Poster Presentation

Initial Hints and Tips
How to Knock Up a Decent Poster

Unit 2 (30%)

Poster presentation and defence: Discuss the development of the physical self and perceptions of physical competence in relation to children's skill acquisition in sport

What is the Purpose of a Poster?

Title
Student Name/Number

PIGS IN SPACE: EFFECT OF ZERO GRAVITY AND AD LIBITUM FEEDING ON WEIGHT GAIN IN CAVIA PORCELLUS

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ABSTRACT:

One ignored benefit of space travel is a potential elimination of obesity, a chronic problem for a growing majority in many parts of the world. In theory, when an individual is in a condition of zero gravity, weight is eliminated. Indeed, in space one could conceivably follow ad libitum feeding and never even gain an gram, and the only side effect would be the need to upgrade one's stretchy pants("exercise pants"). But because many diet schemes start as very good theories only to be found to be rather harmful, we tested our predictions with a long-term experiment in a colony of Guinea pigs (Cavia porcellus) maintained on the International Space Station. Individuals were housed separately and given unlimited amounts of high-calorie food pellets. Fresh fruits and vegetables were not available in space so were not offered. Every 30 days, each Guinea pig was weighed. After 5 years, we found that individuals, on average, weighed nothing. In addition to weighing nothing, no weight appeared to be gained over the duration of the protocol. If space continues to be gravity-free, and we believe that assumption is sound, we believe that sending the overweight — and those at risk for overweight — to space would be a lasting cure.

INTRODUCTION:

The current obesity epidemic started in the early 1960s with the invention and proliferation of elastane and related stretchy fibers, which released wearers from the rigid constraints of clothes and permitted monthly weight gain without the need to buy new outfits. Indeed, exercise today for hundreds of million people involve only the act of wearing stretchy pants in public, presumably because the constrictive pressure forces fat molecules to adopt a more compact tertiary structure (Xavier 1965).

Luckily, at the same time that fabrics became stretchy, the race to the moon between the United States and Russia yielded a useful fact: gravity in outer space is minimal to nonexistent. When gravity is zero, objects cease to have weight. Indeed, early astronauts and cosmonauts had to secure themselves to their ships with seat belts and sticky boots. The potential application to weight loss was noted immediately, but at the time travel to space was prohibitively expensive and thus the issue was not seriously pursued. Now, however, multiple companies are developing cheap extra-orbital travel options for normal consumers, and potential travelers are also creating news ways to pay for products and services that they cannot actually afford. Together, these factors open the possibility that moving to space could cure overweight syndrome quickly and permanently for a large number of humans.

We studied this potential by following weight gain in Guinea pigs, known on Earth as fond of ad libitum feeding. Guinea pigs were long envisioned to be the "Guinea pigs" of space research, too, so they seemed like the obvious choice. Studies on humans are of course desirable, but we feel this current study will be critical in acquiring the attention of granting agencies.

MATERIALS AND METHODS:

One hundred male and one hundred female Guinea pigs (Cavia porcellus) were transported to the International Space Laboratory in 2010. Each pig was housed separately and deprived of exercise wheels and fresh fruits and vegetables for 48 months. Each month, pigs were individually weighed by duct-taping them to an electronic balance sensitive to 0.0001 grams. Back on Earth, an identical cohort was similarly maintained and weighed. Data was analyzed by statistics.

RESULTS:

Mean weight of pigs in space was 0.0000 +/- 0.0002 g. Some individuals weighed less than zero, some more, but these variations were due to reaction to the duct tape, we believe, which caused them to be alarmed push briefly against the force plate in the balance. Individuals on the Earth, the control cohort, gained about 240 g/month ($p = 0.0002$). Males and females gained a similar amount of weight on Earth (no main of effect of sex), and size at any point during the study was related to starting size (which was used as a covariate in the ANCOVA). Both Earth and space pigs developed substantial dewlaps (double chins) and were lethargic at the conclusion of the study.

CONCLUSIONS:

Our view that weight and weight gain would be zero in space was confirmed. Although we have not replicated this experiment on larger animals or primates, we are confident that our result would be mirrored in other model organisms. We are currently in the process of obtaining necessary human trial permissions, and should have our planned experiment initiated within 80 years, pending expedited review by local and Federal IRBs.

ACKNOWLEDGEMENTS:

I am grateful for generous support from the National Research Foundation, Black Hole Diet Plans, and the High Fructose Sugar Association. Transport flights were funded by SPACE-EXES, the consortium of wives divorced from insanely wealthy space-flight startups. I am also grateful for comments on early drafts by Mañana Athletic Club, Corpus Christi, USA. Finally, sincere thanks to the Cuy Foundation for generously donating animal care after the conclusion of the study.

LITERATURE CITED:

NASA. 1982. Project STS-XX: Guinea Pigs. Leaked internal memo.

Sekulić, S.R., D. D. Lukač, and N. M. Naumović. 2005. The Fetus Cannot Exercise Like An Astronaut: Gravity Loading Is Necessary For The Physiological Development During Second Half Of Pregnancy. Medical Hypotheses. 64:221-228

Xavier, M. 1965. Elastane Purchases Accelerate Weight Gain In Case-control Study. Journal of Obesity. 2:23-40.

