Replication Review for Coordinated Exploration in Concurrent Reinforcement Learning

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Abstract

This is a replication attempt for a a paper on seed sampling. Seed sampling is a way to provide a stable and efficient mechanism for exploring the state action space for multi-agent reinforcement learning algorithms. In the replicated paper, 3 exploration methods are compared, using a common multiple agent learning algorithm : Upper Control Bounds, Thompson Sampling, and Seed Sampling. I show that the results for that paper can be replicated and that they are more computationally efficient alternative to Thompson sampling while providing better diversity than UCB methods.

1. Introduction

There are multiple approaches to exploration in single agent settings. These approaches may not always extend well to multiple agent settings. There are 2 single agent methods which have had some success: Upper Control Bound (Auer et al., 2009) and PSRL (Bayesian) methods (Strens, 2000) There have been recent attempts to extend these approaches to multi agent settings.

In this project, I attempt to replicate the findings in (Dimakopoulou & Roy, 2018). In this paper 3 approaches are compared: UCB based multiple agent approaches, Thompson Sampling and seed sampling. Seed sampling is based on the single agent PSRL approach. In the UCB approach, as presented in the paper, the agents do not coordinate directly on exploration. Instead, they maintain a shared prior and at the the beginning of an episode will generate an MDP model using an upper control bound approach. Two agents, for which the shared prior is currently the same, will construct the same MDP and thus will have the same policy for the episode.

In the Thompson sampling approach, at each time step, a potential MDP is constructed on the transitions and/or Rewards, based on posteriors obtained for the priors updated by the transitions/rewards seen up to this point. Each agent then samples independently from the distribution of possible MDPs based on the posteriors to take the next step. In seed sampling, an MDP is constructed at the beginning of each episode, similarly to Thompson sampling, and this is used to generate a policy for the episode. So the main difference between Thompson sampling and seed sampling is that seed sampling samples per episode, and Thompson sampling samples per time step.

The paper presented two types of seed sampling: standard Gaussian seed sampling and Martingalean Gaussian seed sampling. The results for both as presented int the paper were pretty much identical, so I only tried to reproduce the results for the standard Gaussian seed sampling. The difference between seed sampling and Thompson sampling is that seed sampling adds an additional small amount of randomness at the beginning of an episode and then generates a policy for the entire episode, similar to the UCB approach the paper describes.

An important consideration is that, in terms of the paper's construction of the problem, an MDP (could be an approximation) must be solved for all three methods. For UCB and seed sampling, it's done once per episode, for Thompson sampling it's every time step. Every agent creates it's own policy, although that policy could be equal to another agents policy.

Seed sampling gets it's name from the addition of a

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small seed (in the paper the seed is distributed as z_k $Bernoulli(p)$ for the bipolar chain example and z_k $N(0,1)$ for the other problems. A seed is only sampled once per episode. How a seed is incorporated in the MDP sampling is problem specific.

Here is a table which shows how to view the approach of each in terms of how often the MDP is solved and how it achieves (or doesn't achieve) diversity.

Algorithm Family	Diversity?	MDP Solved
UCB	No	Once Per Episode
Thompson Sampling	Yes	Every Timestep
Seed Sampling	Yes	Once Per Episode

Each set of three approaches is tested on three simple problems.

1) A bipolar chain, illustrated in Figure ??, is constructed as $-10 \longleftrightarrow -1 \longleftrightarrow ... \longleftrightarrow -1 \longleftrightarrow 10$. The chain can be reversed. So there are 3 rewards: -10, 10, -1 and 2 actions: left, right. All transitions are deterministic. The -10 and 10 states are also stopping states. Rewards are not noisy in this scenario, but which end has the reward of -10 and which end has the reward of 10 is random (Bernoulli, as above.) If a single agent hits either the -10 reward or the 10 reward, it is assumed that is known instantly by all agents, which will use the policy for the true MDP after that.

Here is an image from the paper showing a bipolar chain:

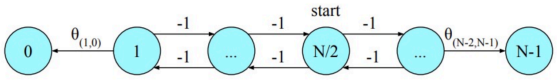

Figure 1. Graph of Bipolar Chain Example.

2) Parallel chains, illustrated in Figure 2, are constructed as a a set of singly linked lists with a common node at one end. All nodes have 0 rewards except the the end nodes. Those have rewards that are distributed as $N(0, 100 + c)$ where c is a unique integer in 1 .. # of nodes. So, you could sort them to have rewards of $N(0, 101)$, $N(0, 102)$ ... I didn't sort them to have more generalizable results. The actual reward obtained is a noisy (distributed normally) sample from the reward for the node. The same chains are used for an entire run for all algorithms, but a new set of chains and rewards are sampled for each run. All transitions are deterministic.

