How to Present with Power and Insight

Michael Laughter
and
Clint Stivers

The Communication Center

First, Prepare Your Research and Topic

- Analyze audience
- Streamline material
- Create one to three main points
- Think: Problem / Solution
- Define relevant point(s) for audience

Anticipate Questions

- Introduce topic through importance to field
- Think: who, what, where, when, why, how
- Make material accessible through graphics
- Vary speed of delivery
- Gauge comprehension
- Adjust accordingly
- Bring it back to your discipline

Never Forget:

You—not your media—are your presentation

Use Your Physical Space

- Establish control
- "Aim" your voice
- Implement "Speaker's Triangle"
- Keep your eye on your audience
- Control gestures
- Vary information delivery methods
- Adjust physical stance to screen location

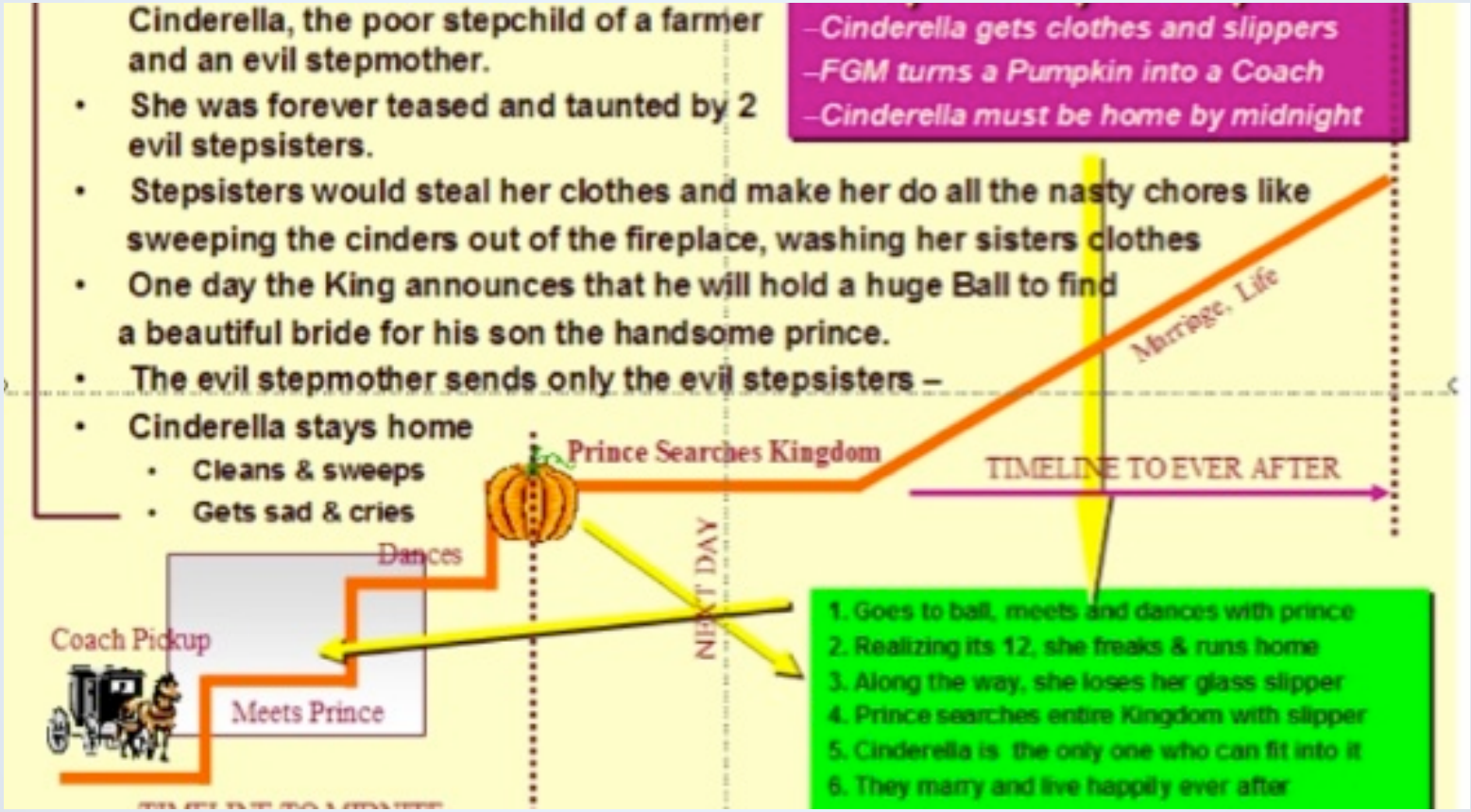
Use Slides Only for Emphasis

- Do not overwhelm
- Obey “Rule of Seven”
- Modulate creativity, color, animation
- Avoid “reading”
- Use slides to remind of importance, relevance
- Make last slide “count”