If you can read this you must be nocturnal…

Your name here, and names of others
Place the name of your institution here

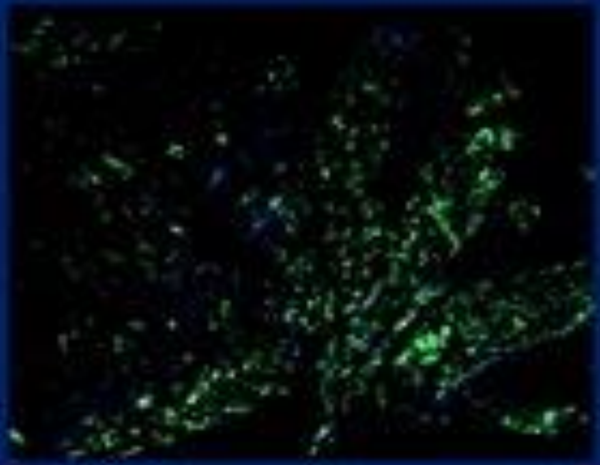
Abstract

Introduction

Questions

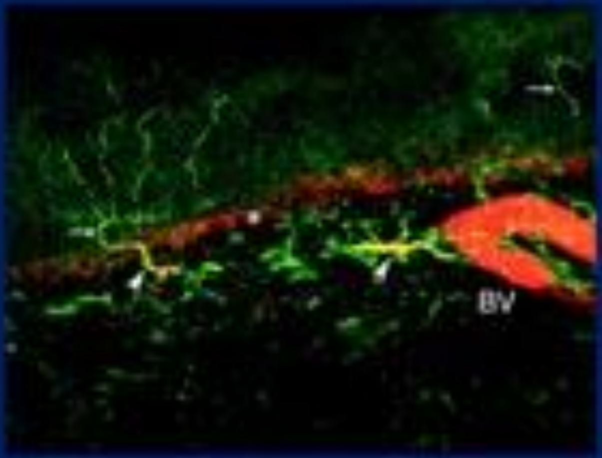
Hypothesis

Results



Methods & Materials

Results



Methods & Materials

Discussion

Conclusion

References

Acknowledgements

O⁶-Benzylguanine Inhibits Tamoxifen Resistant Breast Cancer Cell Growth and Resensitizes Breast Cancer Cells to Anti-Estrogen Therapy

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Abstract

Endocrine therapies using anti-estrogens are least toxic and very effective for breast cancers, however, tumor resistance to tamoxifen remains a stumbling block for successful therapy. Based on our recent study on the involvement of the DNA repair protein MGMT in pancreatic cancer (Clin Cancer Res. 15, 6087, 2009), here, we investigated whether MGMT overexpression mediates tamoxifen resistance. Specifically, we determined whether administration of MGMT inhibitor [O⁶-benzylguanine (BG)] at a non-toxic dose alone or in combination with the anti-estrogens (tamoxifen/fulvestrant) curtails human tamoxifen resistant breast cancer cell growth. Further, we also determined whether BG sensitizes breast cancers to tamoxifen using tamoxifen resistant cells.

MGMT expression was found to be increased in breast cancer cells relative to normal breast epithelial cells. Also, MGMT levels were significantly higher in tamoxifen resistant MCF-7 compared to the parent cells. Silencing of the ER-α expression using a specific siRNA resulted in augmentation of MGMT mRNA and protein levels by 2 fold. We also observed an inverse correlation between MGMT and p53 levels in breast cancer cell lines; moreover, p53 downregulation was accompanied by increased MGMT expression. Other experiments showed that BG alone or BG in combination with tamoxifen or fulvestrant decreased ER-α expression, whereas tamoxifen alone and fulvestrant alone increased and decreased the same respectively. However, all these treatments increased the $p21^{cip1}$ mRNA and protein expression significantly. BG inhibited tamoxifen resistant breast cancer growth in a dose-dependent manner and it also resensitized resistant breast cancer cells to anti-estrogen therapy (TAM/ICI). These combinations also enhanced the cytochrome C release and the PARP cleavage, indicative of apoptosis. In breast cancer xenografts, BG alone or a combination of BG with tamoxifen or fulvestrant caused significant tumor growth delay and immunohistochemistry revealed that BG inhibited the expression of MGMT, ER- α, ki-67 and increased $p21^{cip1}$ staining. These findings suggest that MGMT inhibition may provide a novel and effective approach for overcoming tamoxifen resistance.

Introduction

Recent advances in breast cancer research have identified key pathways involved in the repair of DNA damage induced by chemotherapeutic agents. The ability of cancer cells to recognize DNA damage and initiate DNA repair is an important mechanism for therapeutic resistance and has a negative impact on therapeutic efficacy. A number of DNA-damaging alkylating agents attack the nucleophilic O⁶ position on guanine, forming mutagenic and highly cytotoxic interstrand DNA crosslinks. The DNA repair enzyme O⁶-alkylguanine DNA alkyltransferase (AGT), encoded by the gene MGMT, repairs alkylation at this site and is responsible for protecting both tumor and normal cells from alkylating agents. MGMT is expressed constitutively in normal cells and tissues. In breast tumors, MGMT gene expression is elevated and levels are up to 4-fold higher than in the normal breast. Interestingly, it has been shown that tamoxifen accelerates proteasomal degradation of MGMT in human cancer cells. In 1991, Pegg, Moschel, and Dolan observed that O⁶ benzylguanine (BG) inhibited AGT and potentiated the cytotoxicity of both chloroethylating agents and methylating agents. In a series of important observations, they fully characterized the interaction between BG and AGT and its therapeutic impact. They showed that BG binds AGT, transferring the benzyl moiety to the active-site cysteine [29]. The reaction is very rapid and more potent than any other previously known AGT inhibitor. BG is not incorporated into DNA in living cells and reacts directly with both cytoplasmic and nuclear AGT. Because BG is a psuedosubstrate for MGMT which results in the covalent transfer of benzyl group to the active site cysteine, the MGMT protein is degraded after each reaction. This stoichiometric reaction mechanism effectively depletes the AGT content in tumors and the associated repair of alkylation damage. BG is currently undergoing clinical trials in various cancers to increase the efficacy of alkylating agents.

Interestingly, several observations suggest an inverse correlation between the levels of MGMT and p53 tumor suppressor proteins where wild-type p53 suppresses transcription of human MGMT expression. Unfortunately, p53 function is often inactivated or suppressed in human cancers; therefore, restoration of wt-p53 activity is essential for the success of some treatments. However, whether or not this is mediated by suppression of MGMT expression has yet to be determined. To date, the cross-talk between MGMT and ER-alpha (and the link to p53 expression) has not been explored in drug (i.e., tamoxifen) resistant breast tumors. The anti-estrogen tamoxifen is the most commonly used treatment for patients with estrogen receptor positive breast cancer. Although many patients benefit from tamoxifen in the adjuvant and metastatic settings, resistance to this endocrine therapeutic agent is an important clinical problem. The primary goal of present study was to investigate the mechanisms of anti-estrogen drug resistance and to design new therapeutic strategies for circumventing this resistance. The results show that MGMT expression is increased in TAM-resistant breast cancers and inhibition of MGMT by BG significantly improves TAM-sensitivity.

Results

Prolonged Treatment of Tamoxifen Increases MGMT Expression: We developed a tamoxifen resistant MCF-7 cell line by using prolonged treatment of tamoxifen on the parental ER-positive breast cancer cell line, MCF-7. Tamoxifen-resistant MCF-7 cells proliferate at rates similar to the parental MCF-7. Prolonged treatment of tamoxifen onto MCF-7 cells increased MGMT expression compared to parental MCF-7 cells by 2 fold (Fig.1).

