Translating Short Segments with NMT: A Case Study in English-to-Hindi

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Abstract

This paper presents a case study in translating short image captions of the Visual Genome dataset from English into Hindi using out-of-domain data sets of varying size. We experiment with three NMT models: the shallow and deep sequence-to-sequence and the Transformer model as implemented in Marian toolkit. Phrase-based Moses serves as the baseline.

The results indicate that the Transformer model outperforms others in the large data setting in a number of automatic metrics and manual evaluation, and it also produces the fewest truncated sentences. Transformer training is however very sensitive to the hyperparameters, so it requires more experimenting. The deep sequence-to-sequence model produced more flawless outputs in the small data setting and it was generally more stable, at the cost of more training iterations.

1 Introduction

In recent years, neural machine translation (NMT) systems have been gaining more popularity due to their improved accuracy and even more fluency compared with "classical" statistical machine translation systems such as phrase-based MT (PBMT), see e.g. the shared tasks of WMT and IWSLT (Bojar et al., 2017; Cettolo et al., 2017). The major advantages of NMT include the consideration of the entire sentence, capturing similarity

of words, and the capacity to learn complex relationships between languages. At the same time, it has been observed that NMT is more sensitive to the shortage of or noise in the parallel training data (Koehn and Knowles, 2017).

Our goal is to create the Hindi version of Visual Genome (Krishna et al., 2017).¹

Hindi, with 260 million speakers, is the fourth most widely spoken language on the planet (after Chinese, Spanish and English). Hindi is a morphologically rich language (MRL), with e.g. the gender category being reflected in the forms of nouns, verbs and also adjectives (Sreelekha S and Bhattacharyya, 2017). The structural and morphological differences between English and Hindi result in translation difficulties (Tsarfaty et al., 2010).

Visual Genome is a dataset of images, captions and relations. As such, it is potentially useful for many NLP and image processing applications. The Hindi version would allow to exploit this dataset e.g. to create Hindi image labellers or other practical tools.

The textual part of Visual Genome consists primarily of short sentences or noun phrases that were manually attached to rectangular regions in an input image. In the current version, Visual Genome contains 108K distinct images with 5.4 million such labelled regions in total. On average, an image is thus associated with 50 text segments. Text segments can repeat across images and indeed, when de-duplicated, the set of unique strings reduces to 3.15 million unique segments.

Even with this de-duplication, this set remains too big to be translated manually. It is thus natural to attempt to translate this dataset automatically and in this paper, we are trying to find the best base-

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¹http://visualgenome.org/

line translation. In the future, we want to include also information available in the context of each of the labels: either the text descriptions of nearby regions or directly the visual information in a form of multi-modal translation (Matusov et al., 2017; Calixto et al., 2012; Huang et al., 2016).

The paper is organized as follows. Section 2 reviews related work on neural MT and English-Hindi translation. Section 3 describes our experimental setting: data, models and their parameters. Section 4 provides automatic and manual evaluation of the translations and Section 5 discusses the results in closer detail. We conclude in Section 6.

2 Related Work

Singh et al. (2017) have compared two neural machine translation models, convolutional sequence to sequence (ConvS2S) and recurrent sequence to sequence (RNNS2S) for English↔Hindi machine translation task. They have used the IITB corpus for training (see Section 3.1) and also for development and test data. The RNNS2S model was trained using Nematus (Sennrich et al., 2017) and ConvS2S using Fairseq (Gehring et al., 2017), an open source library developed by Facebook. In their evaluation, ConvS2S was better when targetting English (BLEU scores: RNNS2S: 11.55, ConvS2S: 13.76) but RNNS2S was better when targetting Hindi (BLEU scores: RNNS2S: 12.23, ConvS2S: 11.73). As our experiment scope is limited to English to Hindi translation, we have not tried the ConvS2S.

Wang et al. (2017) use the encoder-decoder framework with attention (Bahdanau et al., 2015) for their submission to the Workshop on Asian Translation (WAT) 2017 shared task and observe considerable gains for English-to-Hindi compared to PBMT. Similarly to other works, they benefit from subword units (Sennrich et al., 2016a) and back-translation (Sennrich et al., 2016b), as well as model ensembling.

