Problem 5 In [1]: import load helper import pandas as pd import matplotlib.pyplot as plt import numpy as np import importlib from torch import tensor import distributions In [19]: fname = '5.daphne' graph = load helper.graph_helper(fname) %cat 5.daphne (let [m (sample (normal 0 5)) s (sample (uniform-continuous 0.01 (abs m)))] (observe (normal 0 s) 7) In [3]: import bbvi importlib.reload(bbvi) from bbvi import graph bbvi algo12 In [25]: init concentration = tensor(2.) init rate = tensor(1./0.5)d init = distributions.Gamma(concentration, rate) In [27]: q=d init support = np.linspace(1e-6, 10, 100)log pdf = np.zeros like(support) for idx,c in enumerate(support): log pdf[idx] = q.log prob(tensor(c)) pdf = np.exp(log pdf)In [28]: sr = pd.Series(pdf) sr.index = support sr.plot() plt.xlabel('\$X\$') plt.ylabel('\$p(X|Y)\$')plt.title(\ '{} \n initial proposal for s \n'.format(fname) +\ 's \$\sim\$ Gamma' +\ '[concentration={:1.2f}, rate={:1.2f}]'.format(init_concentration,init_rate) Text(0.5, 1.0, '5.daphne \n initial proposal for s \ns \$\\sim\$ Gamma[concentration=2.00, rate=2.00]') Out[28]: 5.daphne initial proposal for s s ~ Gamma[concentration=2.00, rate=2.00] 0.7 0.6 0.5 0.4 0.3 0.1 0.0 10 Х In [7]: %%time T=5000 L=50 1r=0.05 r, logW, sigma = bbvi.graph bbvi algo12(graph,T=T,L=L,lr=lr, init local env={'prior dist':{'sample2':d init}}, do log=False) t=0, Q after step={'sample2': Gamma(concentration: 2.049999952316284, rate: 1.8545866012573242), 'sample1': Nor mal(loc: 0.04999998211860657, scale: 4.993239402770996)} t=500, Q after step={'sample2': Gamma(concentration: 3.5841071605682373, rate: 0.6521859765052795), 'sample1': Normal(loc: -0.03162112832069397, scale: 0.5565510988235474)} t=1000, Q after step={'sample2': Gamma(concentration: 3.9007184505462646, rate: 0.4390002489089966), 'sample1': Normal(loc: -0.01562013104557991, scale: 0.20264212787151337)} t=1500, Q after step={'sample2': Gamma(concentration: 3.9578874111175537, rate: 0.501619815826416), 'sample1': Normal(loc: 0.01076040044426918, scale: 0.15789341926574707)} t=2000, Q after step={'sample2': Gamma(concentration: 4.0830841064453125, rate: 0.509914755821228), 'sample1': Normal(loc: 0.001771264709532261, scale: 0.16390740871429443)} t=2500, Q after step={'sample2': Gamma(concentration: 4.188406944274902, rate: 0.5608922839164734), 'sample1': Normal(loc: -0.026647645980119705, scale: 0.16605576872825623)} $\texttt{t=3000, Q after step=\{'sample2': Gamma(concentration: 4.373668670654297, rate: 0.5812458395957947), 'sample1': all the step={'sample2': Gamma(concentration: 4.373668670654297, rate: 0.58124588395957947), 'sample2': all the step={'sample2': Gamma(concentration: 4.373668670654297, rate: 0.58124588395957947), 'sample2': all the step={'sample2': Gamma(concentration: 4.373668670654297, rate: 0.581245889, rate: 0.581245889, rate: 0.58124589, rate: 0.5812489, rate: 0.5812489,$ Normal(loc: 0.050263628363609314, scale: 0.16615404188632965)} t=3500, Q after step={'sample2': Gamma(concentration: 4.557319164276123, rate: 0.6205235719680786), 'sample1': Normal(loc: 0.0379907488822937, scale: 0.17913062870502472)} t=4000, Q after step={'sample2': Gamma(concentration: 4.736571311950684, rate: 0.6485102772712708), 'sample1': Normal(loc: -0.028357677161693573, scale: 0.16197428107261658)} t=4500, Q after step={'sample2': Gamma(concentration: 4.986073970794678, rate: 0.6990025639533997), 'sample1': Normal(loc: 0.02570241130888462, scale: 