Knocking Down ERα Enhances MGMT Expression in Tamoxifen Resistant Breast Cancer Cells: It is not known whether ERα and MGMT transcriptionally regulate each other in tamoxifen resistant breast cancer cells. We therefore investigated whether down regulation of ERα has any effect on endogenous MGMT expression in these cells. As expected, downregulation of ERα using specific siRNA significantly reduced ERα protein levels in these cells. Western blot analysis was performed and the results in the left panel (Fig. 2A) shows that silencing of ERα increases MGMT expression in these cells, and interestingly, the results in the right panel (Fig.2B) show increased MGMT mRNA levels were increased as assessed by qRT-PCR. These data suggest that ERα–mediated signaling functions to repress MGMT gene expression in breast cancer cells.

Transcriptional Regulation Between MGMT and p53: Previously, it was reported that p53 negatively regulates MGMT in breast cancer cells. Therefore, we addressed whether or not silencing the p53 enhances endogenous MGMT transcription. Tamoxifen resistant MCF-7 cells were transfected with either p53 siRNA (p53-KD) (Fig.2C) or MGMT siRNA (MGMT-KD) (Fig.2D) along with Non-specific siRNA (NS). MGMT expression was consistently increased in p53 knock down cells, with different experiments showing a – fold augmentation (Fig. 2A) and as expected, knocking down MGMT decreased MGMT transcription where as p53 mRNA levels were unaffected in MGMT knockdown cells (Fig.2D). These results confirm that p53 can regulate MGMT at the transcriptional level.

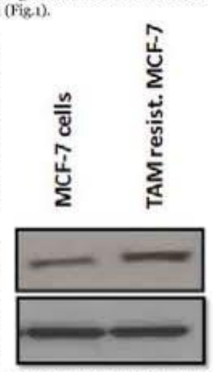


Figure 1. MCF-7 parental and tamoxifen resistant MCF-7 cell pellets were prepared, proteins were isolated and MGMT expression was detected by western blot analysis. Tamoxifen resistant MCF-7 breast cancer cells significantly increased MGMT expression compared to MCF-7 parental cells.

O⁶-Benzylguanine Plays a Dual Role in Tamoxifen Resistant MCF-7 Cells: Contrasting with the experiments above, next, we studied whether or not knocking down MGMT has any effect on ERα transcription. As expected, knocking down MGMT decreased MGMT gene transcripts. However, it was interesting to find that ERα gene transcription was also reduced after MGMT silencing. (Fig.2E). These data demonstrate that BG has the ability to attenuate the not only the MGMT, but also the ERα transcription, indicating a possible dual role for MGMT blockers in these breast cancer cells.

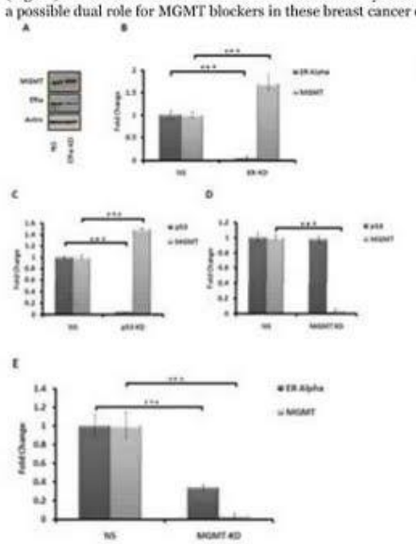


Figure 2. (A) Tamoxifen resistant MCF-7 cells were transfected with ERα siRNA (100nM) (ERα-KD) and NS siRNA (100nM) (NS), and cells were harvested 72h post transfection. Total proteins were isolated and ERα and MGMT expression was determined by western blot analysis. MGMT protein was significantly increased in ERα knock down cells (B) Tamoxifen resistant MCF-7 cells were transfected with ERα siRNA (100nM) (ERα-KD) and NS siRNA (100nM) (NS), and cells were harvested 72h post transfection. Total RNA was isolated and MGMT and ERα transcription was determined by qRT-PCR. MGMT transcription was significantly increased in ERα knock down cells. (C) Total RNA was isolated from non-specific siRNA (NS) (100nM) and p53 siRNA (20 nM) knock down tamoxifen resistant MCF-7 breast cancer cells. MGMT and p53 transcription was determined by qRT-PCR. (D) Total RNA was isolated from non-specific siRNA (NS) (100nM) and MGMT siRNA (100nM) knock down tamoxifen resistant MCF-7 breast cancer cells. MGMT and p53 transcription was determined by qRT-PCR. There is an inverse correlation between MGMT and p53 in tamoxifen resistant breast cancer cells (C & D).

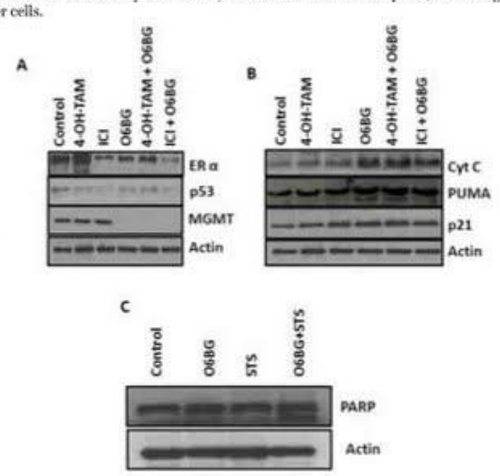


Figure 3. (A) Tamoxifen resistant MCF-7 breast cancer cells were treated in presence or absence of BG (50 μg) and 48h post treatment 4-OH-TAM (1μM), ICI (1μM) either alone or in combination with BG. 24h post treatment cells were harvested and proteins were isolated and western blot analysis was performed. (A) ERα, p53 and MGMT expressions (B) Cytochrome C, PUMA and p21 was determined by western blot analysis (C) tamoxifen resistant MCF-7 cells were treated with or without BG for 48h and later treated with staurosporin (5 μM/L) for 6 hrs PARP cleavage was determined by western blot analysis.

