confounders X of concern.
- Balance: to make the distributions the same between treatment and control groups
- Multidimensional covariate balance is difficult to measure

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Searching for the Correct Propensity Score Model

- People use methods to simplify the problem of searching for the best set of matches: propensity score (pscore)
- This simplification turns the problem into a polynomial time problem: $\mathbf{O}(N^2 log(N))$ for pair matching
- How do we know what is the correct propensity score model?
- Matching on the "correct" pscore obtains covariate balance–it's a tautology!
- Trail-and-error specification search for the best pscore
- number of possible matched datasets grows exponentially with N.
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Genetic Matching (GenMatch)

Genetic matching is a new general method for performing multivariate matching. GenMatch:

- algorithmically maximizes the balance of observed potential confounders across matched treated and control units
- uses the pscore (if one has one) and weights covariates so that balance is maximized
- uses an evolutionary search algorithm to determine the weight each covariate is given
- genetic algorithm developed by Sekhon and Mebane (1998) is used.

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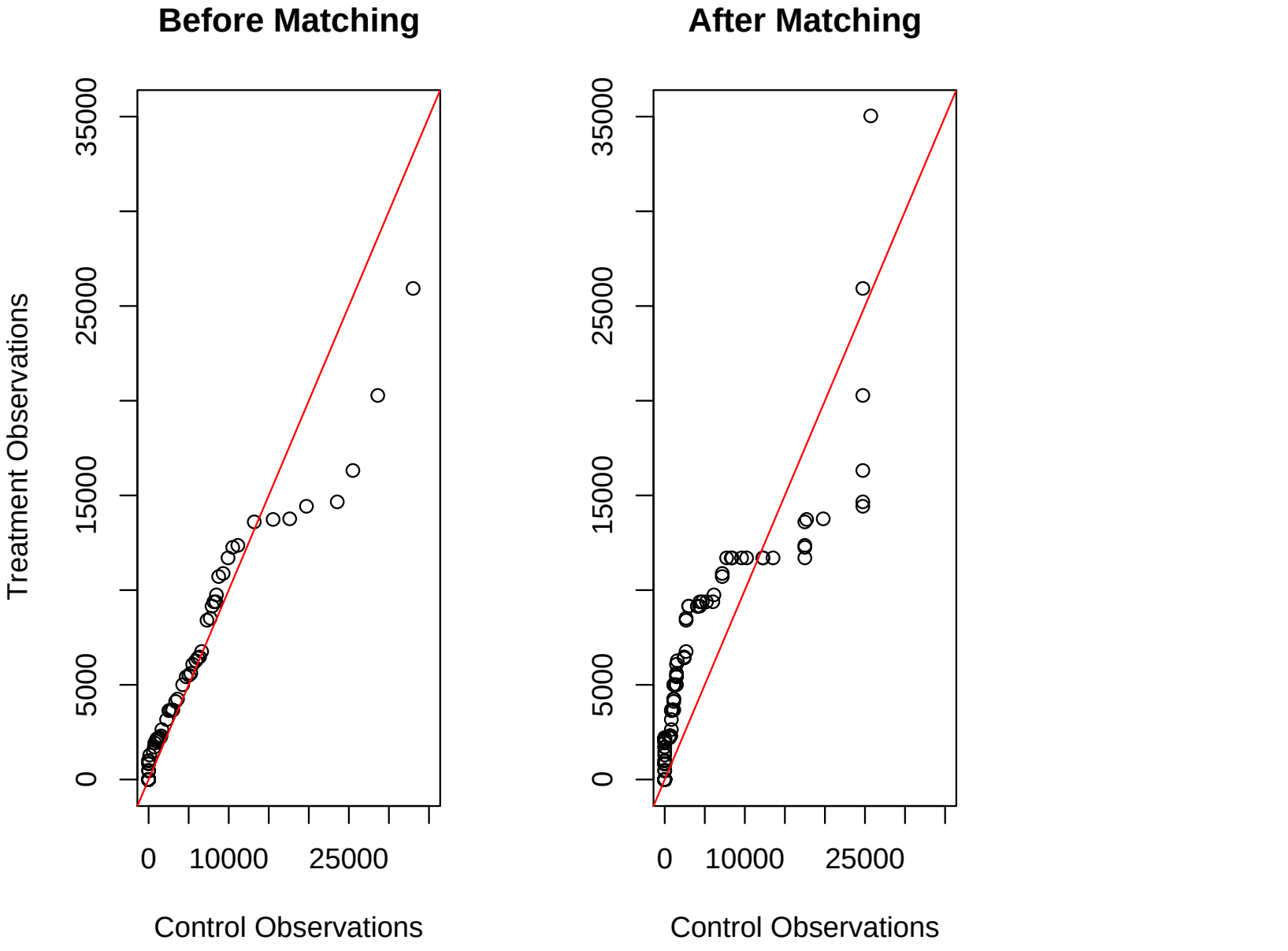
Pscore Matching Example

```
library(Matching)
data(lalonde)

Y  <- lalonde$re78   #the outcome of interest
Tr <- lalonde$treat  #the treatment of interest

# pscore model
glm1  <- glm(treat~age + educ + black +
             hisp + married + nodegr + re74  + re75,
             family=binomial, data=lalonde)

# Matching
rr1  <- Match(Y=Y, Tr=Tr, X=glm1$fitted)
```

