Lab-Test

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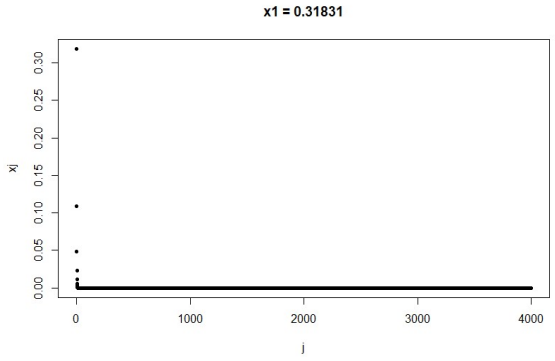
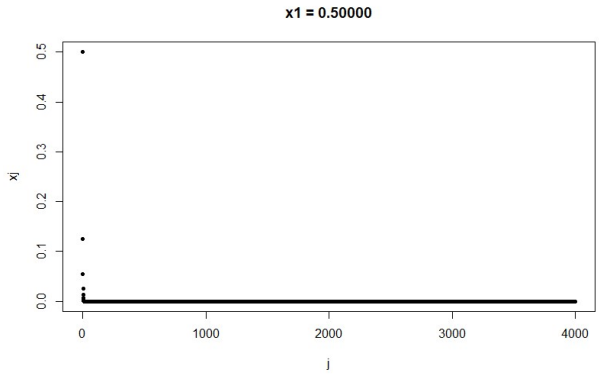
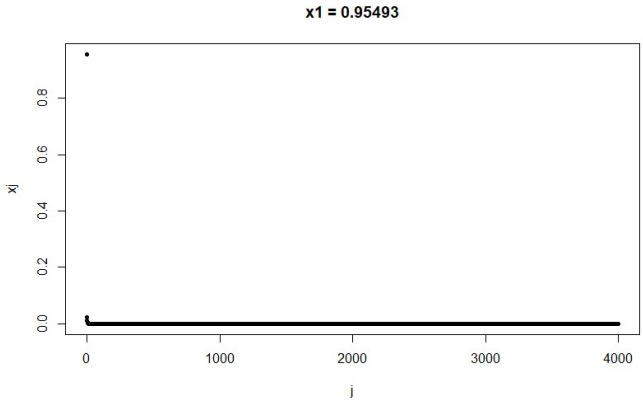
1.

b) For all the values of x_1, the sequences converge to zero.