O6-Benzylguanine Modulates p53 Down-Stream Targeted Protein Expressions: Encouraged by the results reported, we investigated the effect of combination therapy on endogenous MGMT, p53, and ERα protein expressions. As expected, BG decreased MGMT expression, while combination therapy (4-OH-TAM or ICI combined with BG) significantly decreased both MGMT and ERα expressions. BG alone or in combination with tamoxifen or ICI decreased ER-α expression, whereas tamoxifen alone and ICI alone increased and decreased the same respectively (Fig.3A). p53 expression was slightly altered after ICI treatment. The reduction in p53 expression by ICI alone was reversed when BG was combined (Fig.3A). We investigated the effect of BG on proteins which are involved in cell cycle regulation, apoptosis in tamoxifen resistant breast cancer cells. All these treatments significantly increased the $p21^{cip1}$ protein expression (Fig.3B). PUMA expression was also increased with these treatments. Hence, PUMA may have translocated to the mitochondria, cytochrome C is released (Fig.3B), and apoptosis was triggered in these cells in presence of combination therapy. PARP cleavage is seen in BG treated cells in presence of staurosporin as an indicative of apoptosis (Fig.3C). Therefore, this data suggest that BG promotes cell cycle arrest and can induce apoptosis by modulating p53 function.

O6-Benzylguanine Modulated Transcriptional Targets in Tamoxifen Resistant Breast Cancer Cells: The effect of combination therapy on endogenous MGMT mRNA levels ws aso stuid. Quantitative real-time PCR (qRT-PCR) resulted that anti-estrogens (TAM/ICI) increased the MGMT expression while the combination therapy decreased it compared to control levels. ERα transcription was decreased compared to controls with all these treatments (Fig.4A). Surprisingly, p21 and PUMA mRNA was significantly increased in the presence of combination treatments (Fig.4B &C). These results suggests that p53 mediated target gene transcription was affected by the drug combinations in breast cancer cells (Fig. 3 & 4).

O6-Benzylguanine Enhances p21 Transcriptional Activity in Tamoxifen Resistant Breast Cancer Cells: In order to investigate the effect of BG on p53 function, we performed luciferase reporter assays. Tamoxifen resistant MCF-7 breast cancer cells were transfected with p21 luc promoter construct in presence or absence of BG (target gene of p53). These results clearly demonstrate that BG significantly enhanced p21 transcriptional activity by 4-5 fold in these cells (Fig.4D).

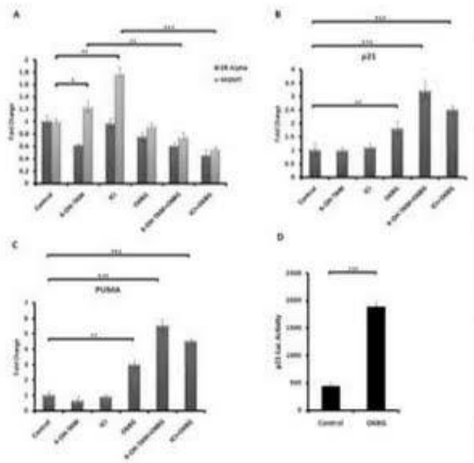
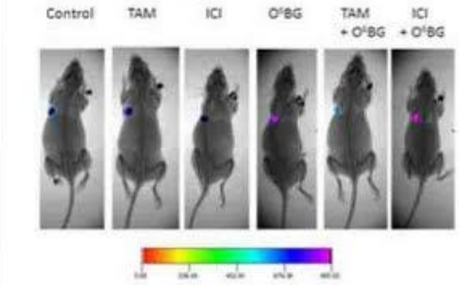


Figure 4. Tamoxifen resistant MCF-7 breast cancer cells were treated in presence or absence of BG (50 μg) for 48h and later 4-OH tamoxifen and ICI (1μM) was either alone or in combination with BG and 24h later cells were harvested and total RNA was isolated. (A) MGMT and ERα (B) p21 transcription (C) PUMA transcription was determined by qRT-PCR. 4-OH tamoxifen and ICI induces MGMT transcription. BG induced PUMA and p21 transcription. (D) Tamoxifen resistant MCF-7 breast cancer cells were transfected with p21-luc construct and 6h later treated with BG and 24h later cells were harvested. p21 transcriptional activity was significantly increased by BG in these cells.

O6-Benzylguanine Inhibits Tamoxifen Resistant Breast Cancer Cell Growth and Increase Resistant Breast Cancer Cell Sensitivity to Anti-Estrogen Therapy (TAM/ICI): Detailed necropsy revealed that all the mice had tumors in the breast. The data summarized in Table 1 show the daily BG alone or in combination with twice weekly tamoxifen/ICI significantly decreased median tumor volume and weight as compared with that seen in tamoxifen/ICI treated and control mice. The combination of BG with tamoxifen or ICI produced the greatest decrease in median tumor volume as compared with control mice (83.99 mm^3, 9.33 mm3 (TAM+BG), respectively; p< 0.0001); (83.99 mm^3, 31.60 mm^3 (ICI+BG), respectively; p<0.0001). Tumor weight was also significantly reduced in mice treated with combination therapy as compared with control mice (81.23 mg, 22.30 mg (TAM+BG), respectively, p<0.0005); (81.23 mg, 51.57 mg (ICI+BG), respectively, p<0.0005). (Table.1). Body weight was not changed among all treatment groups as compared with control mice. No visible liver metastases were present (enumerated with the aid of a dissecting microscope) in all treatment groups.

Histology and IHC Analysis: We next determined the *in vivo* effects of BG (alone or in combination) with tamoxifen/ICI. Tumors harvested from different treatment groups were processed for routine histological and IHC analysis. Tumors from mice treated with BG alone or in combination with tamoxifen/ICI exhibited a significant decrease in MGMT, ERα, ki-67 as compared with tumors treated with tamoxifen/ICI alone or control group. p53 expression was not much altered in these treatment groups. In sharp contrast, the expression of p21 was significantly increased in tumors from mice treated with BG either alone or in combination with tamoxifen/ICI. The images were analyzed by ImageJ (NIH) and MGMT, ERα, p53, p21 and ki-67 expressions were quantified by the ImmunoRatio plugin. (Fig.5).