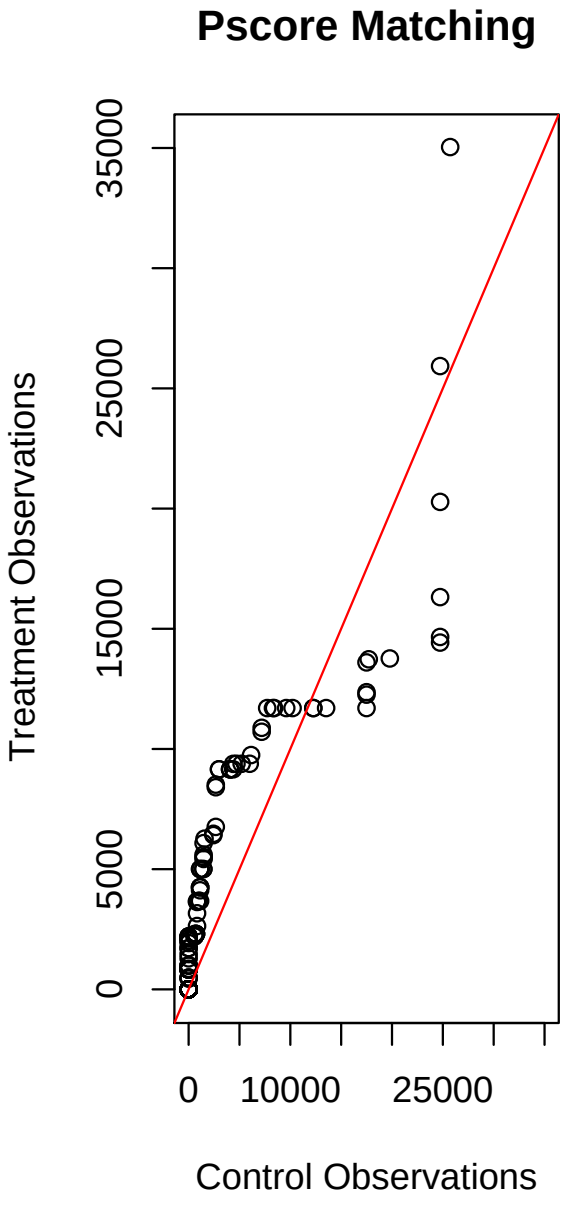
QQ Plot of Before and After Pscore Matching

