

# Supplementary Material for “Energy-Based Learning for Scene Graph Generation”

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## 1. Quantitative Studies

We present the complete results of our experiments using both the mR@K[2] and the R@K[3] metrics in Table 1.

**Visual Genome.** VCTree, Motif and IMP models, suffer a small drop in regular R@K [3] performance when trained using the energy-based loss. This can be attributed to the heavy-tailed distribution of Visual Genome dataset [1]. Our model predicts granular and informative relations which get penalized on the R@K metric due to biased ground truth annotations. When comparing the mR@K metric [2] our model fares significantly better. For an unbiased scene graph generation framework such as VCTree-TDE, our model is able to improve on both the mR@K and the R@K metrics. We plot the difference in predicate level R@100 performance (sorted in descending order of sampling fraction) of a Motif model trained using the energy-based loss and the cross-entropy loss in Figure 1, along with the sampling fractions of the relations in the visual genome

dataset in Figure 2. We observe that for generic relations such as on with a large number of training samples, the baseline model has slightly higher recall. However, granular relations with a smaller number training samples have significantly higher recall rates.

**GQA.** We observe an almost consistent improvement in both R@K and mR@K. This is primarily due to removing the frequency bias component which leads to relatively unbiased predictions. We plot difference in predicate level R@100 performance of the energy-loss based model and the cross entropy based model in Figure 3 and the corresponding sampling fractions of the relations in Figure 4. Note that the sampling fractions in Figure 4 were plotted using a log-scale on the y-axis for clarity. To keep the visualization simple, we do not plot relations where both the energy model and the baseline model have zero recall. We observe a similar trend where our model performance is comparable to baseline on relations with more labels and significantly better on relations with lesser annotations.

Dataset	Model	Method	PredCls						SGCls						SGDet					
			R@K			mR@K			R@K			mR@K			R@K			mR@K		
