

UNIVERSITI TEKNOLOGI MARA

**PREDICTION OF NOVEL ANGIOGENESIS
INHIBITORS USING *IN SILICO* METHOD**

ABU MUSA BIN SULAIMAN

Dissertation submitted in partial fulfilment of the
requirements for the
Bachelor of Pharmacy (Hons.)

Faculty of Pharmacy

2017

ACKNOWLEDGEMENT

Final year project could be very draining if a student failed to manage his time very well. I would like to acknowledge myself for being able to finish this final year project in time. But it all would not be a reality if it wasn't because of my kind supervisor, Dr. Fazlin Mohd. Fauzi for being attentive enough to listen to my ramblings whenever I feel like giving up pharmacy and keeping up with my constant laziness.

I would also like to thank my final year project partner, Anis Sheezen Shamsir for choosing me to be her project mate. It wasn't easy dealing with me and my excuses but she still pulls through. I wish nothing but the best for her.

Finally, I would like to thank my faculty for giving me this opportunity to execute this project, my family for being supportive enough even though they understand nothing but still tried to help especially my math teacher sister, Samirah Sulaiman, and also my friends who able to keep up with my sudden burst of laughter and crying and then laughter again that occurred out of nowhere whenever I'm trying to finish this project. Thank you so much.

ABSTRACT

Angiogenesis plays an important role in tissue repair and could cause all kinds of complications when its balance is disturbed. Cancer and angiogenesis are closely related and inhibiting angiogenesis in cancer is heavily studied. Humanized monoclonal antibodies such as bevacizumab are one of many angiogenesis inhibitors available in the market. However, it is administered intravenously and the treatment can be very expensive. The purpose of this study is to build a computational model that first analyzes protein-ligand binding patterns of anti-angiogenesis drugs for the purpose of predicting a novel angiogenesis inhibitor. 12 different angiogenesis receptors were studied and compounds associated with them were obtained from the ChEMBL database and served as the training set. 8 different prediction models were built, which were from the combination of different fingerprints (ECFP_4, FCFP_4, PubChem, MACCS) and machine learning algorithms (Naïve Bayes, Decision Tree). The combination of MACCS-Decision Tree performed the best, with sensitivity and specificity values of 0.92 at rank 5. The MACCS-Decision Tree model was then subjected to external validation where 4 compounds; Shiraiachrome-A, 11,11'-dideoxyverticillin, Quercetin and TKI-31, obtained from scientific literature were tested. The model was able to predict the correct target for 3 of the compounds. This goes to show that the model can be used to discover novel anti-angiogenesis drugs. Future work should include the *in vivo* or *in vitro* validation of the *in silico* result.

Table of Contents

LIST OF TABLES	iii
LIST OF FIGURES	iv
LIST OF ABBREVIATION	vi
CHAPTER 1	1
INTRODUCTION	1
1.1 Introduction	1
1.2 Problem Statement	2
1.3 Hypothesis of the Study	2
1.4 Objective of the Study	3
1.5 Significant and Limitation of Study	3
CHAPTER TWO	4
LITERATURE REVIEW	4
2.1 Angiogenesis and Cancer: A brief history	4
2.2 Formation of tumor blood vessels	5
2.3 Endogenous angiogenic factors	6
2.3.1 Vascular endothelial growth factors (VEGFs)	6
2.3.2 Platelet-derived growth factors (PDGFs)	7
2.3.3 Transforming growth factor beta (TGF- β)	8
2.3.4 Matrix metalloproteinases (MMPs)	8
2.4 Structure of tumor blood vessels	9
2.4.1 Chaotic blood flow	9
2.4.2 High vascular permeability	9
2.4.3 Non-uniform surface markers	10
2.4.4 Dysfunctional lymphatics	10
2.5 Classification of angiogenesis inhibitors	10
2.5.1 Direct inhibitor of angiogenesis	11
2.5.2 Indirect inhibitor of angiogenesis	11
2.6 Currently available monoclonal antibody anti-angiogenesis drug: Bevacizumab	12
2.7 In-silico approaches and drug discovery	14
CHAPTER THREE	16

CHAPTER 1

INTRODUCTION

1.1 Introduction

According to the World Health Organisation (WHO), cancer arises from a single mutated cell that later metastasized into cancerous cells and develop tumour. In metastasis, cancer cells will travel from where it first started (primary cancer) via blood and lymphatic systems and form new metastatic tumours in other parts of the body. The transformation of a normal cell to a tumour cell is a multiple stage process.

From the World Cancer Report 2014, cancer is among the major causes of morbidity and mortality around the world, with approximately 14 million new cases and 8.2 million deaths in 2012. The number is projected to increase by 70% over the next twenty years.

There are various treatment options available in treating cancer and one known method is through inhibiting the angiogenesis process. Angiogenesis is the process of new blood vessels formation from a pre-existing blood vessel. It provides nutrients for the tumours to grow and later spread to other parts of the body. Currently, one of the widely-used angiogenesis inhibitors available in the market is bevacizumab, a humanized monoclonal antibody, which binds to VEGF (vascular endothelial growth factor) and stops the binding to VEGFR (VEGF receptor), marketed in the form of injection.