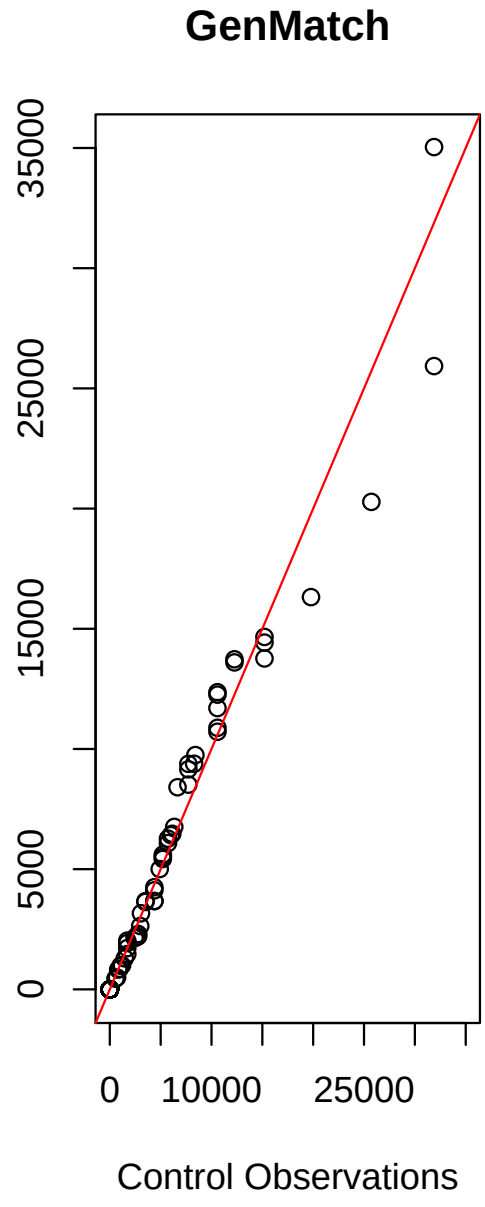


GenMatch Matching Example

```
X  <- cbind(age, educ, black, hisp, married, nodegr,
            re74, re75, u74, u75)

BalanceMatrix <- cbind(age, I(age^2), educ, I(educ^2),
                  black, hisp, married, nodegr, re74 ,
                  I(re74^2), re75, I(re75^2), u74, u75,
                  I(re74*re75), I(age*nodegr),
                  I(educ*re74), I(educ*re75))

gen1 <- GenMatch(Tr=Tr, X=X,
                  BalanceMatrix=BalanceMatrix)

mgen1 <- Match(Y=Y, Tr=Tr, X=X, Weight.matrix=gen1)
```

QQ Plot of Pscore and GenMatch





Properties of Matching Algorithms

- When can matching confounders make bias worse? e.g., what if the propensity score model is incorrect?
- All affinely invariant matching methods have the Equal Percent Bias Reduction (EPBR) property under some conditions.
- If X are distributed with ellipsoidal distributions, then the EPBR property holds for affinely invariant matching methods (Rubin and Thomas 1992).
- There is an extension to a restricted class of mixtures (Rubin and Stuart 2006): discriminant mixtures of proportional ellipsoidally symmetric distributions.

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Equal Percent Bias Reduction (EPBR)

- Let Z be the expected value of X in the matched control group. Then we say that a matching procedure is EPBR if

$$E(X|T=1) - Z \quad = \gamma \{E(X|T=1) - E(X|T=0)\}$$

  for a scalar $0 \leq \gamma \leq 1$.
- We say that a matching method is EPBR for X because the percent reduction in the mean biases for each of the matching variables is the same.
- In general, if a matching method is not EPBR, then the bias for some linear function of X is increased.
- We may care about nonlinear functions of X.

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Genetic Matching Computationally Intensive

- Raessler and Rubin (2005) use GenMatch for a dataset with over 2 million observations
- Political get-out-the-vote databases also have millions of observations
- Marketing data has millions of observations and thousands of covariates
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To Optimize the Software

- Computationally intensive functions are written in C/C++
- Parallelize the outer loop and vectorize the inner loop
- Extensive use of BLAS and Lapack libraries
- The GenMatch function is parallelized, it can make use of multiple CPUs or nodes via the snow package: simple network of workstations
- Parallel execution is tricky: unexpected bottlenecks such as a cache-bottleneck when executing SSE3 instructions via BLAS
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Using Multiple Computer Chips to Run `GenMatch`

