

Homework 4b Submission

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```
In [2]: %load_ext autoreload
%autoreload 2
import numpy as np
from scipy.special import factorial
import pandas as pd
import matplotlib.pyplot as plt
from tqdm import tqdm_notebook
```

The autoreload extension is already loaded. To reload it, use:
%reload_ext autoreload

1.

(a)

i.

$GS_f = \infty$ because the sensitivity is unbounded and so a single point can arbitrarily change the mean.

ii.

$\min_{x \in S} LS_f(x) = \infty$ for the same reasons as above - regardless of any of the other points (i.e. x s.t. we get minimum local sensitivity), a single additional point can arbitrarily change the resulting mean. (For example, to increase the mean by k , the new point should be $\mu_{old} + nk$.)

iii.

$RS_f^H = \frac{b-a}{n}$ because a single point can change only by $b - a$ while remaining in H , and so the average can only change by that divided by n .

iv.

We can construct an explicit Lipschitz extension by simply clipping each point to $[a, b]$ and then taking the mean and adding Laplace noise with sensitivity $\frac{b-a}{n\epsilon}$. This will be increasingly biased as the original data is farther from $[a, b]$, but the sensitivity will remain the same, and on H this agrees with f .

(b)

i.

$GS_f = \infty$ because, for any large N , we can construct a dataset with $\frac{n}{2}$ data points at 0, and $\frac{n}{2}$ datapoints at N , and then shifting a single point from 0 to N shifts the median by N , for any arbitrary N .

ii.

$\min_{x \in S} LS_f(x) = 0$ because if we create a dataset with 3 points at 0, no matter how much we change any single point, the other two will still be 0 and so the median will be unchanged.

iii.

$RS_f^H = b - a$ because every point must fall in $[a, b]$, and so the largest possible change in median would be from a to b . (This example is possible if half the points minus 1 are at a , and the other half are at b , and then we move one from b to a)

(c)

i.

$GS_f = n - 1$ because if every node was previously disconnected (meaning the value was $n - 1$) we can connect a new node to every old node, meaning that now 0 nodes are disconnected.

ii.

$\min_{x \in S} LS_f(x) = 1$ because if every node in the graph is already connected, the addition of a new node cannot disconnect any existing nodes. The most it can do is add a node with no edges. (Note that our definition of node sensitivity in this case is a little weird, because if we're talking about deleting nodes rather than adding, the minimum local sensitivity is actually 0, if all edges exist between all nodes.)

iii.

$RS_f^H = d$ because the greatest change from adding a single node would be that all existing nodes are unconnected, and then a single new node is added that connects to d other nodes. (It can't connect to more than that because it must be in H). Thus the query can only decrease by d .

2.

Below is the R code, reproduced. I'm porting it into Python.

```
In [16]: def nll(w, b, x, y):
          pi = 1/(1 + np.exp(-b - w*x.reshape(-1)))
          llik = y*np.log(pi + 1e-9) + (1-y)*np.log(1e-9 + 1-pi)
          return - llik
```

```
In [96]: def gaussianReleaseNoise(sensitivity, epsilon, delta, size=1):
          scale = sensitivity*np.sqrt(2*np.log(1.25/delta))/epsilon
          noise = np.random.normal(scale=scale, size=size)
          return noise
```

```
In [147]: PUMSdata = pd.read_csv("../data/MaPUMS5full.csv")
          Xpums = (PUMSdata['educ'].values).reshape(-1, 1)
          Ypums = PUMSdata['married'].values
          from sklearn.linear_model import LogisticRegression

          import warnings
          warnings.simplefilter("default")
          lr = LogisticRegression(C=10000).fit(Xpums, Ypums)

          print(f"slope = {lr.coef_[0]}, bias = {lr.intercept_}")
          print(f"likelihood = {nll(lr.coef_[0], lr.intercept_, Xpums, Ypums).mean()}")
          w_true = lr.coef_[0][0]
          b_true = lr.intercept_[0]
```

/home/yonadav/anaconda3/envs/tensorflow/lib/python3.7/site-packages/sklearn/linear_model/logistic.py:433: FutureWarning: Default solver will be changed to 'lbfgs' in 0.22. Specify a solver to silence this warning.

FutureWarning)

```
slope = [0.07828201], bias = [-0.61997557]
likelihood = 0.6821270958807131
```

```
In [148]: def calc_clipped_gradient(X, Y, C, w, b, fun=nll):
          dx = 1e-4
          out1 = fun(w, b, X, Y)
          out2 = fun(w, b + dx, X, Y)
          out3 = fun(w + dx, b, X, Y)
          dw = (out3 - out1)/dx
          db = (out2 - out1)/dx
          dw = np.clip(dw, -C, C)
          db = np.clip(db, -C, C)
          return dw, db
```