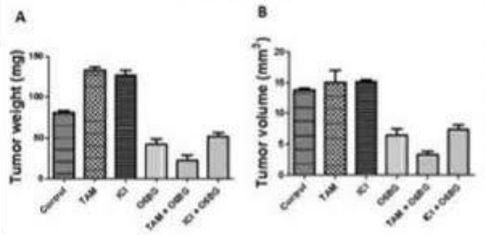
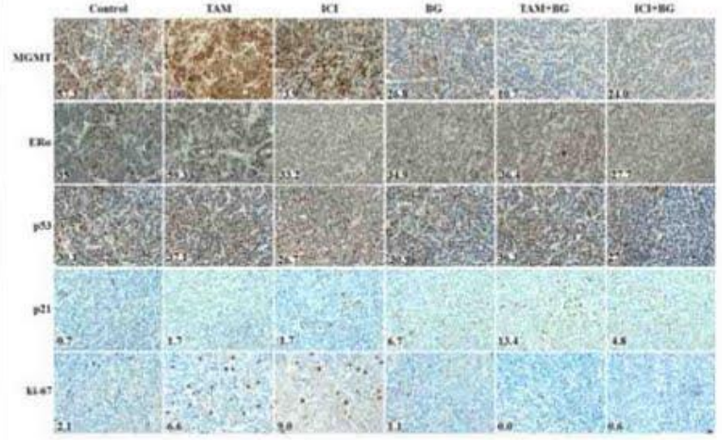


Figure 5. Tumors were harvested from control mice and mice treated with tamoxifen/ICI, BG, or both tamoxifen/ICI and BG. The sections were immunostained for expression of MGMT, ERα, p53, p21 and ki-67. Tumors from mice treated with BG either alone or in combination with tamoxifen or ICI had a significant decrease in the expression of MGMT, ERα and ki-67. p53 expression was not much altered in these treatment groups. In sharp contrast, expression of p21 was significantly increased in all these treatment groups compared to controls. Representative samples (40X) are shown.



Conclusions

1. In the present study, we observed that prolonged treatment with anti-estrogens causes drug resistance by inducing the DNA repair protein O⁶-methylguanine DNA methyltransferase (MGMT).
2. Decreasing the expression of MGMT by exposing breast cancer cells to BG sensitized these cells to anti-estrogen therapy (tamoxifen and ICI 182,780).
3. We also observed that combination therapy of anti-estrogens and MGMT blockers not only overcame the MGMT derived drug (tamoxifen and ICI) resistance but also increased the efficacy of anti-estrogen therapy by decreasing estrogen receptor expression and restoration of the functional activity of p53 in tamoxifen-resistant breast cancer cells.
4. Combination therapy inhibited tamoxifen resistant breast tumor growth *in vivo*.

Acknowledgements

We would like to thank the Florida Department of Health, Bankhead-Coley Cancer Research Program 09BN-10 for their funding of this project.

Arachidonic acid affects aardvark afferents and alters anabolism

Anna N. Mus

Department of Integrative Science, The University of Texas-Pan American

Introduction

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Results

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Discussion

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CSE 3
Fluency with Information Technology (FIT)

Adventures in Computational Thinking

By Wendy Hu

Overview

During this quarter we have learned about Information Technology (IT) Fluency, including proficiency with certain computer applications, foundational computer literacy, principles on which you can build new understanding as IT evolves, high-level reasoning and IT problem solving, and basic web programming (HTML and JavaScript). Computational thinking, data analysis and data presentation have been the main themes throughout.

Visual Programming with Scratch

Scratch is a programming language developed by the Lifelong Kindergarten Group at the MIT Media Lab to help young people learn how to develop computer programs.

The development of Scratch (and its name) was inspired by the scratching process that DJs use to create new sounds and music by rubbing vinyl-style vinyl records back and forth on record turntables, creating new and distinctively different sound out of something that exists.

Computational Thinking

- Computational Thinking is thinking at multiple levels of abstraction
  - For solving problems
  - For designing systems
  - For understanding the power and limits of human and machine intelligence
- Computational thinking also means being able to go above the original whole and constructing a whole of wholes. Or going above the whole and thinking about the whole in a different way.
- The concept of computational thinking is being spearheaded by the Center of Computational Thinking at Carnegie Mellon where their major activity is conducting PRO BEs or PRO Bem-enhanced Explorations.

- There are some very basic statistical concepts that every college educated person should understand.
- These are useful for understanding our grade distributions in classes here at UCSD, current events, and all manner of information in our lives.
- Because this isn't a math class, we have focused on the intuition and use of a very few of the most common statistical metrics.

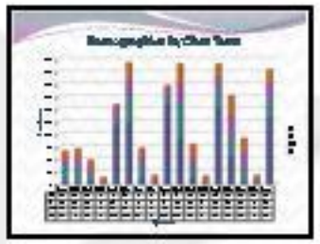


Image Analysis and Manipulation with Photoshop

- Image analysis is the extraction of meaningful information from images; mainly from digital images by means of digital image processing techniques.
- Image analysis tasks can be as simple as reading bar coded tags or as sophisticated as identifying a person from their face.
- Computers are indispensable for the analysis of large amounts of data, for tasks that require complex computation, or for the extraction of quantitative information.

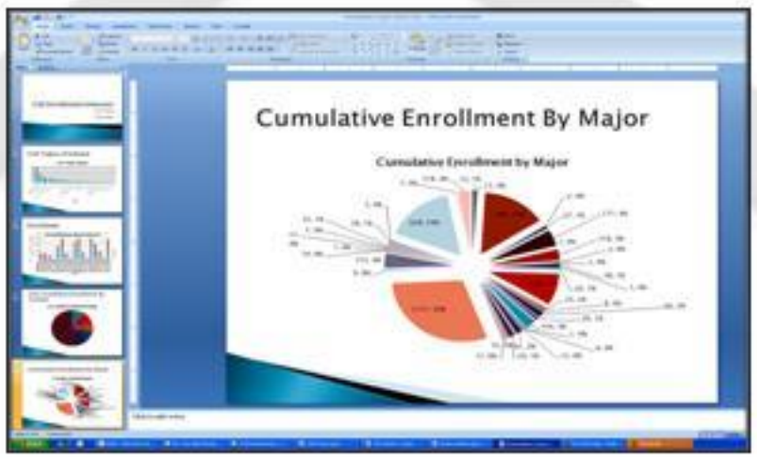
Data Analysis and Visualization with Excel

- One of the most common uses of a spreadsheet is to chart financial information.
- We created an annual budget for ourselves, so we can monitor our spending while here at UCSD and calculate how much discretionary spending money we have each month.
- We were encouraged to use real information (they promised not to ask other than to help check us off!) but if we didn't feel comfortable with that, could feel free to make up numbers - they wouldn't know if it was real anyway!