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1780 Observations				
run time (seconds)	2557	1372	950	749
x CPU/1 CPU run time		0.54	0.37	0.29
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- Memory allocation issue: malloc
- OS X malloc makes system call at 15KB while Linux does at 256KB.
- On OS X, more page faults
- Rewrite functions to make fewer malloc calls (at the cost of more memory usage). Apple's OS X performance group helped with this.
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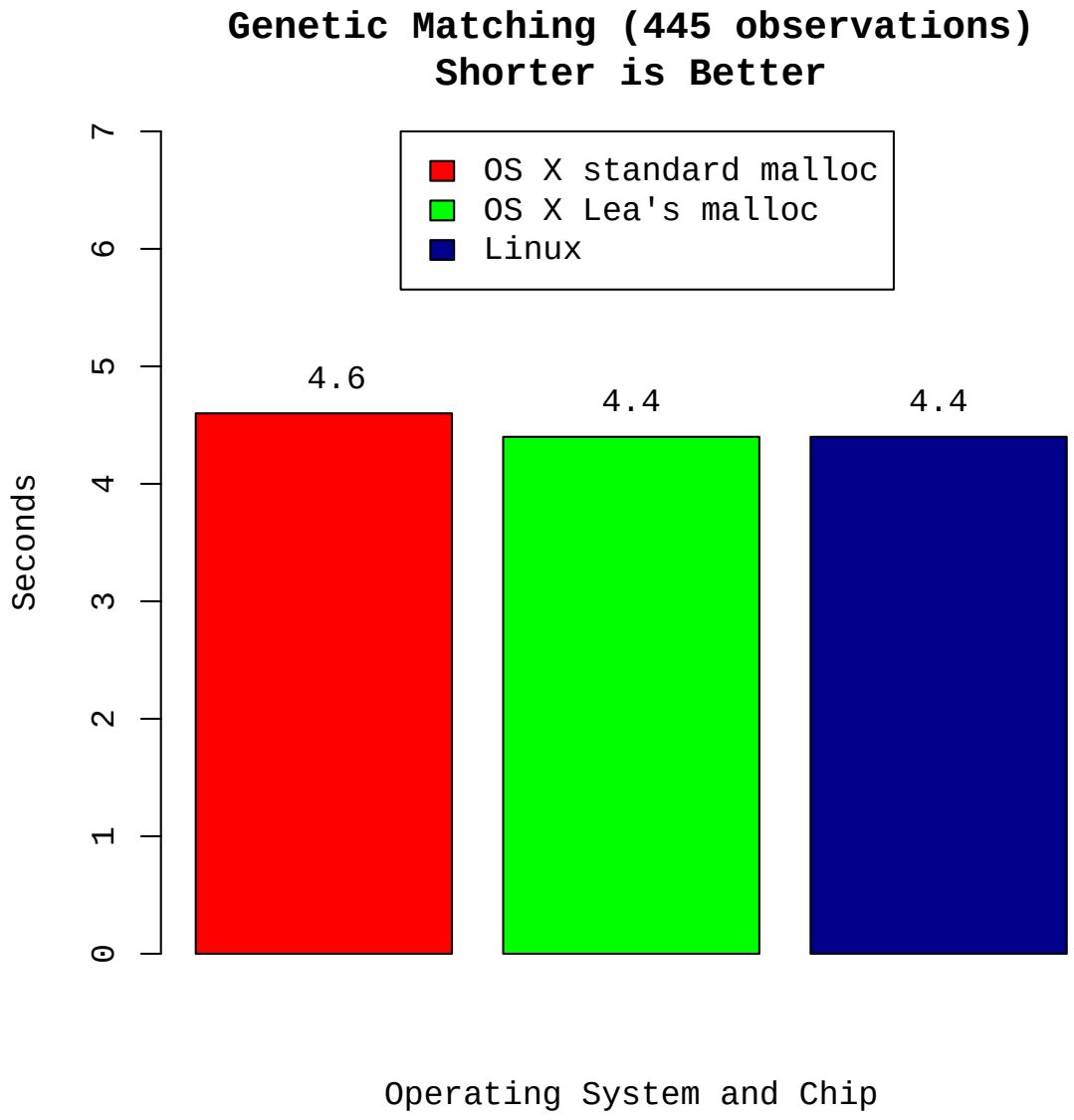