			@20	@50	@100	@20	@50	@100	@20	@50	@100	@20	@50	@100	@20	@50	@100	@20	@50	@100
Visual Genome	VCTree	CE	<b>59.82</b>	<b>65.93</b>	<b>67.57</b>	13.07	16.53	17.77	<b>41.49</b>	<b>45.16</b>	<b>46.1</b>	8.5	10.53	11.24	<b>24.9</b>	<b>32.02</b>	<b>36.3</b>	5.31	7.16	8.35
		EBM	57.31	63.99	65.84	<b>14.2</b>	<b>18.19</b>	<b>19.72</b>	40.31	44.72	45.84	<b>10.04</b>	<b>12.54</b>	<b>13.45</b>	24.21	31.36	35.87	<b>5.67</b>	<b>7.71</b>	<b>9.1</b>
	Motif	CE	<b>58.56</b>	<b>64.38</b>	<b>67.13</b>	12.45	15.71	16.98	<b>35.95</b>	<b>39.18</b>	<b>39.96</b>	6.95	8.58	9.05	<b>25.62</b>	<b>32.97</b>	<b>37.41</b>	5.07	6.91	8.12
		EBM	58.39	65.19	67.33	<b>14.17</b>	<b>18.02</b>	<b>19.53</b>	35.65	39.16	40.04	<b>8.18</b>	<b>10.22</b>	<b>10.98</b>	24.29	31.74	36.29	<b>5.66</b>	<b>7.72</b>	<b>9.27</b>
	IMP	CE	<b>54.34</b>	<b>61.05</b>	<b>63.06</b>	8.85	10.97	11.77	<b>34.02</b>	<b>37.39</b>	<b>38.26</b>	5.4	6.4	6.74	<b>16.34</b>	<b>23.64</b>	<b>28.71</b>	2.2	3.29	4.14
		EBM	54.61	61.49	63.49	<b>9.43</b>	<b>11.83</b>	<b>12.77</b>	34.03	37.24	38.09	<b>5.66</b>	<b>6.81</b>	<b>7.17</b>	18.14	25.86	31.13	<b>2.78</b>	<b>4.23</b>	<b>5.44</b>
	VCTree-TDE	CE	40.12	50.83	54.91	16.3	22.85	26.26	26	33.03	35.97	11.85	15.81	17.99	13.97	19.43	23.34	6.59	8.99	10.78
		EBM	<b>41.62</b>	<b>51.22</b>	<b>54.29</b>	<b>19.87</b>	<b>26.66</b>	<b>29.97</b>	<b>29.53</b>	<b>36.49</b>	<b>38.92</b>	<b>13.86</b>	<b>18.2</b>	<b>20.45</b>	<b>14.66</b>	<b>20.55</b>	<b>24.74</b>	<b>7.1</b>	<b>9.69</b>	<b>11.6</b>
	GQA	Transformer	CE	34.68	50.86	58.46	1.17	2.48	3.69	11.05	14.86	16.42	0.54	0.97	1.29	-	-	-	-	-
EBM			<b>35.61</b>	<b>51.88</b>	<b>59.5</b>	<b>1.28</b>	<b>2.94</b>	<b>4.71</b>	<b>12.14</b>	<b>16.12</b>	<b>17.66</b>	<b>0.68</b>	<b>1.32</b>	<b>1.77</b>	-	-	-	-	-	-
Motif		CE	32.73	47.51	54.32	0.89	1.83	2.75	11.34	15.31	16.93	0.49	0.87	1.18	-	-	-	-	-	-
		EBM	<b>34.9</b>	<b>50.66</b>	<b>57.98</b>	<b>1.04</b>	<b>2.29</b>	<b>3.49</b>	<b>11.64</b>	<b>15.74</b>	<b>17.39</b>	<b>0.57</b>	<b>0.9</b>	<b>1.26</b>	-	-	-	-	-	-
IMP		CE	29.4	42.44	48.49	0.5	0.95	1.34	<b>11.87</b>	<b>15.82</b>	<b>17.44</b>	0.28	0.5	0.65	-	-	-	-	-	-
		EBM	<b>29.85</b>	<b>43.3</b>	<b>49.13</b>	<b>0.57</b>	<b>1.07</b>	<b>1.5</b>	11.64	15.47	17.02	<b>0.34</b>	<b>0.58</b>	<b>0.76</b>	-	-	-	-	-	-