Agrawal and Misra Sharma (2017) evaluate English-Hindi translation quality using several variants of RNN-based neural network architecture and basic units (LSTMs, Hochreiter and Schmidhuber, 1997, and GRUs, Cho et al., 2014b), including the attention mechanism by Bahdanau et al. (2015) and more layers in the encoder and decoder. The bi-directional LSTM model with four layers and attention performs best.

The early models of NMT have suffered from

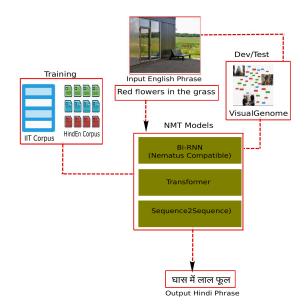


Figure 1: Overall experimental setting.

lower translation quality for long sentences, see e.g. Cho et al. (2014a) and Bahdanau et al. (2015). A recent experiment by Beyer et al. (2017) has however suggested that NMT can perform worse than PBMT also for short segments (insignificantly). It is thus natural to evaluate the effect in our particular setting.

We note that monolingual data plays an important role in boosting the performance of the translation in both PBMT (Brants et al., 2007; Bojar and Tamchyna, 2011) and NMT (Sennrich et al., 2016b; Domhan and Hieber, 2017). We leave these experiments for future work because we would first need to find or select Hindi texts closely matching to the domain of Visual Genome texts.

3 Experiments

The overall framework of our work is shown in Figure 1. The targeted dataset is English text descriptions from Visual Genome but no similar or related data is available in Hindi. So far, we thus used Visual Genome only to select the development and the test set.

We experimented with two parallel corpora as our training data, HindEnCorp and IITB Corpus (see Section 3.1), three NMT models and the PBMT baseline (Section 3.2).

We used the experiment management tool Eman (Bojar and Tamchyna, 2013)² for organizing and running the experiments.

²http://ufal.mff.cuni.cz/eman

Set	#Sentences	#Tokens	
		En	Hi
Train (HindEnCorp)	273.9k	3.8M	5.6M
Train (IITB)	1492.8k	20.8M	31.4M
Dev (Visual Genome)	898	4519	6219
Test (Visual Genome)	1000	4909	6918

Table 1: Statistics of our data.

3.1 Dataset Description

This section describes the processing and usage of the training and development data. We have used HindEnCorp (Bojar et al., 2014) as the training dataset which contains 274k parallel sentences. Additionally, we have explored the very recent "IIT Bombay English-Hindi Parallel Corpus" (Kunchukuttan et al., 2018) which is supposedly the largest publicly available English-Hindi parallel corpus. This corpus contain 1.49 million parallel segments and it includes HindEnCorp.

The development and test sentences were extracted from the Visual Genome. The original dataset contains images and their region annotations and several other formally captured types of information (objects, attributes, relationships, region graphs, scene graphs and question answer pairs). We built our dataset by extracting only the region descriptions, which are generally short sentences or phrases. We selected the development and test segments randomly and prepared the corresponding Hindi translation by manually correcting Google Translate outputs.

The training and test sets sizes are shown in Table 1. Note that the token counts considerably differ from those reported in the corpus descriptions. Here we report the token counts as obtained by the Moses tokenizer and used in all our experiments.

3.2 MT Models Tested

One of the current most efficient NMT toolkits is Marian³ (Junczys-Dowmunt et al., 2016), which is a pure C++ implementation of several popular NMT models. All our experiments thus use Marian models.

3.2.1 Marian's nematus Model (Bi-RNN)

The common baseline NMT architecture is the (shallow) attentional encoder-decoder of Bahdanau et al. (2015). A particularly popular implementation of this model is available in the Nematus toolkit (Sennrich et al., 2017),⁴ which adds some