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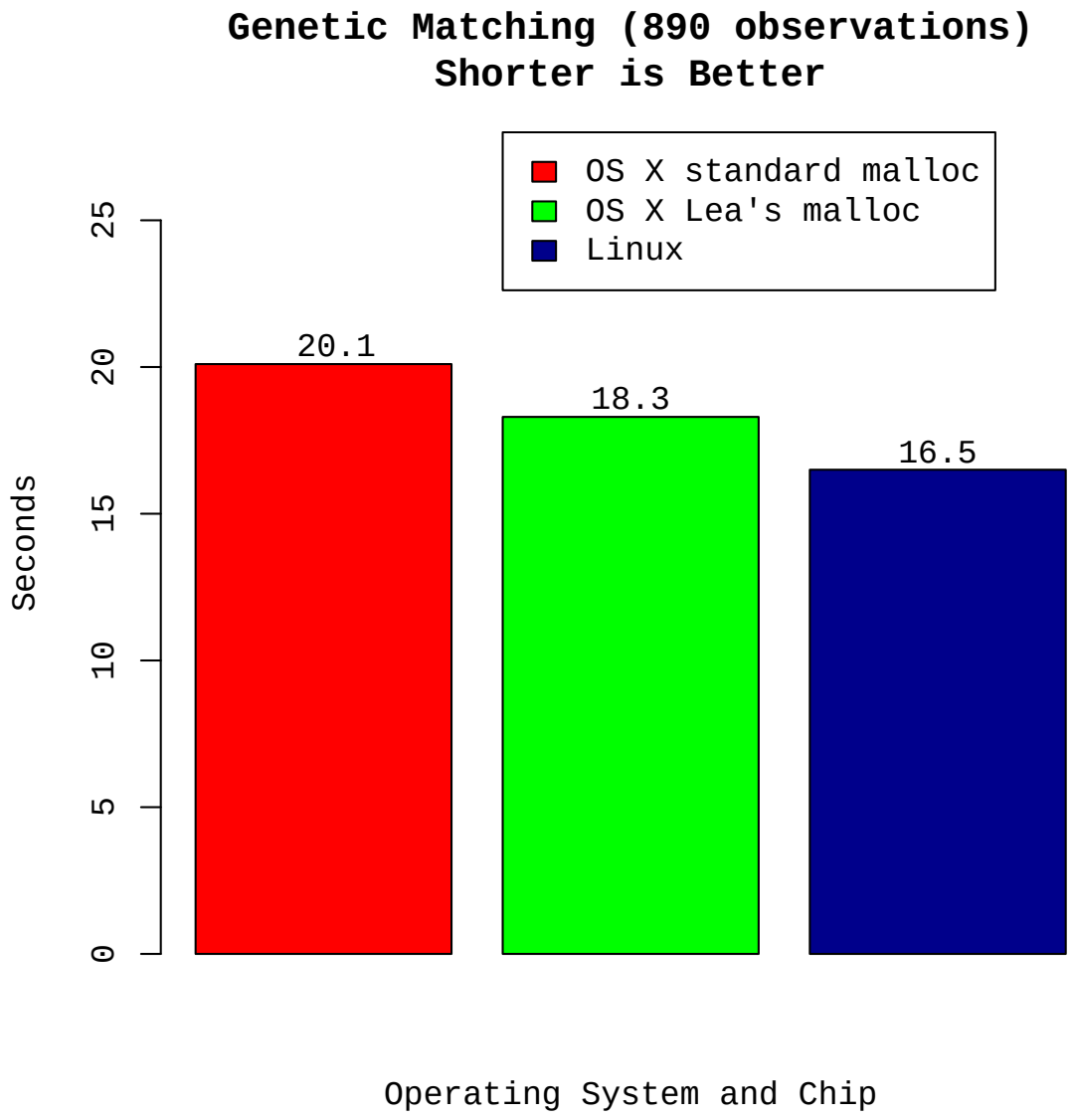