Table 1: **Quantitative Results.** Table shows the R@K and mR@K comparison between models trained using the proposed framework and energy based formulation

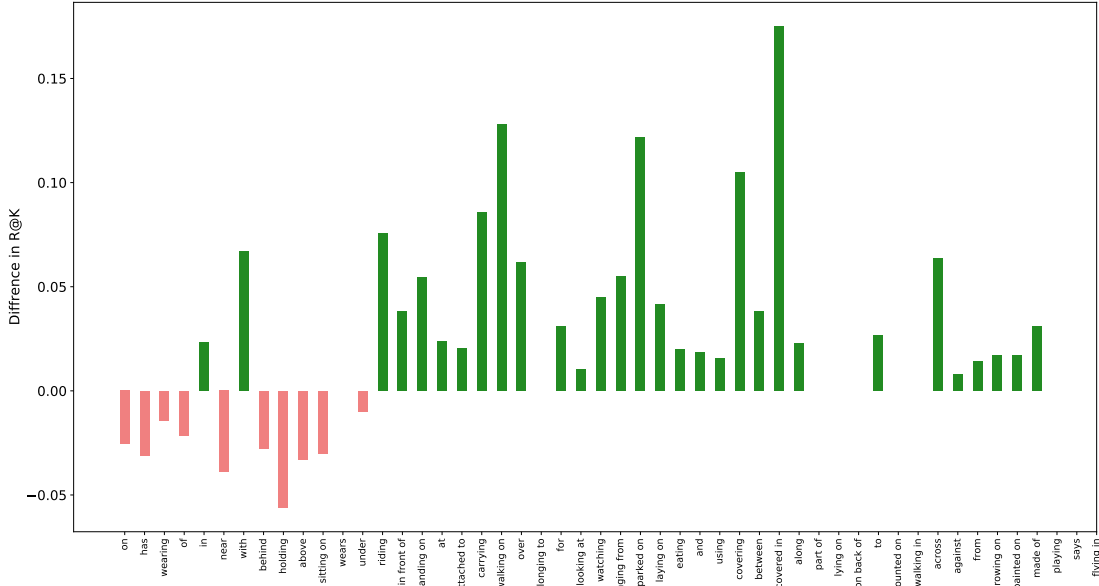


Figure 1: This figure plots the relation wise difference in Recall@100, sorted by descending order of sampling fractions, between a Motif model trained using the proposed energy-based framework and a similar model trained using the standard cross-entropy based framework. The green (red) bars correspond to a relative improvement (regression) in the performance of the energy-based model. We note that using our proposed methodology, we obtain large improvements in the performance of relations with relatively less data. The slight degradation in performance on the commonly occurring relations such as `on` is due to relatively unbiased/granular predictions from energy based models.

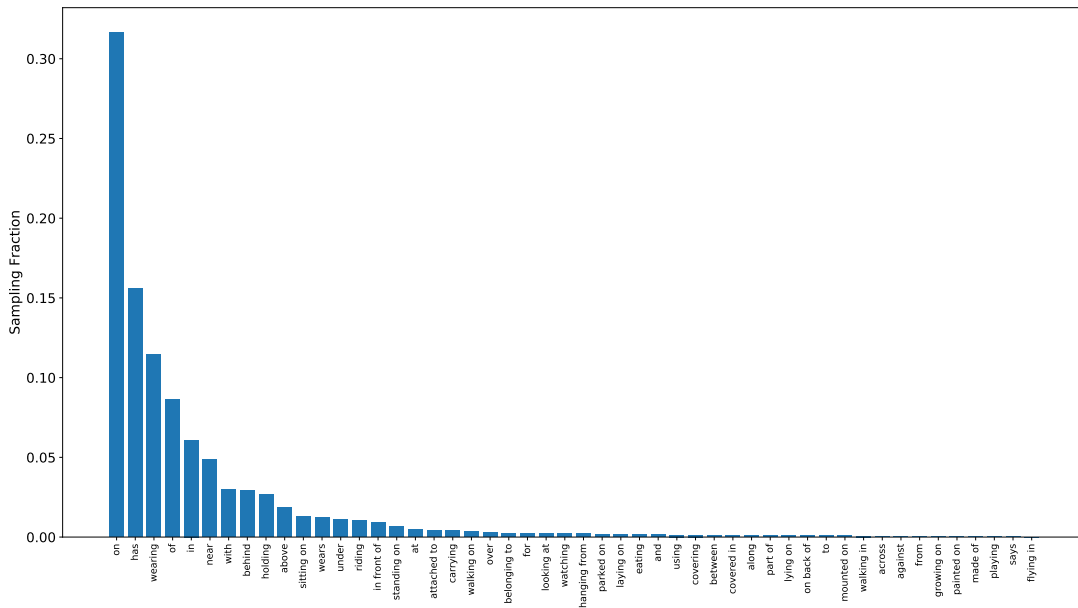


Figure 2: Figure shows the sampling fraction of the different relations in the Visual Genome dataset.

