CONFERENCE ABSTRACT BOOK OPEN ACCESS

WISE National Conference 2024: Endless Exploration

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Abstract:
Our goal at Women in Science and Engineering – University of Toronto Chapter is to support and empower all women in STEM fields and to help them achieve their full potential as future engineers, entrepreneurs, scientists, and leaders. Since its inception in 1999, the organization has developed into one of the largest and highly regarded campus organizations with over 1500 members to champion gender equity, counter biases, and build confidence in all STEM fields. Our annual National Conference aims to empower and inspire individuals to pursue their passions, explore new opportunities, and to make meaningful, lasting connections. One of the events we held at this year's conference is the 5 Minute Thesis (5MT) competition, which challenges undergraduate and graduate delegates to present their research in five minutes to a non-specialist audience. This abstract book features the research that the 5MT competitors presented at the WISE National Conference 2024.

Keywords: 5MT; competitions; conference; gender equality; STEM; WISE; non-specialist audience

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Conference Abstracts
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5MT Abstracts

Efficacy of Machine Learning Video Analysis in a Clinical Brain Computer Interface Setting

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For children living with cerebral palsy, fatigue is an ever present concern, particularly when participating in rehabilitation. Brain-computer interfaces (BCIs) may help complement traditional rehabilitation, but evaluating fatigue still relies on time-consuming or expensive processes. MediaPipe, an open-source machine learning framework, can detect a variety of body landmarks from a single camera angle. The objective of this study was to assess the efficacy of using MediaPipe to analyze physical fatigue in videos of children before and after BCI use in a clinical setting. Three MediaPipe models (Hand, Hand Legacy and Holistic) were used to analyze 200 videos from 35 children performing manual dexterity tasks. All models output similar, low percentages of frames with detected landmarks (26%, 27% and 28%). However, performance for different

participants varied across models. When combining outputs of Hand and Holistic models, the average percentage of frames with landmarks detected increased to 44%. While MediaPipe is an efficient and low cost tool, it is not effective in all clinical scenarios. Four model inhibitors were identified: camera angle, body positioning, motion speed and uncommon objects such as BCI headset. Future investigation of systematic clinical methodologies and techniques such as transfer learning should be done to further assess efficacy.

Investigating the Consequence of Deleting the Mechanoreceptor TRPV4

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Currently, the role of mechanoreceptors in the cellular response to mechanical loading in sub-compartments of the IVD are poorly understood. Previous work has demonstrated that TRPV4, a mechanically-gated cation channel, mediates mechanotransduction in the intervertebral disc (IVD). The IVD is comprised of three sub-compartments: the nucleus pulposus (NP), annulus fibrosis (AF), and cartilage endplates (CEP). We hypothesize that TRPV4 is required for NP tissues to respond to mechanical load in vivo. The present study uses a novel NP-specific TRPV4 knockout mouse in a longitudinal study to characterize the role of TRPV4 in the NP. We collected the lumbar spines of wild-type and NP-specific TRPV4 knockout mice aged to 12 and 22 months, and subsequently used histopathological analysis to compare the severity of age-associated disc degeneration between wild-type and knockout. At 12 months, knockout spines demonstrated minimal observable difference from wild-type spines. However, at 22 months, the knockout spines demonstrated less degenerative changes than the wild-type mice, indicating that the deletion of TRPV4 in NP tissues may have a protective effect against age-associated disc degeneration. These results can direct future research investigating the physiological processes that underlie these histological observations to better characterize the biology of mechanotransduction in the IVD.

Peptide Library Design, Synthesis and Evaluation for Selectively Targeting the CXCR4 Receptor

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Cancer is one of the leading causes of death worldwide. Molecular imaging techniques, such as positron emission tomography (PET), allow for visualization of cancer at the earliest stages. The C-X-C chemokine receptor 4 (CXCR4) is a promising biomarker due to its role in tumor microenvironment interactions and growth in cancer cells. The aim of this project is to use peptides as targeting moieties and develop a library of linear peptide analogues as an antagonist to the receptor. The results from an alanine scan of a recently discovered peptide with micromolar affinity specified three ideal locations for modifications within the eight amino acid peptide sequence. The peptides were designed and then synthesized using manual and automated solid phase peptide synthesis and conjugated via copper free click chemistry to a small molecule containing fluorine. Fmoc-Lys(N_3)-OH was synthesized and incorporated into the peptide sequence allowing for strain promoted alkyne-azide cycloaddition (SPAAC), a subtype of copper-free click chemistry, between the residue and small molecule. The synthesized peptides will be evaluated for their binding affinity through a radioligand-displacement binding assay to the CXCR4 receptor. In the future, the most optimal probe will be radiolabeled with 18F and evaluated with PET imaging in animal models.

