**Summary of Balance for All Data:**

| | Means Treated | Means Control | Std. Mean Diff. | Var. Ratio | eCDF Mean | eCDF Max |
|---|---|---|---|---|---|---|
| distance | 0.544 | 0.276 | 1.077 | 1.62 | 0.301 | 0.462 |
| i.age | 40.51 | 39.628 | 0.096 | 1.141 | 0.037 | 0.109 |
| i.sex | 0.769 | 0.657 | 0.266 | . | 0.112 | 0.112 |
| i.educ | 4.548 | 4.983 | -0.406 | 1.516 | 0.072 | 0.252 |
| i.insu | 1.481 | 1.477 | 0.004 | 1.262 | 0.017 | 0.041 |
| i.drug | 0.99 | 0.977 | 0.14 | . | 0.014 | 0.014 |
| i.seve | 2.76 | 2.529 | 0.263 | 0.858 | 0.058 | 0.09 |
| com.t | 2.933 | 1.715 | 0.81 | 1.526 | 0.135 | 0.381 |
| pcs.sd | 41.311 | 48.274 | -0.665 | 1.309 | 0.204 | 0.377 |
| mcs.sd | 48.852 | 48.429 | 0.043 | 0.99 | 0.02 | 0.059 |

**Summary of Balance for Matched Data:**

| | Means Treated | Means Control | Std. Mean Diff. | Var. Ratio | eCDF Mean | eCDF Max | Pair Dist. |
|---|---|---|---|---|---|---|---|
| distance | 0.544 | 0.384 | 0.641 | 1.913 | 0.142 | 0.375 | 0.642 |
| i.age | 40.51 | 40.635 | -0.014 | 1.224 | 0.03 | 0.087 | 1.114 |
| i.sex | 0.769 | 0.731 | 0.091 | . | 0.038 | 0.038 | 0.913 |
| i.educ | 4.548 | 4.779 | -0.216 | 1.371 | 0.042 | 0.163 | 0.917 |
| i.insu | 1.481 | 1.346 | 0.138 | 2.756 | 0.026 | 0.048 | 0.651 |
| i.drug | 0.99 | 1 | -0.099 | . | 0.01 | 0.01 | 0.099 |
| i.seve | 2.76 | 2.615 | 0.165 | 0.801 | 0.036 | 0.077 | 1.197 |
| com.t | 2.933 | 2.163 | 0.512 | 1.399 | 0.085 | 0.25 | 0.717 |
| pcs.sd | 41.311 | 45.471 | -0.397 | 1.254 | 0.116 | 0.24 | 0.929 |
| mcs.sd | 48.852 | 49.772 | -0.094 | 1.226 | 0.027 | 0.087 | 1.023 |

**Sample sizes**

| | Control | Treated |
|---|---|---|
| All | 172 | 104 |
| Matched | 104 | 104 |
| Unmatched | 68 | 0 |
| Discarded | 0 | 0 |

**Propensity score distributions of unmatched and matched samples**

| | n | mean | sd | median | trimmed | mad | min | max | range |
|---|---|---|---|---|---|---|---|---|---|
| Unmatched | 68 | 0.11 | 0.04 | 0.11 | 0.11 | 0.05 | 0.03 | 0.17 | 0.14 |
| Matched | 208 | 0.46 | 0.23 | 0.43 | 0.45 | 0.26 | 0.1 | 0.99 | 0.89 |
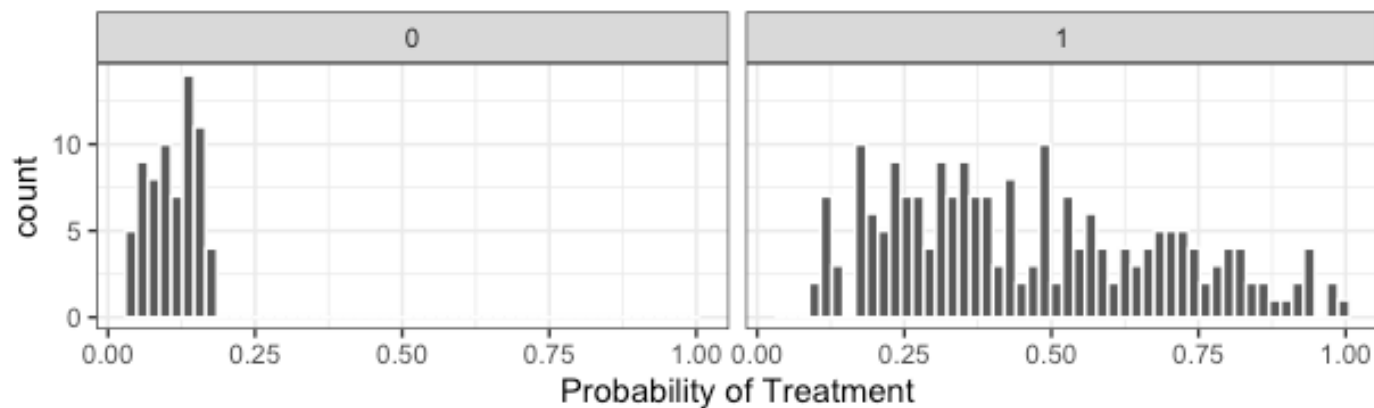
Note: 0=unmatched sample; 1=matched sample

```
> summary(lm_treat1)
Call:
lm(formula = i.aqoc ~ pg, data = dta_m)
```

**Coefficients:**

|             | Estimate | Std. Error | t value | Pr(>\|t\|) |
|-------------|----------|------------|---------|-----------|
| (Intercept) | 0.6346   | 0.0443     | 14.3    | <2e-16    |
| pg          | 0.1442   | 0.0626     | 2.3     | 0.022     |

---
Residual standard error: 0.452 on 206 degrees of freedom
Multiple R-squared: 0.0251,     Adjusted R-squared: 0.0204
F-statistic: 5.3 on 1 and 206 DF    p-value: 0.0223