Parameter	Bi-RNN	S2S	Transformer
beam-size	12	12	12
dec-cell	gru	lstm	_
dec-cell-base-depth	2	4	_
dec-cell-high-depth	1	2	_
dec-depth	1	4	6
decay-inv	_	_	16000
dim-emb	512	512	512
dim-rnn	1024	1024	1024
dropout-rnn	0.2	0.2	_
dropout-src	0.1	0.1	_
dropout-trg	0.1	0.1	_
early-stopping	10	_	_
enc-cell	gru	lstm	_
enc-cell-depth	1	2	_
enc-depth	1	4	6
	irectional	alternating	_
exponential-smoothing	g –	0.0001	_
heads	_	_	8
label-smoothing	_	_	0.1
learning-rate	0.0001	0.0001	0.0003
max-length	50	50	100
normalize	_	_	0.6
optimizer	adam	adam	adam
transformer-dim-ffn	_	_	2048
transformer-dropout	_	_	0.1
transformer-dropout-a		_	0
transformer-postproce	ss –	_	dhn
warm-up	_	_	16000

Table 2: Model configurations.

implementation differences such as a different initial hidden state, a different RNN cell and several others

Marian implements both the training and inference with the Nematus (Sennrich et al., 2017) model and in fact, it can load models trained by the original Nematus.

We call this setup "Bi-RNN" in the following and use it only in shallow (depth 1) setting.

3.2.2 Marian's Sequence-to-Sequence (s2s) Model

A more advanced variation of the RNN-based model allows to use deeper layers in both decoder and encoder and it also differs from the original Nematus model in several features, such as a different layer normalization (Sennrich et al., 2017; Junczys-Dowmunt and Grundkiewicz, 2017).

We denote this model "S2S" in the following and use it only in the deep (depth 4) setting.

3.2.3 Marian's transformer Model

The Transformer model (Vaswani et al., 2017) has been recently proposed to avoid the expensive training of RNNs, relying on the attention mechanism.

As explored by Popel and Bojar (2018) with the

 $^{^3 \}rm http://github.com/marian-nmt/marian$

⁴http://github.com/EdinburghNLP/nematus

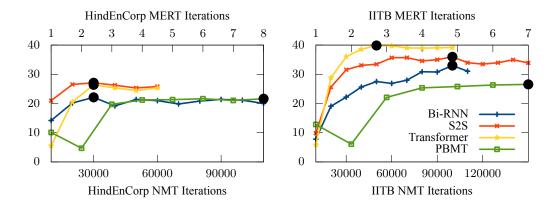


Figure 2: Learning curves in terms of BLEU on dev set. The big black dots indicate which iteration was used for test set translation and evaluation.

original Google implementation,⁵ the model can be more difficult to train but it will likely outperform other architectures in both training time and final translation quality. Indeed, we needed to try 9 different configuration settings for Transformer before we got any reasonable performance, compared to just 3 for S2S and 1 for Bi-RNN.

Marian's implementation should be fully compatible with the original Google one.

The configuration parameters used for training of the models are shown in Table 2.

3.2.4 Common Settings

In all NMT experiments, we used the same BPE (Sennrich et al., 2016a), with 30k merges, joint for English and Hindi and extracted from HindEnCorp only. We also tried to extract the BPE from the respective training corpus (i.e. IITB for IITB models) but the performance was lower, perhaps due to domain differences between the corpora. The HindEnCorp BPEs are thus used in all experiments reported here.

3.2.5 Moses PBMT Baseline

For the purposes of comparison, we also train Moses (Koehn et al., 2007) phrase-based MT system with a 5-gram LM and a lexicalized reordering model, trained with the standard MERT optimization towards BLEU. The alignment is based on lowercase tokens, stemmed to the first 4 characters only.

4 Results

Figure 2 presents the learning curves for all the models evaluated on the development set using the

		Bi-RNN	S2S	Transf.	PBMT
HindEnCorp	BLEU	20.68	26.45	23.91	20.61
	chrF3	32.30	39.52	36.36	36.49
	nCDER	34.04	40.91	38.26	32.71
	nCharacTER	12.27	18.47	23.12	29.05
	nPER	41.76	49.05	47.01	50.40
	nTER	29.63	35.70	33.52	24.78
IITB Corpus	BLEU	31.78	32.81	38.31	25.06
	chrF3	42.63	44.50	51.08	43.09
	nCDER	44.49	44.91	51.78	37.54
	nCharacTER	-14.76	-47.00	25.07	37.55
	nPER	51.86	52.04	59.60	55.17
	nTER	40.62	41.44	49.05	32.76

Table 3: Results on the test set, multiplied by 100. Best model according to each automatic metric in bold. Metrics with the prefix "n" were flipped (100-score) to make better scores higher. The negative numbers for nCharacTER happen when the original CharacTER score is over 1.