	Per Year	Per Month	Per Week	Per Day
INCOME:				
Student Loans	$6,470.00	$1,705.00	$393.23	$56.23
Parents	$1,200.00	$100.00	$25.00	$3.57
Total Income:	$10,670.00	$1,805.00	$418.23	$59.81
Expenses:				
Federal Expenses				
Student Loans	$0.00	$0.00	$0.00	$0.00
Health Insurance	$0.00	$0.00	$0.00	$0.00
Books & Supplies	$400.00	$34.00	$7.85	$1.12
Parking	$107.00	$9.00	$2.08	$0.30
Living Expenses:				
Rent	$2,340.00	$195.00	$45.00	$6.43
Utilities	$480.00	$40.00	$9.23	$1.32
Renter's Insurance	$0.00	$0.00	$0.00	$0.00
Gas	$480.00	$40.00	$9.23	$1.32
Cell Phone	$312.00	$26.00	$6.00	$0.86
Food	$2,340.00	$195.00	$45.00	$6.43
Gym	$336.00	$28.00	$6.46	$0.92
Total Expenses:	$6,107.00	$1,509.00	$348.25	$49.75
Spending Money:	$563.00	$46.92	$10.83	$1.55

Presentation of Information with Word & PowerPoint

Presenting complex raw data into easily understandable charts and graphs displaying it through the filters of PowerPoint and Word.



Making Information Available to the World with HTML and Web Pages

- The World Wide Web is a system of interlinked hypertext documents contained on the Internet.
- With a web browser, one can view web pages that may contain text, images, videos, and other multimedia and navigate between them using hyperlinks.
- Using concepts from earlier hypertext systems, English physicist Sir Tim Berners-Lee, now the Director of the World Wide Web Consortium, wrote a proposal in March 1989 for what would eventually become the World Wide Web.[1]
- He was later joined by Belgian computer scientist Robert Cailliau while both were working at CERN in Geneva, Switzerland. In 1990, they proposed using "HyperText to link and access information of various kinds as a web of nodes in which the user can browse at will",[2] and released that web in December.[3]
- "The World-Wide Web (W3) was developed to be a pool of human knowledge, which would allow collaborators in remote sites to share their ideas and all aspects of a common project."[4]

Enhanced Indoor Tracking using Bayesian filters and past movement patterns

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I. Research Aim

- The aim of this research is to create an algorithm that enhances Wi-Fi tracking capability in an indoor environment.
- The **HABITS** (History Aware Based wi-fi Indoor Tracking System) algorithm will allow for real-time continuous tracking in areas where this was not previously possible due to signal black spots. Historical movement patterns will be used to probabilistically facilitate this.

II. Positioning Systems

- Positioning is a process to obtain the spatial position of a target.
- In recent years the need has arisen for the development of Location Based Services (LBS) which work in an indoor environment. Large public buildings; universities, hospitals and shopping centres have become target areas.
- Due to the poor performance of Satellite and Cellular systems indoors, a separate system is required.
- 802.11 Wi-Fi networks as specified by the IEEE are available in many large buildings. The signals transmitted by the Access Points (APs) provide a readily available network of signals which may be used for positioning

III. Ekahau

- The Ekahau RTLS (Real Time Location System) is used to provide the position of a Wi-Fi device.
- It does not rely on proprietary infrastructure or readers in order to track devices.
- The existing 802.11 Wi-Fi network is used for all tracking with signal strengths of the Access Points (APs) being recorded as shown in fig 1.

Fig 1: Heat Map showing areas of similar RSS values

- Ekahau Site Survey records RSSI data of the test area.
- This data is mapped to a model which shows the areas where a Wi-Fi enabled device may travel (Fig 2).

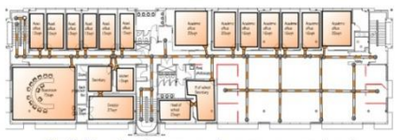

Fig 2: Map showing areas where a user may travel

- The observed Wi-Fi signal strength data is recorded at each location. A probability is then assigned to each location based on this data as Fig 3 shows.

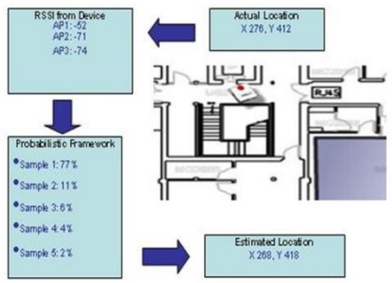

Fig 3: Probabilistic estimation in Ekahau

IV. Multisensor data Fusion

- Multi sensor data fusion can facilitate bringing together data from different sources.
- Using a combination of the live data from Ekahau, historical movement data and dead reckoning information, an enhanced live track may be produced which would be continuous (Ekahau has 5 sec updates at its fastest) and would continue to track when signals were poor - black spots.
- A number of filtering techniques may be used to produce a new estimate of the state of a system.

V. Bayesian Filtering

- Bayes filter is commonly used in robotics as a method to infer the position of a robot.
- This recursive algorithm enables a position estimate to be continuously updated by including the most recent sensor readings.
- A general form of the Bayes filter, which may be used for a discrete case like this, is outlined in pseudo code below.

General Algorithm for Bayes Filtering

1 Algorithm_filter($bel(x_{t-1})$, u_t, z_t):
2 for all xt do
3 $\overline{bel}(x_t) = \sum p(x_t \mid u_t, x_{t-1})\, bel(x_{t-1})$ (PREDICTION STEP)
4 $bel(x_t) = \eta\, p(z_t \mid x_t)\, \overline{bel}(x_t)$ (UPDATE STEP)
5 end for
6 return $bel(x_t)$

Inputs belief $bel(x_{t-1})$ at t-1; most recent control u_t + measurement z_t.
Output is the belief $bel(x_t)$ at time t.

VI. HABITS Overview and Context

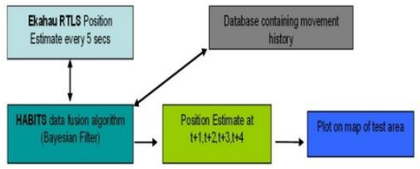

Fig 4: HABITS overview

Figure 4 gives the flow of data in HABITS.

- The Ekahau API enables a position estimate from the Ekahau system to be fed into the fusion algorithm.
- This information will then be compared to the data stored in the historical database.
- From this a prediction of the movement steps for the next 5 seconds will be calculated.
- These predicted positions will be plotted on the map. Figure 5 shows the context in which HABITS will be used.

Fig 5: Context of HABITS

VII. Implementation Graphing/ Mapping

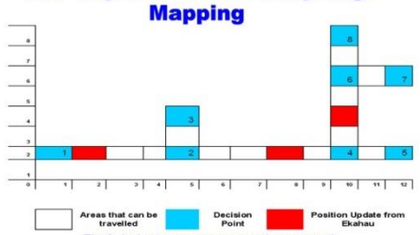

Fig 6: Indoor map represented as a graph

- The test area would need to be mapped in a similar way to Ekahau. These maps would contain all the possible routes that a person may travel.
- A graph may be used as a means of representing the movement of people indoors (Fig 6).
- This graph of the area will be used along with the historical movement data of a person (Fig 7) in order to calculate the transition matrix

Movement History of User 1			
	Morning	Afternoon	Evening
Day 1	12467	5645,5467	76421
Day 2	12467	768,867	76421
Day 3	12467	768,867	76421
Day 4	12467	7645	5421

Fig 7: Historical movement sequences through the nodes.