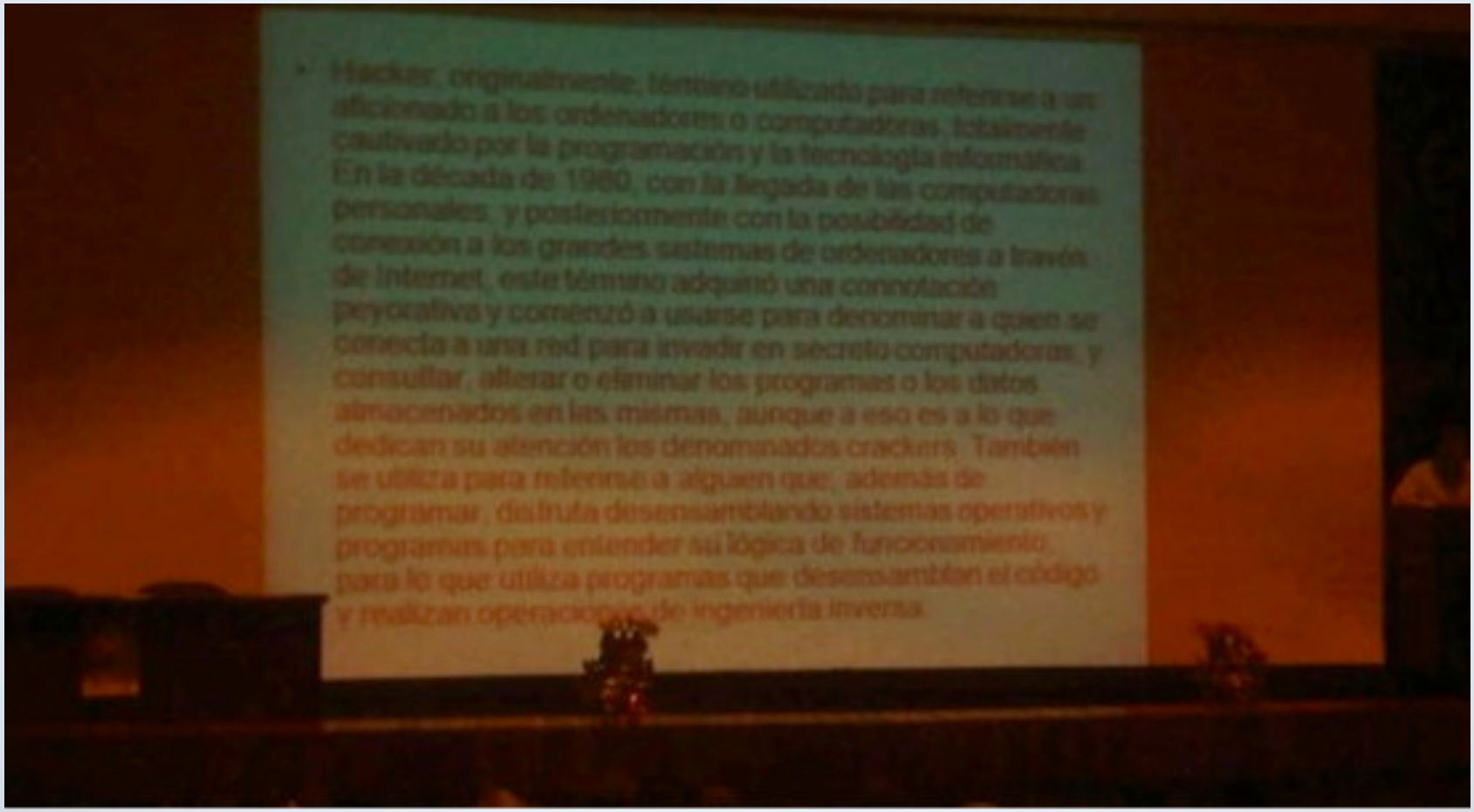
Design Principles

- Less is More
- Arrangement/Layout
- Alignment
- Font
- Color
- Contrast

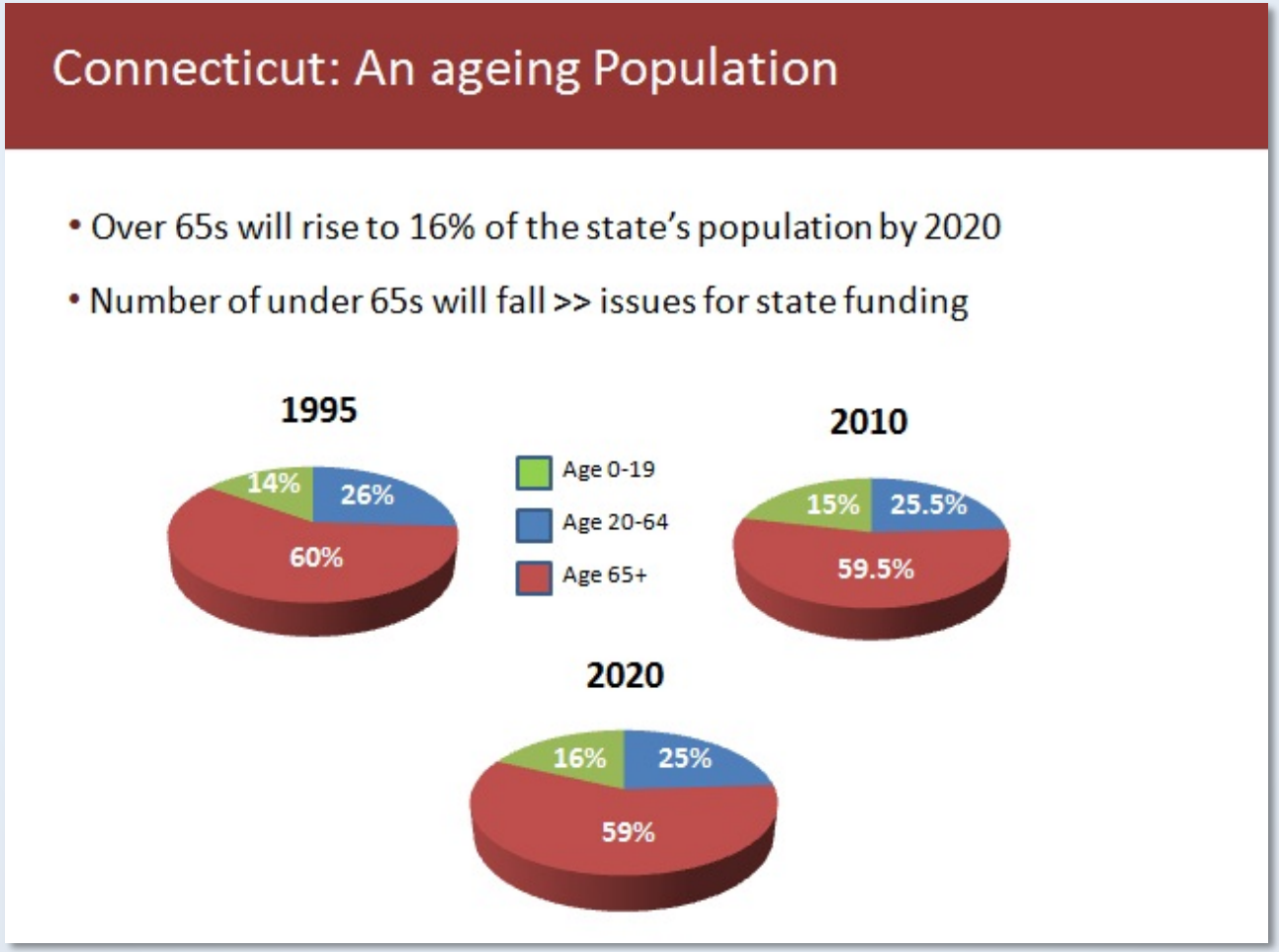
Death by PowerPoint



Not a Novel


Hacker, originalmente, término utilizado para referirse a un
aficionado a los ordenadores o computadoras, totalmente
cautivado por la programación y la tecnología informática.
En la década de 1980, con la llegada de las computadoras
personales, y posteriormente con la posibilidad de