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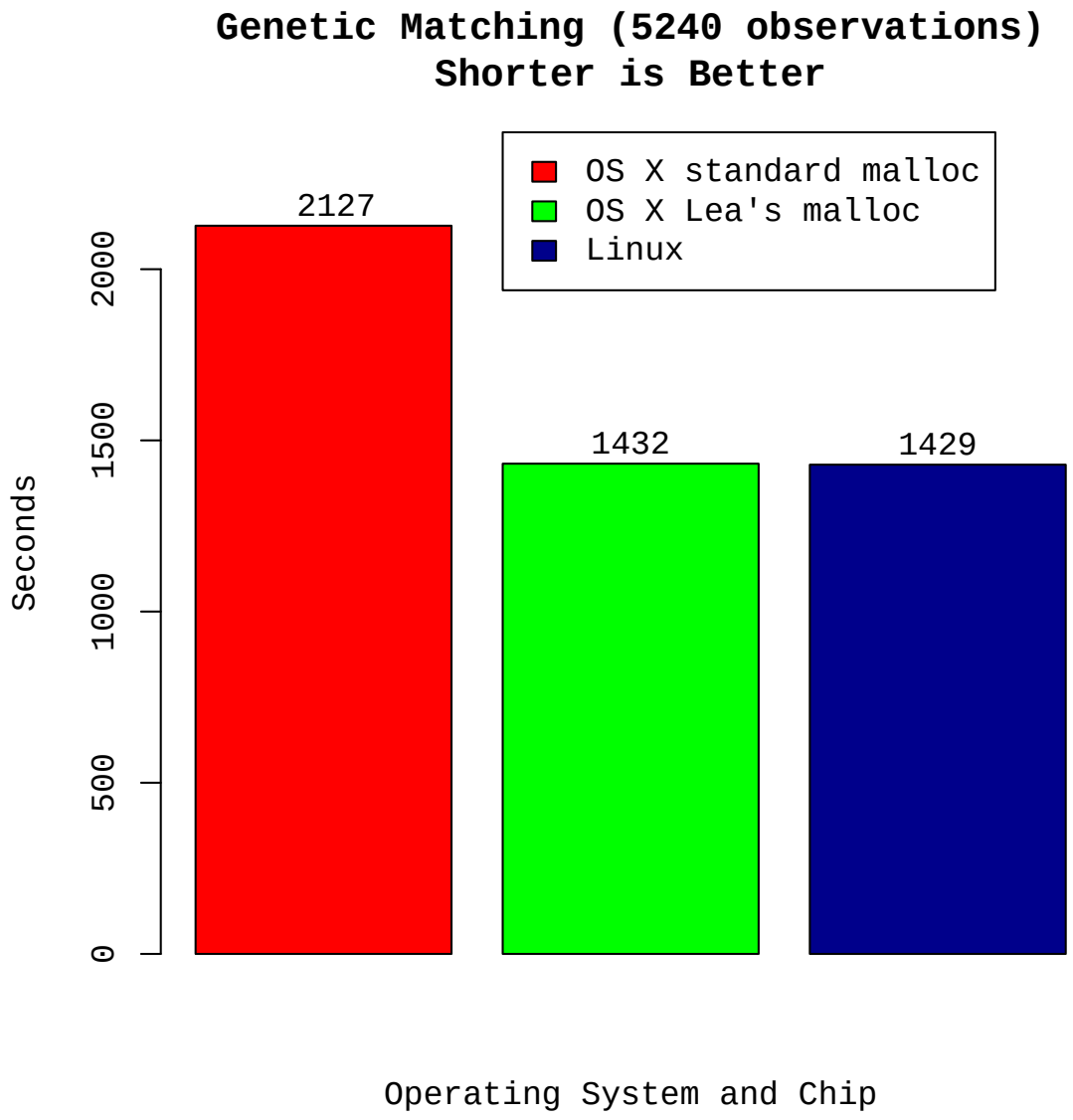