Computational Hit-Finding for Casitas B-Lineage Lymphoma B

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Drug discovery is a lengthy process through which new therapeutic entities are identified using computational, experimental, and clinical techniques. An early but important stage in the development of small-molecule drugs is to screen large libraries of drug-like molecules against the desired protein target. Computational methods can significantly accelerate this stage by providing unmatched access to large and more diverse chemical spaces. Such methods also leverage improved physics-based

methods, as well as advancements in machine learning. The Critical Assessment of Computational Hit-Finding Experiments (CACHE) is an open-science project that provides benchmarking challenges designed to find the most efficient computational methods for hit-identification. The most recent challenge required participants to find hits for Casitas B-Lineage Lymphoma B (CBL-B), an important immunotherapeutic anticancer target. To find hits for CBL-B, analysis of reference structural data was firstly performed to identify key interactions between CBL-B and a known binder. After protein preparation, a library of commercial compounds was docked in the CBL-B structure using the Glide docking tool (Schrödinger). The best hits were then filtered to prioritize poses with low strain-energies and no intramolecular clashes. The prioritized compounds were then visually inspected, and 150 compounds were finally submitted to CACHE organizers for controlled in-vitro testing.

Screening for Chemical Inhibitors of Fungal Pathogen Transporter PHO84

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In 2022, the World Health Organization released a list of fungal pathogens to address the rising threat of fungal infections, especially among the immunocompromised population. Despite this emerging threat, fungi receive less attention than other microbial pathogens, like bacteria, even though their resistance to current fungicides is also on the rise. Many species of fungi, pathogenic included, have homologues of *Saccharomyces cerevisiae* phosphate transporter PHO84 that are essential for survival but are specific to fungi. By finding small molecule inhibitors of this transporter, it may be possible to develop new classes of specific fungicides. The NOVACore chemical library was screened in 3 strains of *S. cerevisiae* expressing PHO84 homologues of *Cryptococcus neoformans*, *Candida albicans*, and *Candida glabrata*, respectively. The growth inhibition screen found three hits for the *C. neoformans* receptor, ten for *C. albicans*, and thirteen for *C. glabrata* that completely inhibited growth. Of these, two were overlapping hits for all 3 receptors. Many of the hits were azole-class compounds, which are known to be promising antifungals, and should be retested in the fungal pathogen itself. Furthermore, pathogen-derived PHO84 receptors were shown to respond to agricultural antifungal agents like chlorothalonil, and testing of further existing and novel compounds is warranted.

Conflicts of Interest

The authors declare that they have no conflict of interests.

Authors' Contributions

AC: served as Co-Chair for the conference and gave final approval of the version to be published.
AH: served as Co-Chair for the conference and gave final approval of the version to be published.
SJ: served as a Business Relations Director for the conference, assisted authors with their abstract submissions, reviewed the abstract submissions and ensured that they adhered to correct formatting standards, drafted the conference abstract booklet, and gave final approval of the version to be published.
SK: served as a Business Relations Director for the conference and gave final approval of the version to be published.
AM: served as a Business Relations Director for the conference and gave final approval of the version to be published.
EZ: served as a Business Relations Director for the conference and gave final approval of the version to be published.

Acknowledgements

We acknowledge and thank the rest of the WISE 2023-2024 Conference Team for their hard work in putting together an amazing conference, as well as the executive team and volunteers who helped run the conference. In addition, we would like to thank our 5MT judges, who graciously volunteered their time to judge the competition.

Funding

Funding for the WISE National Conference 2024 was supported by Magna International, Qualcomm, Intuit, CIBC, Amazon Robotics, Ontario Power Generation, Procter & Gamble, Accenture, Tetra Tech, Vector Institute, Mastercard, Metrolinx, General Motors, MDPI, Definity, Synopsys and Professional Engineers Ontario.

Article Information
Managing Editor: Jeremy Y. Ng
Article Dates: Received Mar 01 24; Published Mar 15 24

Citation
Please cite this article as follows:
Khurana S, Joulaei S, Mansoor A, Zhou E, Chow A, Huynh A. WISE National Conference 2024: Endless Exploration. URNCST Journal. 2024 Mar 15: 8(3). https://urncst.com/index.php/urncst/article/view/586
DOI Link: https://doi.org/10.26685/urncst.586