BLEU score (Papineni et al., 2002). (PBMT training is displayed in terms of MERT iterations on the secondary x axis.)

For NMT, we validated the model every 10000 iterations and ran the training until the cross-entropy has not improved for 10 consecutive validations. For each model, we selected the iteration where the highest BLEU score was reached and translated the test set with this model.

4.1 Automatic Evaluation

Table 3 provides automatic scores of the models in several metrics (Papineni et al., 2002; Snover et al., 2006; Leusch and Ney, 2008; Popović, 2015; Wang et al., 2016).⁶ We see that on the smaller HindEn-

⁵http://github.com/tensorflow/tensor2tensor

⁶Note that the exact scores are *heavily* dependent on the to-kenization. We collect outputs from all our system after detokenization and tokenize if needed by the metric (chrF3 and CharacTER do not expect tokenized text). We report the scores when Moses tokenizer was used. Using e.g. the Hindi tokenization from IndicNLP, http://github.com/anoopkunchukuttan/indic_nlp_library, leads to sub-

Corp, S2S performs best except in CharacTER and PER where the outputs of PBMT score best. On the larger IITB Corpus, Transformer wins in all metrics except again CharacTER. We suspect that the different evaluation by CharacTER could be an artifact of the Devanagari script used in Hindi.

PER, position-independent error-rate, reflects the overlap of exact word forms used in the reference and the hypothesis, suggesting that PBMT performs reasonably well in terms of preserving words, although the fluency is probably worse.

It should be noted that the automatic scores can be affected by the fact that our test set was created by manual revision of Google Translate outputs. The underlying model of Google Translate is however unknown. Also, we have only one reference translation and it is well known that with more reference translations, automatic evaluations are more reliable (Finch et al., 2004; Bojar et al., 2013).

4.2 Manual Evaluation

To validate the automatic scoring, we manually annotated 100 randomly selected segments as translated by the NMT models.⁷

In this annotation, each annotated segment gets exactly one label from the following set:

Flawless for translations without any error (typesetting issues with diacritic marks due to different tokenization are ignored),

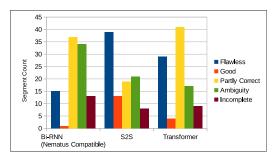
Good for translations which are generally OK and complete but need a small correction,

Partly Correct for cases where a part of the segment is correct but some words are mistranslated,

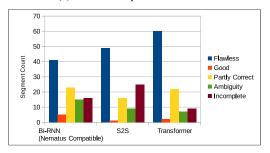
Ambiguity for segments where the MT system "misunderstood" a word's meaning, and

Incomplete for segments that run well but stop too early, missing some content words. This category also includes the relatively rare cases where the NMT model produced just a single word, unrelated to the source.

The results are summarized in Figure 3.



(a) HindEnCorp-trained models



(b) IITB-trained models

Figure 3: Manual evaluation summary.

The manual annotation generally confirms the automatic scores. On HindEnCorp, S2S has the highest number of Flawless segments and Bi-RNN performs worst, having the majority of outputs only Partly Correct and suffering most from Ambiguity.

On IITB, the performance of all the models is generally much better, with 40–60 of the 100 annotated segments falling into the Flawless category. Transformer is a clear winner here and S2S suffers from surprisingly many Incomplete segments.

Some translation samples are shown in Figure 4.

5 Analysis and Discussion

We assumed that PBMT may perform better on short segments. In order to test this assumption, we divided the 1000 test segments into 5 groups based on the source segment length. Group boundaries were chosen to achieve reasonably balance distribution and at least a minimal size for automatic scoring:

Source length:	1–3	4	5	6	7–12
Segment count:	73	380	282	165	100

Figure 5 plots BLEU scores evaluated on each group of segments separately. We see that our assumption does not hold and that there is no clear tendency in translation quality based on source sentence length. In the small data setting (HindEn-Corp), PBMT scores well sentences of length 4 and

stantially lower scores, e.g. BLEU of 7 instead of 20. Fortunately, these BLEU scores correlate very well (Pearson of 0.94) with our scores.