Quantum Computing

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Until Quantum Computing

- Parallel computing and vectorization
- Block-algorithms: the Matchby function
- A wide variety of matching procedures are supported, and in the future `optmatch` will be also
- Design issue for R:
  - The malloc problem impacts BLAS performance
  - Block-algorithms: R interface with SQL
  - Software engineering support...offload this to Parrot/JAVA?
  - Support to extend R internally is needed
- Software available at `http://SEKHON.BERKELEY.EDU` and on CRAN

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  - Support to extend R internally is needed
- Software available at `http://SEKHON.BERKELEY.EDU` and on CRAN

Until Quantum Computing

- Parallel computing and vectorization
- Block-algorithms: the Matchby function
- A wide variety of matching procedures are supported, and in the future `optmatch` will be also
- Design issue for R:
  - The malloc problem impacts BLAS performance
  - Block-algorithms: R interface with SQL
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Mahalanobis Distance

- The most common method of multivariate matching is based on the Mahalanobis distance. The Mahalanobis distance measure between any two column vectors is defined as:

$$md(X_i, X_j) = \left\{(X_i - X_j)' S^{-1} (X_i - X_j)\right\}^{\frac{1}{2}}$$

  where X_i and X_j are two different observations and S is the sample covariance matrix of X.
- Mahalanobis distance is an appropriate distance measure if each covariate has an elliptic distribution whose shape is common between treatment and control groups (Mitchell and Krzanowski 1985, 1989).
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More General Method of Measuring Distance

- A more general way to measure distance is defined by:

$$d(X_i, X_j) = \left\{ (X_i - X_j)' \left(S^{-1/2}\right)' W S^{-1/2} (X_i - X_j) \right\}^{\frac{1}{2}}$$

  where W is a $k \times k$ positive definite weight matrix and $S^{1/2}$ is the Cholesky decomposition of S which is the variance-covariance matrix of X.
- All elements of W are zero except down the main diagonal. The main diagonal consists of k parameters which must be chosen.
- This leaves the problem of choosing the free elements of W. For identification, there are only $k - 1$ free parameters.