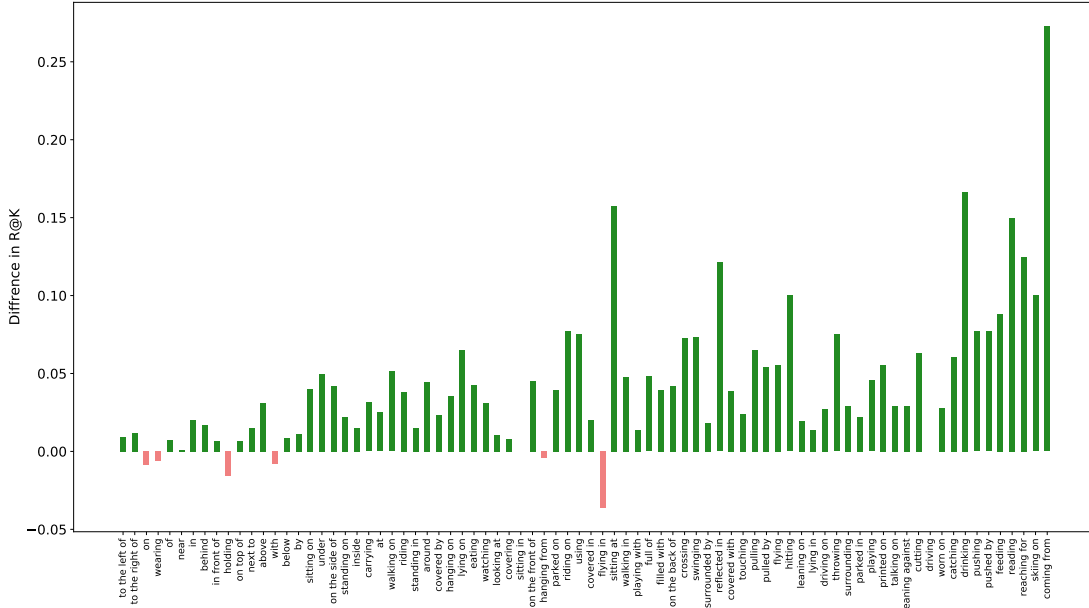


Figure 3: This figure shows the performance difference in relation wise recall on a Motif model trained using an energy loss and using a cross-entropy loss on the GQA dataset sorted in descending order of sampling fractions. We observe that for commonly occurring relations in the dataset, the performance of the baseline and proposed framework is comparable. As we move to the left, we observe larger improvements in performance from energy-based training.

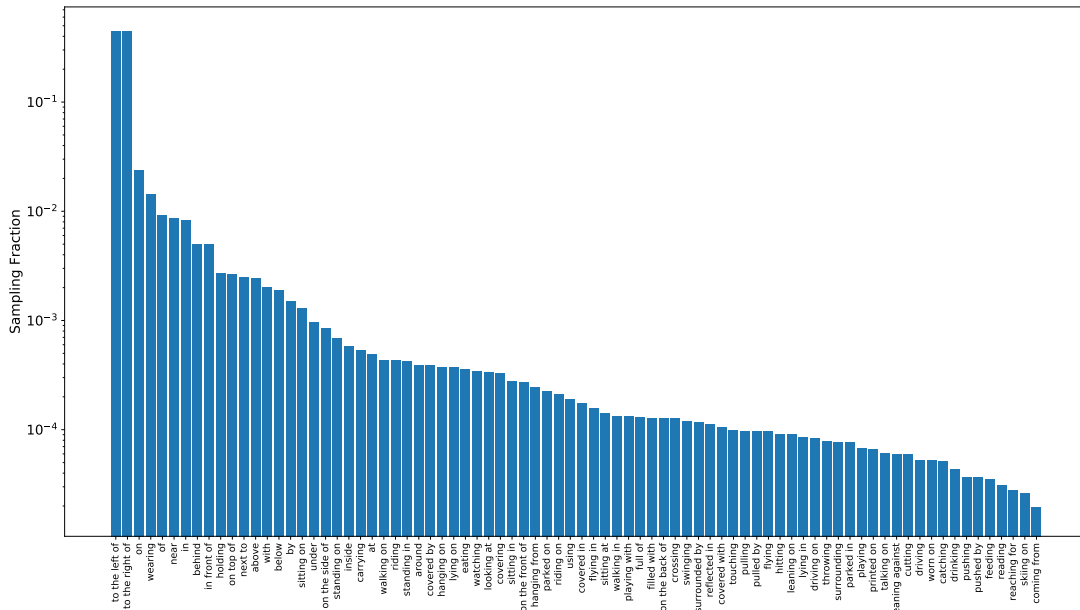


Figure 4: This figure shows the sampling fraction for relation labels in the GQA dataset. The graph is plotted using a log-scale on the y-axis due to a large disparity in the sample fractions. The linear downward trend depicted in the plot corresponds to an exponential reduction in the occurrence of the less frequently occurring relations.

## References

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- [3] Rowan Zellers, Mark Yatskar, Sam Thomson, and Yejin Choi. Neural motifs: Scene graph parsing with global context. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 5831–5840, 2018. [1](#)