Here is an image from the paper showing a set of parallel chains:

3) Maximum reward path. This is constructed as a graph with nodes connected with probability p and rewards that are normally distributed. For the purposes of the example in the paper, rewards are distributed as $lnr_e|\theta_e$ $N(ln\theta_e - \sigma^2/2, \sigma^2)$. The graph sample structure itself is an Erdõs-Rényi graph with N =100 and probability of an edge $p = 2\frac{lnN}{N}$ Rewards are noisy, similarly to parallel chains, but with a slightly different normal distribution. Transitions between nodes, once a graph has been sampled, are deterministic. The agent doesn't know the structure of the graph a priori. The same graph is used for an entire run, but new graphs are sampled between runs.

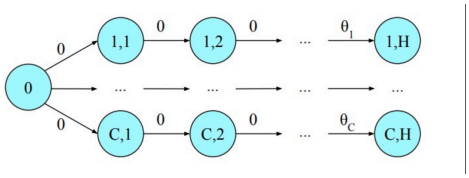

Figure 2. Graph of Parallel Chains Example.

All episodes are finite horizon.

2. Background/Related Work

There is the paper that is being reviewed, of course. There is also a follow on paper, that looks interesting: (Dimakopoulou et al., 2018) This is concerned with more scalable approaches to seed sampling. The approach is similar, but extended to allow for function approximators, such as neural networks.

In addition, there has also been some interesting work on model ensembles. This was in terms of neural networks, but that work could end up being complimentary to this: (Hinton et al., 2015)

Finally, I find this approach to be a bit similar to noise injection to improve the generalization of neural networks for image processing: (Zur et al., 2009) This makes me wonder if a way to remove the need to fully solve an an MDP each time might be to view this as a way to add noise in order to generalize the learning of the agents.

3. Approach

Although this is a multiple agent problem, the seed sampling paper treated actions as occurring within discrete time steps, so it wasn't necessary to use a distributed (including multi-threaded) approach. So, I decided to take advantage of the fairly nice POMDPs.jl framework in Julia.

Steps:

- Solve the true MDP using some method.

  For the bipolar chain, I used the POMDPs.jl framework just for simulation, but I used Q-learning for solving the MDPs, that i wrote myself, but for the parallel chains and maximum reward path, I implemented a full parameterized MDP model using the POMDPs.jl interfaces for each and took advantage of the sparse value iteration solver provided. The true MDP model is used for the simulation portion and also to provide rewards mapping.

- At the appropriate time, generate an MDP and solve it to get a policy for an episode.

  POMDPs.jl value iteration solvers don't handle stochastic rewards well (as expected), so I wrapped the true MDP function to produce the noisy response for the problem statements. I used a single MDP for the bipolar chain case, which was unknown by the agents. For parallel chains and maximum reward path, the true MDP was generated. In the case of parallel chains, random rewards were generated. In the case of maximum reward path, both the structure of the graph and the reward means were generated. This did mean that, especially in the case of a single agent, results could be very stochastic.

- Use the POMDPs.jl methods to run a simulation on an instance of the true MDP generated for the problem, providing a function policy that matches the exploration method. For the bipolar and parallel chains, this stops as soon as it hits a goal state. For the maximum reward path a complete exploration (up to the horizon) was necessary.

  Each successive time step will see a new agent started, so if there are k agents, there would be one agent started at each time step t_1, t_2, ..., t_k. Each agent can take X ~Poisson(1) actions at each time step.

- Repeat for multiple runs, stepping through different #'s of agents. Calculate the average regret.

3.1. Prior Updates

- Bipolar chain The bipolar chain didn't really need a prior, since there were just the two big rewards: -10 and 10, and all the rest where -1. As soon as one of the endpoints was hit, the simulation could end and all agents would just go immediate towards the 10 reward.

- Parallel chains The prior update strategy wasn't mentioned for this problem in the paper, so I used a standard sample gaussian prior update for this problem.

$$\mu_{posterior} = \frac{\sigma_p^2}{(\frac{\sigma^2}{n} + \sigma_p^2)}\mu_s + \frac{\sigma_s^2}{(\frac{\sigma^2}{n} + \sigma_p^2)}\mu_p$$

$$\sigma_{posterior} = (\frac{1}{\sigma_p^2} + \frac{n}{\sigma^2})^{-1}$$

  where μ_s is the sample mean, μ_p is the prior mean, μ is the true mean, σ_s is the sample standard deviation, σ_p is the prior standard deviation, and σ is the true standard deviation σ and μ are assumed known, by the problem definition.