conexión a los grandes sistemas de ordenadores a través
de Internet, este término adquirió una connotación
peyorativa y comenzó a usarse para denominar a quien se
conecta a una red para invadir en secreto computadoras, y
consultar, alterar o eliminar los programas o los datos
almacenados en las mismas, aunque a eso es a lo que
dedican su atención los denominados crackers. También
se utiliza para referirse a alguien que, además de
programar, disfruta desensamblando sistemas operativos y
programas para entender su lógica de funcionamiento,
para lo que utiliza programas que desensamblan el código
y realizan operaciones de ingeniería inversa.

Arrangement/Layout



Source: *The LACS Training Blog*. <http://lacstrainingblog.com/2012/04/26/presentations-tips-for-effective-powerpoint-design/>. 2012.

Arrangement/Layout

Falling Annual Crime Incidents 1999-2010

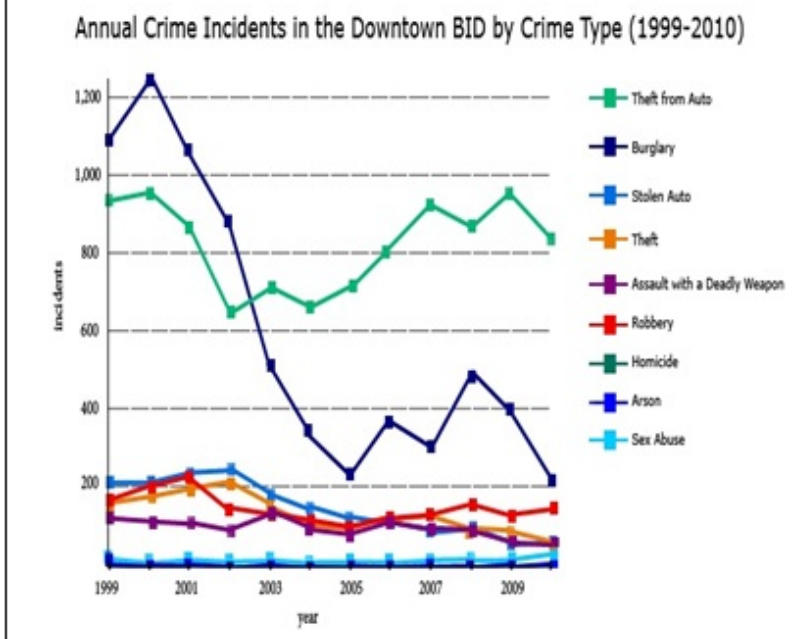
- Crime is falling *across the board*

  (42% fall overall 1999-2010)

- Largest falls: *burglary* and *theft from cars*

  (82% and 16% respectively)