⁷We excluded PBMT from this annotation because its BLEU scores were low; we are now reconsidering this decision given the good performance in PER.

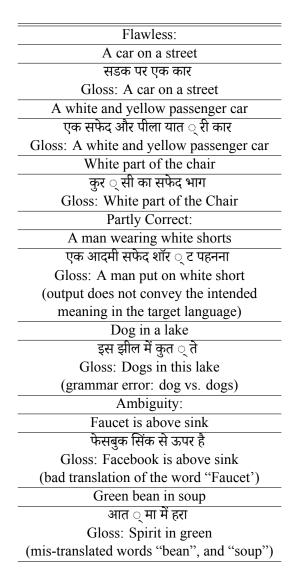


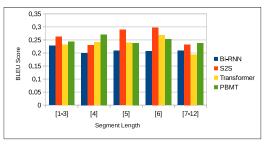
Figure 4: Sample segment translations and their manual classification.

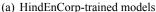
then on sentences over 7 words. In other cases, S2S wins. With the IITB training corpus, Transformer wins and PBMT loses across all lengths.

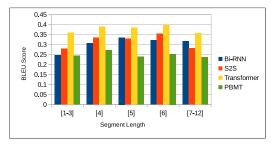
A generally interesting property of NMT is its ability to correctly predict the sentence length (Shi et al., 2016). We take a look at this by considering both the relation of our candidate translations with the source and with the reference.

Figure 6 plots the length of the translation for individual source segments sorted by length. We see that the target length varies a lot across segments and also different NMT models. In general, outputs are longer than sources but the length of the source is not really followed by any of the models.

We observed on the HindEnCorp training data that some of the NMT models tended to cut off sentences too short in early iterations. To examine this, we checked the difference in length be-







(b) IITB-trained models

Figure 5: Translation quality for groups of segments based on their source length.

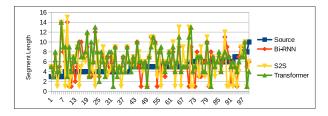


Figure 6: Source and candidate translation lengths for individual segments in the subset of 100 manually-evaluated segments. Segments are sorted by source length. The models were trained on the IITB corpus.

tween the candidate and the reference throughout the iterations. The distribution of length differences was however not skewed in any way and the only observable pattern was that the differences get smaller as the training progresses. We plot the differences for the converged runs over the whole 1000 segments in the test set in Figure 7. We see that all the NMT models are very similar, producing output slightly longer (peak at +2) than the reference. The PBMT is optimized well and the peak is located at zero difference between the candidate and reference length. The interesting pattern in NMT outputs of slightly fewer segments with odd differences (+1, +3 and +5) has still to be explained.

6 Conclusion

We have applied the state-of-the-art neural machine translation models and the phrase-based

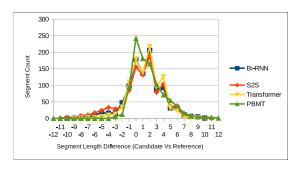


Figure 7: Segment length difference (candidate vs reference) of the IITB-trained models. The positive numbers indicate that candidate is longer than the reference.

baseline to English-to-Hindi translation. Our target domain were relatively short segments appearing in descriptions of image regions in the Visual Genome.

The results indicate that with smaller data (274k parallel segments, 3.8M English tokens), the deep sequence-to-sequence attentional model is the best choice, although the PBMT baseline seemed to perform well in two of the tested automatic metrics, CharacTER and PER. With large parallel data available, Transformer should be preferred and all NMT models clearly outperform PBMT. We have not yet explored the effect of adding monolingual data.

A deeper analysis has not revealed any difference in performance for shorter or longer segments, but the manual annotation suggested that the performance of NMT models varies across individual segments. The overall performance is thus perhaps too crude and it would be suboptimal to decide for a single model.

In the future, we will focus on the possibilities of multi-modal translation (Matusov et al., 2017; Calixto et al., 2012; Huang et al., 2016) to improve translation quality using the Visual Genome images or other contextual information available. Our ultimate plan is to release a machine-translated Hindi version of Visual Genome.

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