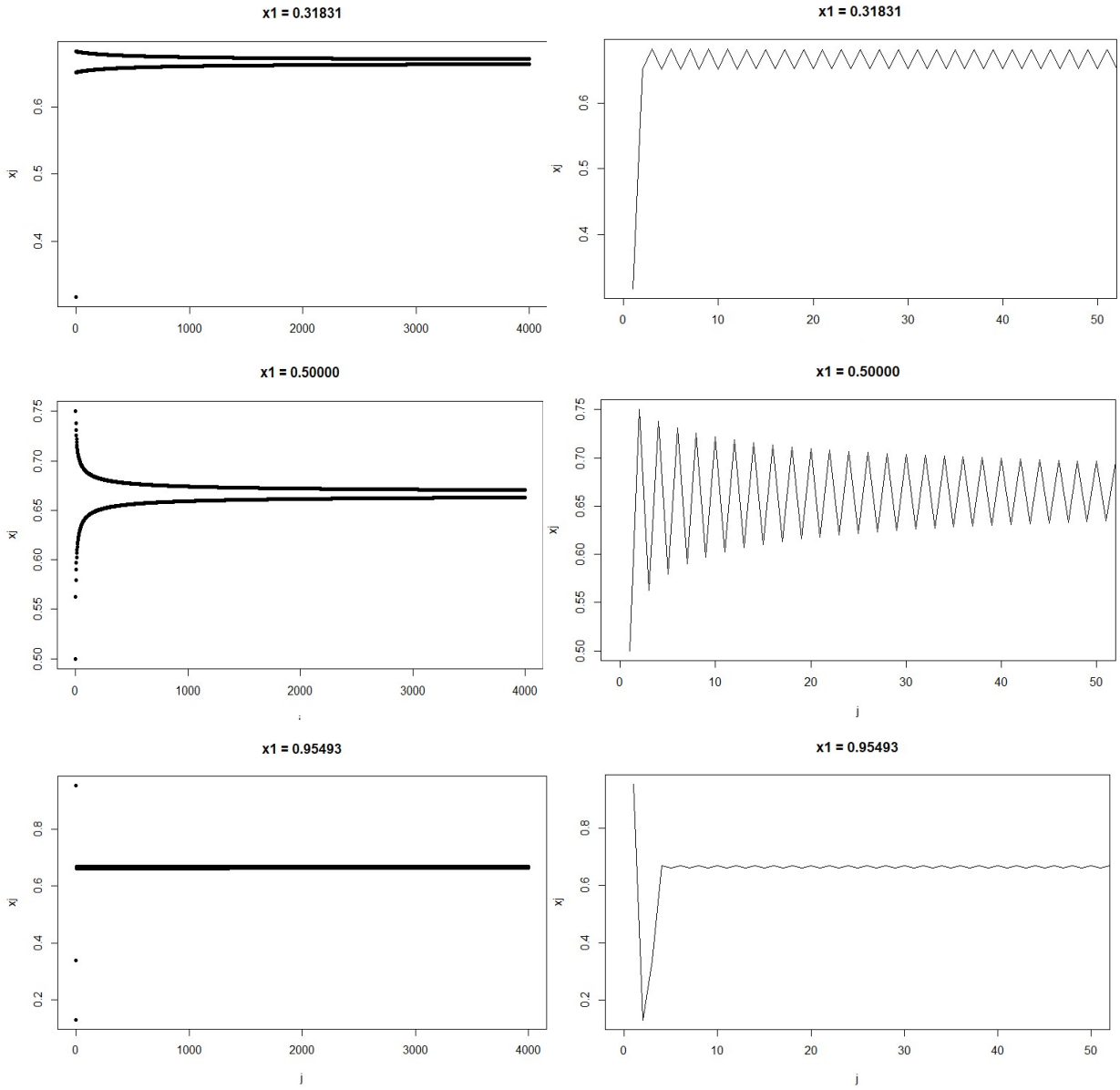






The plots show that the sequence converges to zero very quickly.

c) For r=3, the sequences seem to converge to a different point while also oscillating.



The sequence is called a logistic map and for values r>3.5, the sequence seems to show chaotic behaviour.

2.

a) Used the algorithm given in the lecture slides, full implementation in R-code.

Generating one sample (repeat 100000 times for the question given).

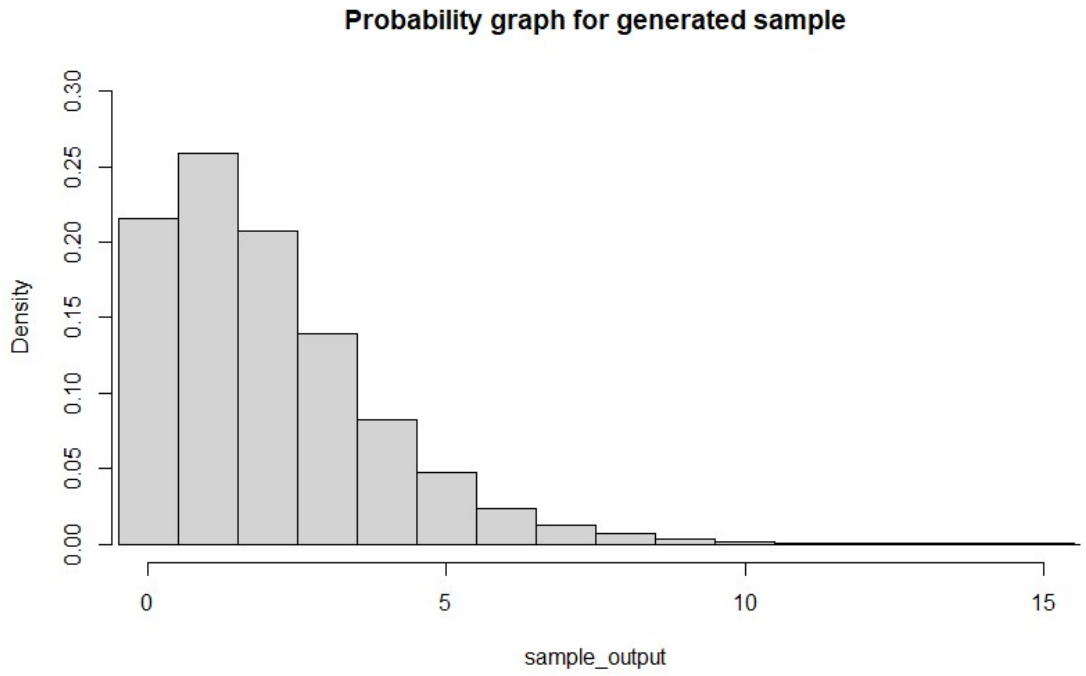
U ~ U (0,1)

X <- 0

while (F(X) < U) {X <- X + 1}

Using sample function would be faster if allowed to be used.

b) Mean=1.99993



c) P values from i =0 to 10 are given below in order.

0.21604, 0.25849, 0.20757, 0.13917, 0.08278, 0.04725, 0.02347, 0.01273, 0.00665, 0.00302, 0.00140

3.

a)

```
> print(model$coefficients)
          (Intercept)                   age               anaemia  creatinine_phosphokinase              diabetes
         1.018493e+01          4.741907e-02         -7.470452e-03          2.222294e-04          1.451498e-01
    ejection_fraction  high_blood_pressure             platelets       serum_creatinine          serum_sodium
        -7.666250e-02         -1.026794e-01         -1.199624e-06          6.660933e-01         -6.698107e-02
                  sex               smoking                  time
        -5.336580e-01         -1.349222e-02         -2.104463e-02
```

Residual deviance: 219.55 on 286 degrees of freedom.

b) For interaction between diabetes and serum_creatinine.

Residual deviance: 217.91 on 285 degrees of freedom.

c) Deviance difference in two models will follow chi-square distribution with df=1.

We get test-statistic=1.6421, p-value=0.20032. Since the p-value is large enough, we can ignore the interaction term and choose common slope.

d) Significant parameters: age, ejection_fraction, serum_creatinine, serum_sodium, time.

e) probability of death = 0.62538, eta = 0.51245

f) Here false negative means prediction is one (i.e., person has died) while true value is zero (person is alive). False -ve rate = 0.03448.