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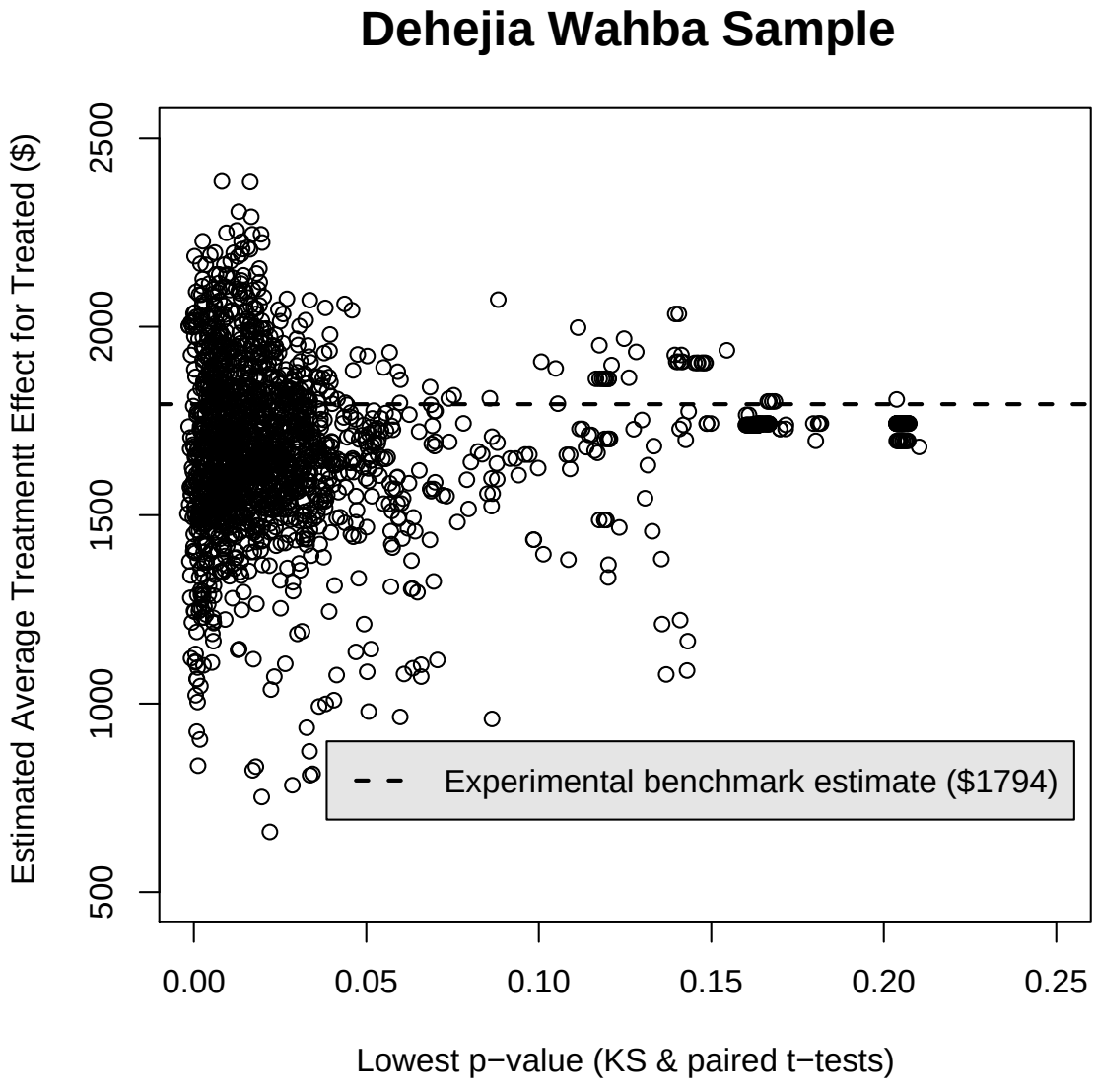
Dehejia Wahba Sample
Estimated Average Treatmentt Effect for Treated ($)
500
1000
1500
2000
2500
0.00
0.05
0.10
0.15
0.20
0.25
Lowest p−value (KS & paired t−tests)
Experimental benchmark estimate ($1794)

Parameterization

- GenMatch uses the propensity score if it is known or if it can be estimated.
- The propensity score is estimated and its linear predictor, $\hat{\mu}$, is matched upon along with the covariates X once they have been adjusted so as to be uncorrelated with the linear predictor.
- Combining is good because:
  - Propensity score matching is good at minimizing the discrepancy along the propensity score
  - Mahalanobis distance is good at minimizing the distance between individual coordinates of X (orthogonal to the propensity score) (Rosenbaum and Rubin 1985).

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  - minimize the largest discrepancy
  - minimize the mean or median discrepancy
  - minimize some other quantile
  - restrict the above to only uniformly improving moves
- By default, the algorithm attempts to minimize the largest discrepancy at every step (minimizing the infinity norm).
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- There are many different ways of measuring balance and I cannot summarize the vast literature here.
- The choice of balance statistics will be domain specific. E.g., use randomization inference if you can as Bowers and Hansen (2005) do.
- But the measures should be sensitive to different departures from balance.
- It is important the maximum discrepancy be small. "*p*-values" conventionally understood to signal balance (e.g., 0.10) are often too low to produce reliable estimates.
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Measures of Balance

- Algorithm uses cumulative probability distribution functions of a variety of standardized statistics which are often thought to be test statistics
- Formal hypothesis tests of balance should not be conducted because no measure of balance is a monotonic function of bias and because balance should be optimized without limit.
- However, descriptive measures of discrepancy ignore information related to bias
- By default, *t*-tests for the difference of means and nonparametric bootstrap Kolmogorov-Smirnov distributional test statistics are used.
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- The malloc problem effects system BLAS performance
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