VIII. Probablistic Matrices

- The more HABITS is used the more accurate it should become.
- When a critical set of historical movement data has been gathered it can be analysed for patterns.
- Probabilistic functions can be calculated for the decision points. Fig 8 shows the initial probability of moving from one state to a neighbouring one.
- This data will then be used to update the various weights/inputs to the HABITS algorithm .
- Movement patterns of a particular user or type of user can facilitate profiling which can be used for a number of ambient intelligent applications.

Prior State

New State	1	2	3	4	5	6	7	8
1	0.5	0.5	0	0	0	0	0	0
2	0.2	0.5	0.1	0.2	0	0	0	0
3	0	0.5	0.5	0	0	0	0	0
4	0	0.2	0	0.5	0.1	0.2	0	0
5	0	0	0	0.5	0.5	0	0	0
6	0	0	0	0.2	0	0.5	0.15	0.15
7	0	0	0	0	0	0.5	0.5	0
8	0	0	0	0	0	0.5	0	0.5

Fig 8: Transition Matrix

- HABITS can be tested by comparing its tracking capability with the standard Ekahau system in terms of Accuracy, Precision, Yield and Latency.

IX. Publications

- Curran, K., Furey, E., (2007). "Pinpointing Users with Location Estimation Techniques and Wi-Fi Hotspot Technology". Int Journal of Network Management
- Furey, E., Curran, K., Mc Kevitt, P., (2008) "HABITS: A History Aware Based Wi-Fi Indoor Tracking System". PGNET 2008 The 9th Annual Postgraduate Symposium: The Convergence of Telecommunications, Networking and Broadcasting 2008. Liverpool, John Moores University, UK
- Petzold, J., Bagci, F., Trumler, W. And Ungerer, T., 2006. "Comparison of Different Methods for Next Location Prediction". Lecture Notes In Computer Science, pp. 909

SoDA: Somatic Diversification Analysis of antigen receptor recombinations

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1 Introduction

The defining characteristic of adaptive immunity is the somatic diversification of its antigen receptor genes. The genes for the T-cell receptor (TCR) and immunoglobulin (Ig) are formed by a process known as V(D)J recombination, in which transcribable genes are composed by the combinatorial joining of gene segments from two or three classes, depending on the specific locus involved. Detailed knowledge of how specific broadly neutralizing HIV antibodies are formed or of the differences in composition between self and non-self antigen receptors is elusive but important for research in vaccine design and autoimmune disorders. Understanding the details of the composition of specific Ig and TCR and the specific processes they underwent during development can facilitate these research endeavors. Thus, we have developed a web-based software tool that analyzes antigen receptor sequences to identify the V, D and J gene segments used, as well as the recombination sites, point mutations and n- and p-nucleotides introduced. We demonstrate the functionality of the software here with an analysis for differential biases within large samples of Ig classified as autoreactive or not.

2 SoDA – (Somatic Diversification Analysis)

SoDA[1] is an implementation of a 3-dimensional algorithm for aligning multiple contiguous DNA sequences to a master antigen receptor sequence in order to determine:

1: the most likely gene segment composition

2: the rules for combining those segments during the formation of an antigen receptor.

Rules for recombination include:

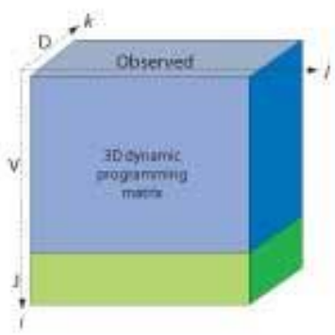
> Identifying recombination sites: some gene segments may undergo exonuclease activity, resulting in a loss of nucelotides in the coding junction.

> Identifying n-nucleotide additions: the enzyme TdT can introduce non-templated nucleotides into the coding junctions.

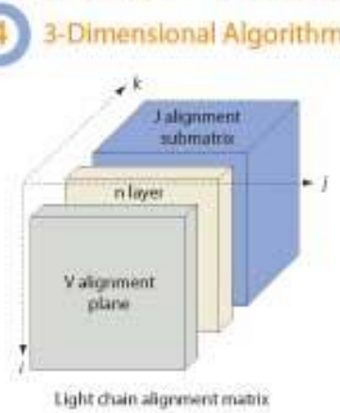
> Identifying somatic mutations: in B-cells, receptor genes undergo somatic hypermutation, whereby random point mutations are introduced in the gene segments.

3 Why is SoDA unique?

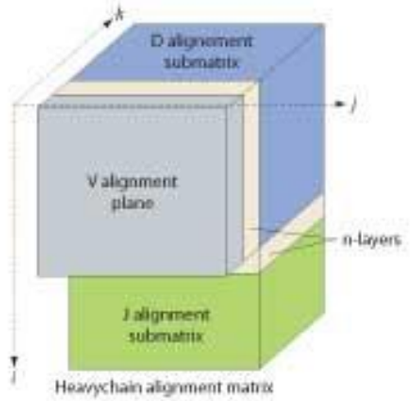
Other bioinformatics solutions already exist (JOINSOLVER[2] and V-QUEST[3]) for approaching this problem, so why build another one? The approach for SoDA is unique in that it relies on dynamic programming, which guarantees an optimal solution. But, unlike typical alignment software, it implements a 3-dimensional algorithm to find it's solution. Formally, SoDA seeks to maximize the likelihood function $P(G,M|T)$, where G = set of gene segments, M=rules for combing those gene segments, T = target sequence, and M(G)=T.



