Title

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# Using Machine learning  modeling to mitigate the Climatic fluctuations on  Angiotensin  converting enzyme (ACE) inhibition activity.

## Abstract.

Currently, the anticipated climatic change hazards redirect  the emergency plans to adapt and control their worldwide risk .That’s why, the continuous data sharing from medical platforms on climate change  should be strengthened, to translate the outcomes of climate change into biological and medical insights .  In this commentary,  we develop an initiative paradigm to model the climatic fluctuations on marine-sourced hydrolysates that affects directly on  ACE inhibition activity in drug industry . On top, the further aim is to regulate a descriptive network starting from the climate change features , passing by the aquatic ecosystem alterations  to finally  predict the Angiotensin  converting enzyme (ACE) inhibition activity on hypertensive patients.  For this,  **(please Mohamed describe the model with professional way in related to the topic showing its compatibility with the scenario of climate change and pharmaceutical).**

## Introduction

Climate change alarm a striking change on human health in different settings especially in various adaptation capacities[1]. For this, scientists from different localities generate enormous amount of data describing both direct and indirect climatic effects in relation to the biomedical research. A factual example that correlates both effects is the water biology. Noteworthy, the recent hypertension cases were founded to be associated with drinking water salinization that is intimately related with climate change [2].

In 2017, scientists have reported the relationship between the structure of peptides and ACE inhibition has not been fully elucidated [4]. With this, we developed a machine learning model that can predict the altered peptides bioactivity in a wake of  temperature fluctuations [3]. In turn,  this unveils the hidden role of climate change on the frequent uncontrolled alteration in the ACE-inhibitory activity.  Therefore, it is of significance to model this alteration for keeping  the sustainable mitigation strategies updated. **(Please Mohamed add a descriptive paragraph about the features that will be used in that trend and I will be further melt it with another descriptive criteria)**

## Algorithm:

## Experimental Results and Discussion:

### Dataset collection

By-products of 120 fresh farmed tilapia (oreochromus niloticus) were collected every month over a year at Kafrelsheikh Governorate, Egypt (One of the most important areas in the production of tilapia in the world). We collected fish byproduct under measured parameters (weight, Sex, length, water quality, ration). Then, they were minced and stored at −30 °C till use. The following steps shows the Enzymatic hydrolysis reaction process for preparing the data samples.

* Thawing the stored by product over night in cold place(4 °C).
* 15% of the samples volume mixed with 50 ml phosphate buffer saline (pH 7.5).
* Pre-incubation at 60 °C for 20 minutes.
* Adding alcalase enzyme (2.5%)to initiate the enzymatic hydrolysis reaction.
* Heating in water bath (90 °C) for 15 minutes.
* Cooling in ice.
* Centrifuge the cooling mixture for twenty minutes at 10000 rpm then the hydrolysis degree was measured to the supernatant according to[27](https://www.nature.com/articles/s41598-017-10890-1#ref-CR27).
* Supernatant extraction then freeze dried and characterized.

### Preparation Phase

Analysis of Tilapia fish by-product and its hydrolysates powder

The contents of tilapia fish by-product and its hydrolysates were measured according to AOAC method[28](https://www.nature.com/articles/s41598-017-10890-1#ref-CR28), The protein content was determined using kjeldal method. Moisture percentage was estimated with drying method. In addition, Ash content was measured by muffle furnace. Within our study, the protein hydrolysates were extracted with alcalase enzyme with appropriate PH and temperature[29](https://www.nature.com/articles/s41598-017-10890-1#ref-CR29).

Amino acid sequence analysis

According to[30](https://www.nature.com/articles/s41598-017-10890-1#ref-CR30), stacking and separating gel were prepared using gel buffer with percentage 4% and 16% respectively. Heating the sample mixture with the buffer till 90 °C for 10 min, then loading into specific wells. Protein standards (1.06 kDa to 26.6 kDa) were also performed on the gels. Fixing, staining and destaining solutions were mixed with gel, after electrophoresis then comparing the resulted protein bands with the standard ones[31](https://www.nature.com/articles/s41598-017-10890-1#ref-CR31).

### Tricine SDS-PAGE analysis

According to [30](https://www.nature.com/articles/s41598-017-10890-1#ref-CR30), we performed Tricine-SDS-PAGE by preparing gel buffer with 4% and 16% stacking and separating gel respectively, then fixing solution was added to gels. After that staining solution was added before the destaining solution. Comparing the resulted bands with standard protein bands.

### Measuring the ACE inhibition Activity:

(Adjust the protocol) will be added

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## Results

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## Discussion

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## Conclusion and Future work

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## References:

[1] X.-N. Zhou. **Potential impacts of climate change on human health**Advances in Climate Change Research (in Chinese), 6 (4) (2010), pp. 235-240.

[2] Hoque MA, Scheelbeek PFD, Vineis P, Khan AE, Ahmed KM, Butler AP. **Drinking water vulnerability to climate change and alternatives for adaptation in coastal region of Southeast Asia**.Global Environmental Change. 2016;136:247–263. doi: 10.1007/s10584-016-1617-1.

[3]  Elaziz, Mohamed Abd  Hemdan, Ahmed Monem  Hassanien, AboulElla  Oliva, Diego Xiong, Shengwu 2017/09/07 Analysis of Bioactive Amino Acids from Fish Hydrolysates with a New Bioinformatic Intelligent System Approach Scientific Reports 10860  7 1

[4] Ceren Daskaya-Dikmen , Aysun Yucetepe , Funda Karbancioglu-Guler 1, Hayrettin Daskaya 2 and Beraat Ozcelik  Angiotensin-I-Converting Enzyme (ACE)-Inhibitory Peptides from Plants. Nutrients 2017, 9, 316; doi:10.3390/nu9040316