0.1748143434524536)} CPU times: user 5min 40s, sys: 904 ms, total: 5min 41s Wall time: 5min 42s In [8]: elbo = logW.mean(1)pd.Series(elbo).plot() plt.xlabel('t') plt.ylabel('ELBO') plt.title(' $\{\}$ \n Best ELBO $\{:1.2f\}$ \n T= $\{\}$ | L= $\{\}$ | Adam, lr= $\{\}$ '.format(fname,elbo.max(),T,L,lr)) Text(0.5, 1.0, '5.daphne \n Best ELBO -11.25 \n T=5000 | L=50 | Adam, lr=0.05 ') Out[8]: 5.daphne Best ELBO -11.25 T=5000 | L=50 | Adam, Ir=0.05 0 -50 -100-150-200-250-300-3501000 2000 3000 4000 5000 In [9]: pd.Series(elbo[-200:]).plot() plt.xlabel('t') plt.ylabel('ELBO') plt.title(' $\{\}$ \n Best ELBO $\{:1.2f\}$ \n T= $\{\}$ | L= $\{\}$ | Adam, lr= $\{\}$ '.format(fname,elbo.max(),T,L,lr)) '5.daphne \n Best ELBO -11.25 \n T=5000 | L=50 | Adam, 1r=0.05 Out[9]: 5.daphne Best ELBO -11.25 T=5000 | L=50 | Adam, lr=0.05 -11.4-11.6-11.8-12.0-12.2-12.4-12.6-12.825 100 125 150 175 200 In [10]: r = np.array(r)probs = np.exp(logW)probs /= probs.sum() posterior_r = (probs * r).sum() $posterior_r2 = (probs * r**2).sum()$ std r = np.sqrt(posterior r2 - posterior r^{**2}) In [11]: print('{} posterior s {:1.3f} | std s {:1.3f}'.format(fname,posterior r,std r)) 5.daphne posterior s 7.494 | std s 4.833 Interestingy we see that the best ELBO is not the final one. The size of the mini match L might affect the fluctuations of the ELBO over t... In [12]: trace = r.flatten() pd.Series(trace).plot() plt.xlabel('time t, sample l') plt.ylabel('s') plt.title('{} \n Trace \n T={} | L={} | Adam, lr={} '.format(fname,T,L,lr)) Text(0.5, 1.0, '5.daphne \n Trace \n T=5000 | L=50 | Adam, 1r=0.05 ') Out[12]: 5.daphne Trace T=5000 | L=50 | Adam, Ir=0.05 40 35 30 25 u 20 15 10 5 0 50000 100000 150000 200000 250000 time t, sample I We can see here the samples in the tails of the posterior. The logW is very small for high s (e.g. 30-40+ range), and so the posterios probability is low in these regions. In [40]: Q = sigma['Q_best_t'] q = Q['sample2'] learned concentration = q.concentration.detach().numpy() learned rate = q.rate.detach().numpy() support = np.linspace(1e-6, 25, 100)log_pdf = np.zeros_like(support) for idx,c in enumerate(support): log pdf[idx] = q.log prob(tensor(c)) pdf = np.exp(log pdf)pdf scaled = pdf / pdf.sum() sr = pd.Series(pdf)sr.index = supportsr.plot() plt.xlabel('\$X\$') plt.ylabel('\$p(X|Y)\$') plt.title(\ '{} \n posterior of s (learned proposal) \n'.format(fname) +\ 's \$\sim\$ Gamma' +\ '[concentration={:1.2f}, rate={:1.2f}]'.format(learned concentration,learned rate) Text(0.5, 1.0, '5.daphne \n posterior of s (learned proposal) \ns \$\\sim\$ Gamma[concentration=3.82, rate=0.5 Out[40]: 1]') 5.daphne posterior of s (learned proposal) s ~ Gamma[concentration=3.82, rate=0.51] 0.12 0.10 0.08 0.06 0.04 0.02 0.00 10 15 20 We can overlay the learned distribion on the empirical (binned) posterior, and compare (taking care to scale appropriately). Outliers with high enough logW in the sampling can shift the proposal. I think that having a different divergence than KL, perhaps that is more robust to outliers, would perhaps mitigate this. In [41]: counts_bins = np.histogram(r.flatten(), weights=probs.flatten(), bins=200) counts, bins = counts_bins[0], counts_bins[1] idxs = (counts > counts.max()*0.005)In [42]: support = bins[1:][idxs] log pdf = np.zeros like(support) for idx,c in enumerate(support): log pdf[idx] = q.log prob(tensor(c)) pdf = np.exp(log pdf)In [84]: fig = plt.figure fig(figsize=(12, 6), dpi=80) axes = plt.bar(bins[1:][idxs],counts[idxs],color='gray',label='Binned logW weighted posterior samples') plt.title('Problem {} \n Importance sampling \n importance sampling weighted counts from proposal'.format(fname plt.ylabel('Counts \$p(X|Y)\$') plt.xlabel('X (s for this model)') = pdf / pdf.sum() #* counts[idxs].max() pdf scaled axes = plt.scatter(support,pdf_scaled,marker='.',zorder=2,color='blue',label='Gamma with learned params (scaled pdf scaled maxmatch = pdf / pdf.max() * counts[idxs].max() axes = plt.scatter(support,pdf scaled maxmatch,marker='.',zorder=3,color='green', label='Gamma with learned par plt.legend(loc='best') <matplotlib.legend.Legend at 0x13776db20> Out[84]: Problem 5.daphne Importance sampling importance sampling weighted counts from proposal Gamma with learned params (scaled to integrate to 1) Gamma with learned params (scaled to match max of binned samples) 0.035 Binned logW weighted posterior samples 0.030 0.025 Counts p(X|Y) 0.020 0.015 0.010 0.005 0.000 5 25 10 20 35 15 30 X (s for this model) We can see how the samples that are outliers, around 15 and 22 push the proposal outward, away from matching the samples around ~2.5-10 In [17]: gamma analytic mean = learned concentration/learned rate print('posterior mean from sampling {:1.3f} \nanalytical mean of Gamma from fit proposal params {:1.3f}'.format posterior mean from sampling 7.494 analytical mean of Gamma from fit proposal params 7.471 In [18]: gamma analytic std = np.sqrt(learned concentration/learned rate**2) gamma analytic mean = learned concentration/learned rate print('posterior std from sampling {:1.3f} \nanalytical std of Gamma from fit proposal params {:1.3f}'.format(s posterior std from sampling 4.833 analytical std of Gamma from fit proposal params 3.823 If we inspect the program, we can reason that the s will be drawn from a uniform distribution with a low of 0.01 and a high of any positive number (abs m), but values given by a normal centred at zero and a spread of std=5. Visually, s is drawn from a bunch of uniforms that are all starting at 0.01 and go further and further out with less and less probability. Thus there will be a hump where many of the samples will be drawn from, and then decreased probability. I chose to propose Gamma for this, since it has a hump, and is supported on the positive real line. Note that there is some probability in the posterior that we have s < 0.01, whereas the true posterior has zero probability here. The parameters of Gamma can learn this, because it has enough flexibility to allow this. The learned posterior has very minimal probability for s < 0.01, and the little it does have is one reason why the elbo doesn't get driven completely to zero. Programatically, we would like to keep track of the support of s form the program, and choose a distribution that matches this and has some flexibility to drive the KL near zero. For instance, in Pyrro, there is an affine beta distribution, where the support is in between high and low, instead of 0 and 1. We could imaging an shifted "Gamma", "Gamma"_shifted = shift + Gamma_unshifted In general, we have to choose a proposal that has enough support for its random variable. The support of the proposal will always be as much or larger than the support of this random variable in the true posterior. Thus in general, BBVI will overestimate the support. See the remarks on this in Stefano Ermon's Probabilistic Graphical Models Winter class (Stanford 2020-21)