4 3-Dimensional Algorithm



Light chain alignment matrix



Heavychain alignment matrix

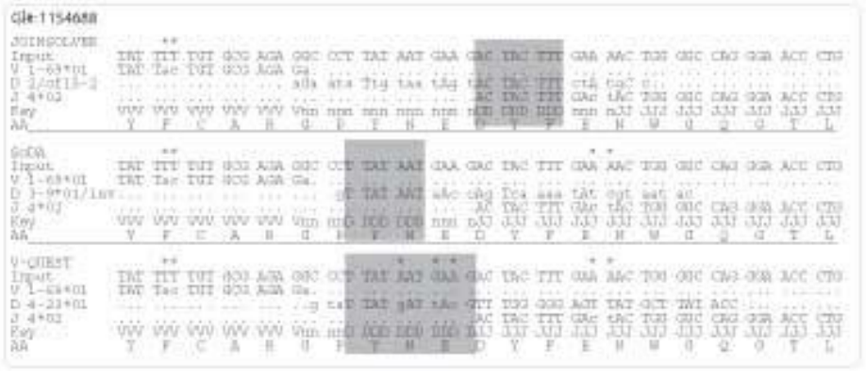
Considering exonuclease activity in the solution adds a constraint to the alignment algorithm: from any point in one gene segment alignment, the traceback path must be able to jump to any point in the contiguous gene segment alignment. For both light and heavy chains, the V alignment is computed in a single plane. Then, the alignment for each contiguous sequence that follows is computed in a 3-dimensional matrix where the alignments run perpendicular to the direction of the alignments for the previous gene segment alignment. This enables the traceback path to jump from any point in one alignment, to any point in the contiguos alignment, thus accounting for the exonuclease constraint. TdT enzymatic activity is captured by the traceback path through the special n-layers.

5 Testing the Algorithm and Results

We tested SoDA using 120 artificial recombination sequences generated by a program that simulates V(D)J recombination. We created 30 sequences at each of four mutation rates: 2.5%, 5%, 10%, and 15%. SoDA proved to be the most reliable in predicting the correct gene segment composition.

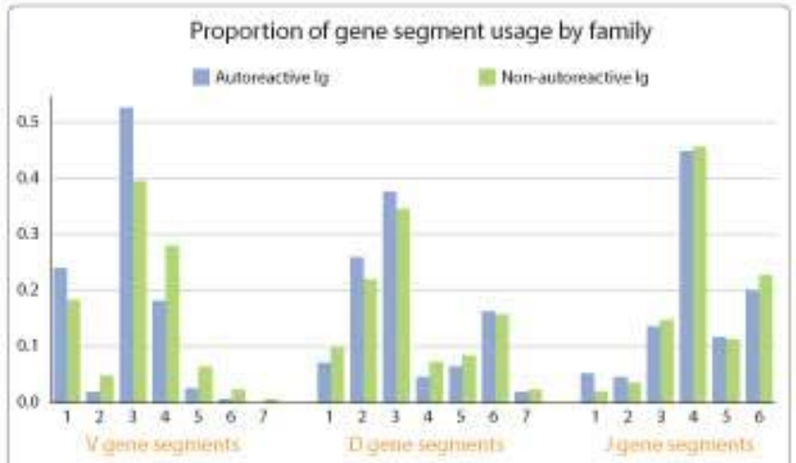
	2.5% mutation			5% mutation			10% mutation			15% mutation		
	SoDA	JS	VQ	SoDA	JS	VQ	SoDA	JS	VQ	SoDA	JS	VQ
V correct	30	30	30	30	26	29	30	25	29	30	23	28
D correct	28	26	16	28	28	10	27	25	18	22	19	16
J correct	30	29	29	30	30	28	29	28	29	28	30	30
VDJ correct	28	26	16	28	25	8	27	20	15	22	15	15

SoDA was designed to find the most likely gene segments as well as the most likely rules that created that rearrangment. So, we tested SoDA against 30 rearrangements from Genbank. Below is the CDR3 region of an Ig rearrangement that arguably shows how SoDA's approach finds the best possible explanation for the gene segments and the rules for combining them:

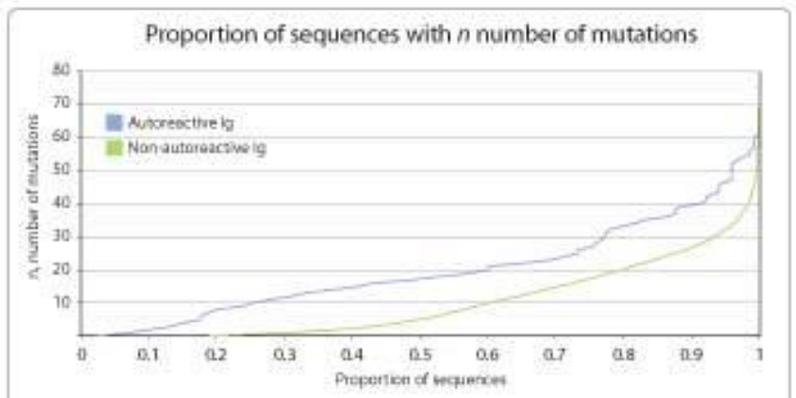


6 Characterizing Autoreactive vs. Non-autoreactive Antibodies

With SoDA, we are able to quatitatively characterize Ig sequences, specifically looking at gene segment usage, CDR3 length, n-nucleotide addition, and mutations. To do this, we downloaded and analyzed approximately 9,450 non-autoreactive Ig and 154 autoreactive Ig sequences from Genbank. Sequences were distinguished and divided into these two groups through keyword searches. Clonal duplicates were removed from each set using an automated procedure that compared several criteria in the sequences.



The differences in segment usage between autoreactive and non-autoreactive Ig are contrasted here. The differences in V-gene segment usage are statistically significant.



This graph shows the number of mutations present in the evaluated sequences for proportions of the sequences. At each proportion, autoreactive Ig contain more mutations than non-autoreative sequences.

Try out SoDA on the web: http://dulci.org/soda

References

1. Volpe, JM. and Cowell, LG. and Kepler, TB. SoDA: implementation of a 3D alignment algorithm for inference of antigen receptor recombinations. Bioinformatics. 2006; 22(4):438-44.

2. Souto-Carneiro, M.M., et al. Characterization of the human Ig heavy chain antigen binding complementarity determining region 3 using a newly developed software algorithm, JOINSOLVER. J Immunol. . (2004); 172, 6790-6802.

3. Giudicelli, V., et al. IMGT/V-QUEST, an integrated software program for immunoglobulin and T cell receptor V-J and V-D-J rearrangement analysis. Nucleic Acids Res. (2004); 32, W435-W440.

Considerations

- Contrast between text colour and background colour
- White space is nice
- Avoid fancy effects
- Underline or *italicise*?
- Font pleasant to look at
- Edit your text, edit it, then edit it again
- We read top left to bottom right....
- Pleasant on the eye: subtle colours

More Help to Come...

Considerations

You may need to read ahead to complete your poster. Be proactive, seek help if you need it, and DON'T LEAVE IT TOO LATE!