- Maximum Reward Path (Dimakopoulou & Roy, 2018) gives the prior update directly for this problem. They used a single sample update at each time step:

$$\mu_e = \frac{\sigma^2\mu_e + \sigma_e^2(\ln r_e + \frac{\sigma^2}{2})}{\sigma_e^2 + \sigma^2}$$

$$\sigma_e^2 = \frac{\sigma_e^2\sigma^2}{\sigma_e^2 + \sigma^2}$$

4. Experiment results

4.1. Bipolar Chain

For the bipolar chain, I did runs from for 10^k agents for $k = 1..4$. I used N=100 for the number of nodes with the horizon $H = 3 \cdot \frac{N}{2}$

Table 1. Bipolar Chain Regret per Agent Count by Algorithm Type..

	algorithm	agents	regret
1	UCB	1	122.00
2	UCB	10	120.40
3	UCB	100	50.22
4	UCB	1000	5.03
5	UCB	10000	0.50
6	Thompson Sampling	1	225.00
7	Thompson Sampling	10	225.00
8	Thompson Sampling	100	225.00
9	Thompson Sampling	1000	225.00
10	Thompson Sampling	10000	223.01
11	Seed	1	119.60
12	Seed	10	120.14
13	Seed	100	49.82
14	Seed	1000	4.97
15	Seed	10000	0.50

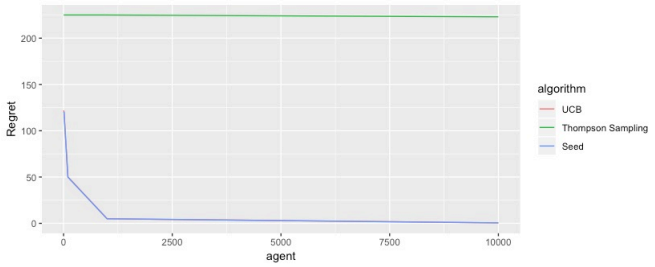

Figure 3. Bipolar Chain Regret per Agent Count by Algorithm Type.

As you can see in Figure 3, and Table 1, there are some small discrepancies. Thompson sampling shows an almost constant regret, only dropping at the end due to the extremely large number of agents, which allows an agent to accidentally hit the end goal, with some higher than 0 probability. In addition, unlike in the paper, UCB was very close to the performance of seed sampling, to the point that they overlap on the graph. This could be that the paper was a little vague about the parallel UCB algorithm used. I implemented a version of UCB1 that used Q and N tables that were common across the agents. Despite this, the improvement when using seed sampling is still quite remarkable, and generally consistent with the improvement shown in the paper.

4.2. Parallel Chains

For parallel chains, I used the number of chains as C=10. Again running 10^k agents for $k = 1..4$

Table 2. Regret per Agent Count by Algorithm Type.

Algorithm	Agent Count	Average Regret
Seed Sampling	1	11.29
Seed Sampling	10	13.49
Seed Sampling	100	5.32
Seed Sampling	1000	1.05
Seed Sampling	10000	0.47
Thompson Sampling	1	14.27
Thompson Sampling	10	12.71
Thompson Sampling	100	5.66
Thompson Sampling	1000	1.07
Thompson Sampling	10000	0.47
UCB	1	18.81
UCB	10	17.15
UCB	100	10.05
UCB	1000	1.45
UCB	10000	0.49

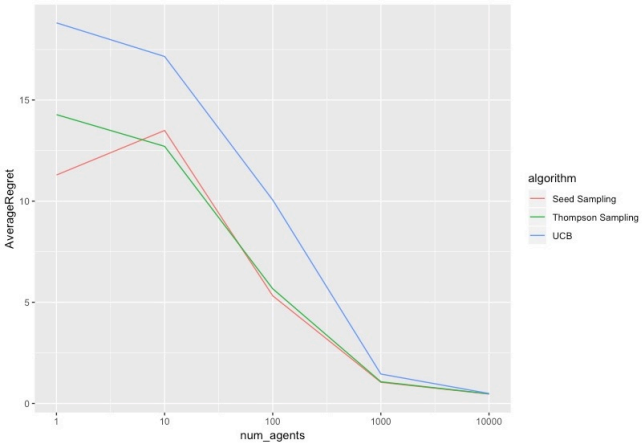

Figure 4. Parallel Chain Regret per Agent Count by Algorithm Type.

As you can see in Figure 4, the results again were fairly close to the paper. My results did converge faster for UCB. As I pointed out above, the exact algorithm they used for UCB wasn't mentioned in the paper, so it could be due to a limitation of the algorithm they chose. For this problem, since the rewards were normally distributed, I just used a 4 sigma upper control bound.

What really makes the results stand our for me is Figure 5. Despite having comparable performance in terms of average regret, seed sampling is computationally much more efficient than Thompson sampling.