```

In [188]: def learn_private_regression(epsilon, X_, Y_, delta=1e-6):
    n = Y_.shape[0]
    batchsize = int(np.sqrt(n))
    steps = int(np.sqrt(n))

    idxs = np.random.permutation(n)
    X = X_[idxs, :]
    Y = Y_[idxs]

    w = 0; b = 0          # starting parameters
    C = 10                 # clipping parameter
    nu_w, nu_b = .0001, .0001 # learning rates

    w_history = [w]
    b_history = [b]

    for i in range(steps):
        batch_start = i*batchsize
        batch_end = min((i + 1)*batchsize, n)
        Xbatch = X[batch_start:batch_end, :]
        Ybatch = Y[batch_start:batch_end]
        dw_clipped, db_clipped = calc_clipped_gradient(Xbatch, Ybatch,
        C, w, b, fun=nll)
        dw_private = dw_clipped + gaussianReleaseNoise(
            sensitivity=2*C, # one sample can shift from -C to C, so d
double sensitivity
            epsilon=epsilon/(2*(batchsize*steps)/n), # two parameters
released, so halve the epsilon for each
            delta=delta,
            size=batchsize,
        )
        db_private = db_clipped + gaussianReleaseNoise(
            sensitivity=2*C, # one sample can shift from -C to C, so d
double sensitivity
            # for each row (constituting its own dataset) we have batc
hsize*steps/n queries, so spread epsilon
            # for that mini-dataset evenly over queries
            # two parameters released, so halve the epsilon for each
            epsilon=epsilon/(2*(batchsize*steps)/n),
            delta=delta,
            size=batchsize,
        )

        dw_private = dw_private.mean(axis=0)
        db_private = db_private.mean(axis=0)
        # update via calculated gradients
        w -= nu_w*dw_private
        b -= nu_b*db_private
        w_history.append(w)
        b_history.append(b)
        if False:
            print(f"w: {w}, b:{b}")
            print(f"Likelihood: {nll(w, b, X, Y).mean()}")
    return w_history, b_history

```

```
In [212]: X, Y = Xpums, Ypums
w_history, b_history = learn_private_regression(.1, X, Y)
w_final, b_final = w_history[-1], b_history[-1]
print(f"w_final: {w_final}, b_final:{b_final}")
print(f"Likelihood: {nll(w_final, b_final, X, Y).mean()}")
```

```
w_final: -0.0906537763390688, b_final:0.10519959855920695
Likelihood: 0.8401312585551419
```

```
In [213]: def accuracy(w, b, X, Y):
          Yhat = 1/(1 + np.exp(-b -w*X.reshape(-1)))
          Yhat = Yhat > 0.5
          return (Yhat == Y).mean()
```

```
In [246]: X, Y = Xpums, Ypums
          trials = 100
          learned_ws = []
          learned_bs = []
          mean_accs = []
          epsilons = np.logspace(-3, 1, 20)
          for eps in tqdm_notebook(epsilons):
              ws = []
              bs = []
              accs = 0
              for t in range(trials):
                  wh, bh = learn_private_regression(eps, X, Y)
                  ws.append(wh[-1])
                  bs.append(bh[-1])
                  accs += accuracy(wh[-1], bh[-1], X, Y)
              mean_accs.append(accs/trials)
              learned_ws.append(ws)
              learned_bs.append(bs)
```

```

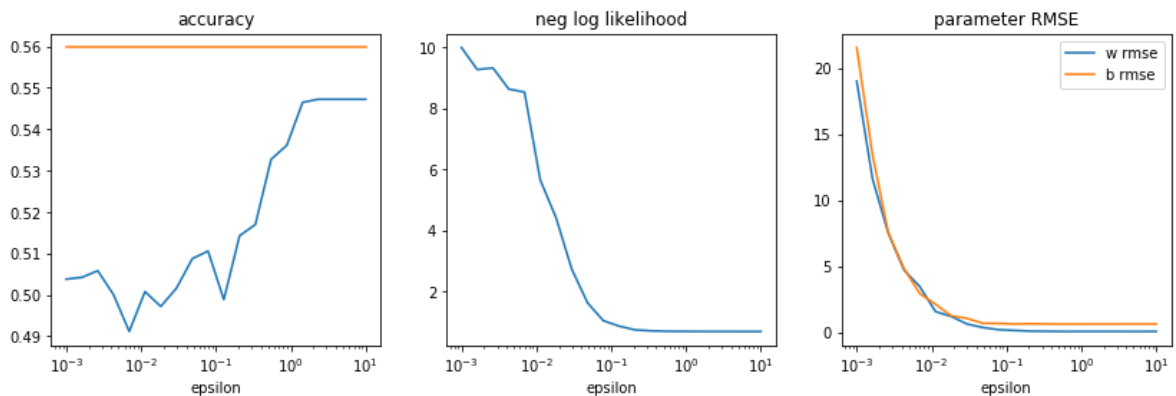
In [248]: plt.figure(figsize=(14, 4))
plt.subplot(1, 3, 1)
plt.title("accuracy")
plt.plot(epsilons, mean_accs)
plt.plot(epsilons, np.ones(epsilons.shape)*accuracy(w_true, b_true, X,
Y))
plt.xlabel("epsilon")
plt.xscale("log")

plt.subplot(1, 3, 3)
plt.title("parameter RMSE")
w_rmse = [np.sqrt(((w_true - np.array(lws))**2).mean(axis=0)) for lws
in learned_ws]
b_rmse = [np.sqrt(((b_true - np.array(lbs))**2).mean(axis=0)) for lbs
in learned_bs]
plt.plot(epsilons, w_rmse, label="w rmse")
plt.plot(epsilons, b_rmse, label="b rmse")
plt.xscale("log")
plt.legend()
plt.xlabel("epsilon")

plt.subplot(1, 3, 2)
plt.title("neg log likelihood")
liks = [np.mean([nll(ws[i], bs[i], X, Y) for i in range(trials)]) for
ws, bs in zip(learned_ws, learned_bs)]
plt.plot(epsilons, liks)
plt.xscale("log")
plt.xlabel("epsilon")

```

Out[248]: Text(0.5, 0, 'epsilon')



As epsilon increases, as we might expect, the accuracy, loss, and learned parameters converge to the true learned parameters.