# Extrapolative Controlled Sequence Generation via Iterative Refinement

Vishakh Padmakumar, Richard Pang, He He, Ankur P. Parikh













#### **Traditional Controlled Sequence Generation**

#### **Traditional Controlled Sequence Generation**

Example: Sentiment (Scale 1 to 5) associated with a review

This place is **just okay**. The wait is **way too long**. The fill and nail art are **decent**, but **not worth the wait**.



#### **Traditional Controlled Sequence Generation**

Problem: Modify the sentiment to be more positive i.e. 3.60



#### Extrapolative Controlled Sequence Generation

Problem: Modify the sentiment to be more positive



#### Extrapolative Controlled Sequence Generation

Problem: Modify the sentiment to be more positive than seen during training



#### Extrapolative Controlled Sequence Generation

Problem: Modify the sentiment to be more positive than seen during training



### Motivation for Extrapolation Setting

In protein design (and other design problems), we might want to generate mutations more stable than those seen during training

### Motivation for Extrapolation Setting

In protein design (and other design problems), we might want to generate mutations more stable than those seen during training



#### Motivation for Extrapolation Setting

In protein design (and other design problems), we might want to generate mutations more stable than those seen during training



#### Key Idea

## **Key Idea:** Learn to make **local edits** to improve the attribute value at train time



# Key Idea: Learn to make local edits to improve the attribute value at train time, and apply these in succession





This place is just okay. The wait is way too long. The fill and nail art are decent, but not worth the wait.





**Control Code** 

Input

Output

This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.

#### **Control Code**

Input

Output

<INC>

This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.

#### **Control Code**

Input

Output

<INC>

This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.



This place is **decent.** The wait is **a little** long. The fill and nail art are **good** but not worth the wait.



This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.

#### Iterative Inference: Example

This place is **just okay**. The wait is **way too long**. The fill and nail art are **decent**, but **not worth the wait**.



#### **Experimental Details**

- Results on 3 different tasks
  - **Natural Language:** Sentiment Control on the Yelp Dataset
  - **Protein Design:** ACE2 Stability and AAV fitness tasks

#### **Experimental Details**

- Results on 3 different tasks
  - **Natural Language:** Sentiment Control on the Yelp Dataset
  - **Protein Design:** ACE2 Stability and AAV fitness tasks
- **Evaluation Metric:** Success rate at editing examples to various target values

in the training and extrapolation regions

#### **Experimental Details**

- Results on 3 different tasks
  - **Natural Language:** Sentiment Control on the Yelp Dataset
  - **Protein Design: ACE2 Stability** and AAV fitness tasks
- **Evaluation Metric:** Success rate at editing examples to various target values

in the training and extrapolation regions

• Aim to generate mutations of the **ACE2 protein** with *higher* stability

- Aim to generate mutations of the **ACE2 protein** with *higher* stability
- Compare performance to two baselines: **Sampling** and **Genhance**

- Aim to generate mutations of the **ACE2 protein** with *higher* stability
- Compare performance to two baselines: **Sampling** and **Genhance** 
  - Generate 10,000 mutants for the protein and compare the library of sequences

- Aim to generate mutations of the **ACE2 protein** with *higher* stability
- Compare performance to two baselines: **Sampling** and **Genhance** 
  - Generate 10,000 mutants for the protein and compare the library of sequences
- Measure stability using the **FoldX** software











#### Iterative Editing Results in Better Extrapolation



#### Iterative Editing Results in Better Extrapolation



### Iterative Editing Results in Higher Quality Candidates Even At the Head of the Distribution

	Iterative Sampling	Genhance	Our Model
All 10k Candidates	-4.326	-4.086	-4.660
Top 1k Candidates	-5.866	-6.030	-6.575
Top 100 Candidates	-6.413	-7.354	-7.938

Average ddG Score of Output Sequences

#### Takeaways

• Through iterative editing, we are able to generate *more* stable proteins and

edit sequences to attribute values beyond the training data range

#### Takeaways

• For more details, including detailed results, inference methods, variation to

the generation hyperparameters, and more, check out our paper!



#### Iterative Inference

#### Iterative Inference: Guided by Editor Likelihood



This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.

Initial Input

#### Iterative Inference: Guided by Editor Likelihood



#### Iterative Inference: Guided by Editor Likelihood



• Based on the available training data, we can train a classifier *f* 

<inc> +

This place is **just okay**. The wait is **way too** long. The fill and nail art are **decent**, but not worth the wait.

Initial Input