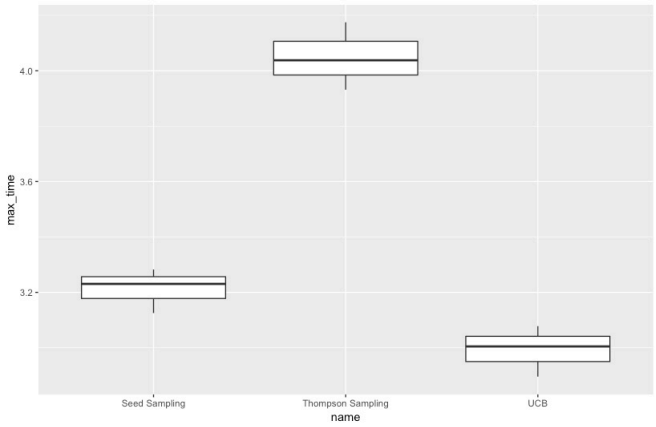

Figure 5. Parallel Chain Time (in minutes) per Run for 10000 Agents by Algorithm Type.

4.3. Maximum Reward Path

For maximum reward path I used number of nodes N=100, with a horizon of H=10.

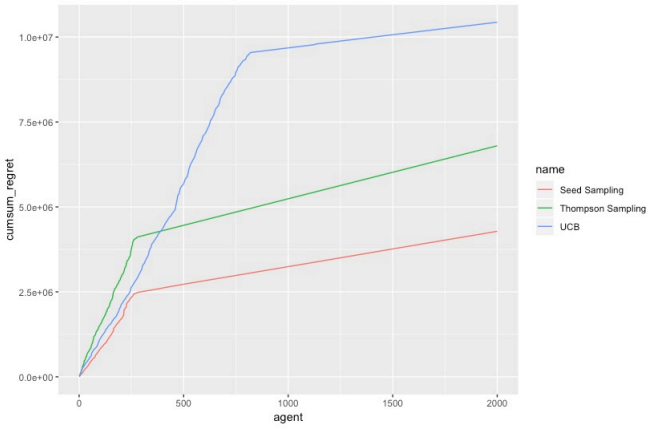

Figure 6. Maximum Reward Path Regret per Agent Count by Algorithm Type.

For this problem, two of the algorithms were switched in performance for me, versus this paper. UCB was performing worse than Thompson sampling. To be honest, I didn't really understand why UCB performed better that Thompson sampling in the paper. I would expect that the lack of exploration that caused the difficulties that UCB had in terms of a lack of diversity in exploration in the parallel chains scenario would carry over to this one.

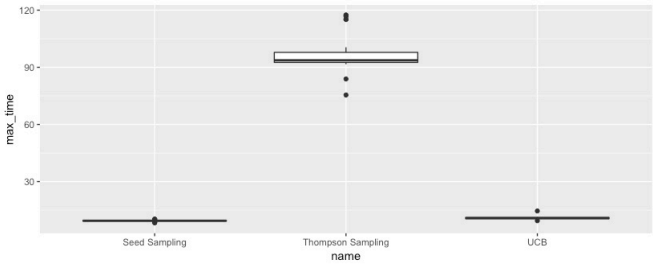

Figure 7. Maximum Reward Path Time (in minutes) per Run for 2000 Agents by Algorithm Type.

This graph was really interesting. You can really see the advantages of seed sampling over Thompson sampling in terms of computation. The cost of solving an MDP on every step is extremely expensive. Since the horizon was 10 for this problem, you can see exactly that magnitude of an increase in the time taken by Thompson sampling. To the point that it would be very prohibitive for large problems.

In the scalable version of this paper, they mention using ensembles of solved MDPs to additionally reduce the amount of computation, since that appears to be the most time consuming portion: (Dimakopoulou et al., 2018) The mechanism wasn't specified, but the idea in that situation seems to be to solve models without the seed, then apply the seed to the solved model. This would imply that the seeding would not be included in the value function itself, and so part of the discounted value, but instead would be applied post hoc to a completed value function a bit like how UCB1 works, a type of random exploration bonus. This is the reverse of the procedure from the (Dimakopoulou & Roy, 2018) paper, which sampled an MDP as a function of the seed.

5. Conclusion

I was able to replicate the findings in the paper. The results aren't exactly the same, but that isn't too surprising given that they aren't specific about the algorithms they compared against. What was really impressive was the gain in computational efficiency by reducing how often MDPs need to be solved. In all cases, seed sampling was much faster than thompson sampling, scaling as the number of episodes vs. the number of time steps. Yet, seed sampling retained much of the benefits of Thompson sampling in terms of providing exploration diversity.

As mentioned above, the ideas here seem to be similar to adding noise to training images to improve generalization. It makes me think that it's likely this idea could be taken out of the Bayesian context and applied to algorithms like UCB1 or MSIE-EB, especially if the PAC guarantees of MSIE-EB could be retained. It seems likely that such a method would use something similar to how you would implement the ensembles mentioned in the (Dimakopoulou et al., 2018) paper.

6. References

References

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