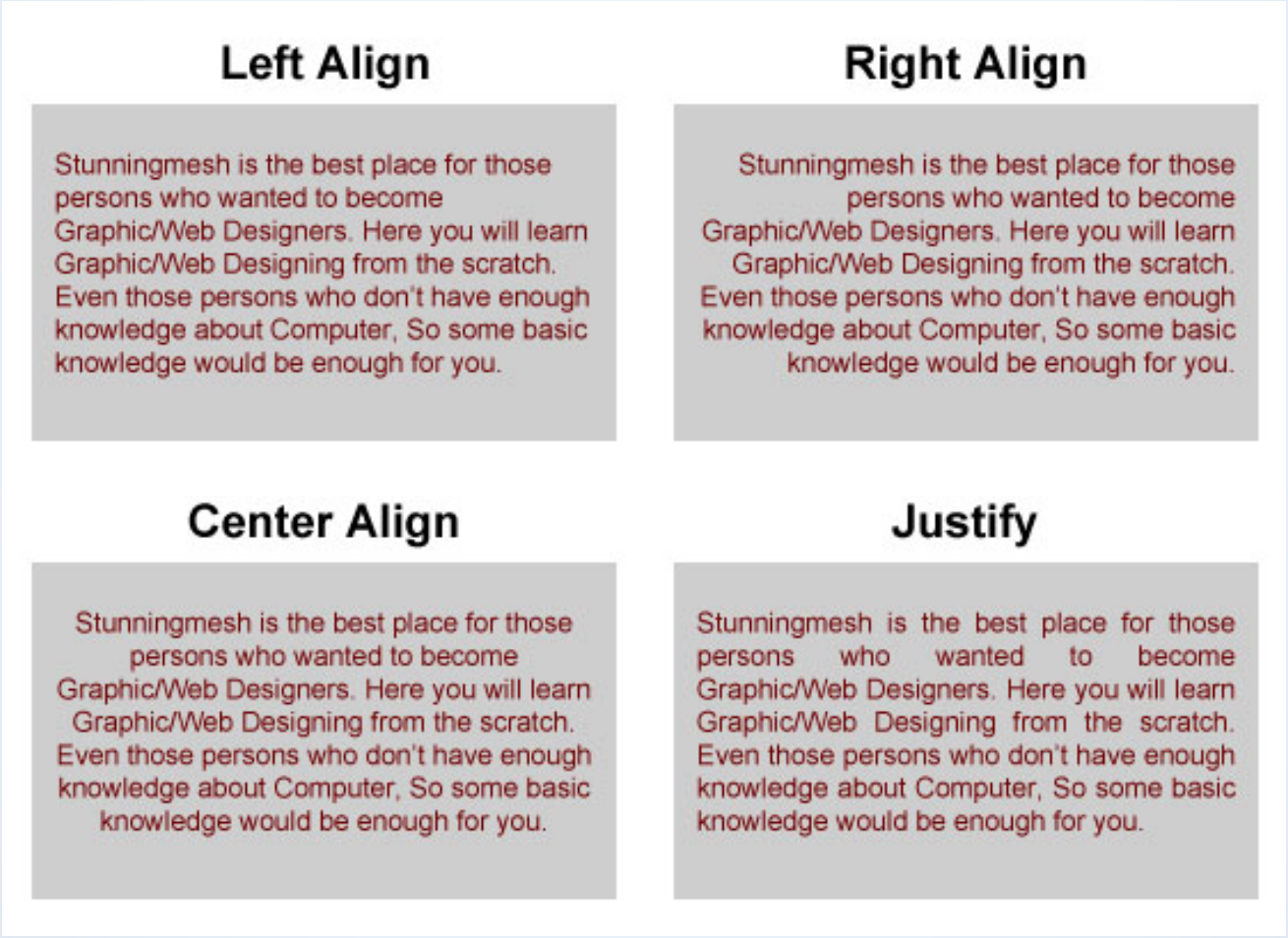
- Other reductions: car theft, theft, robbery, and sex abuse



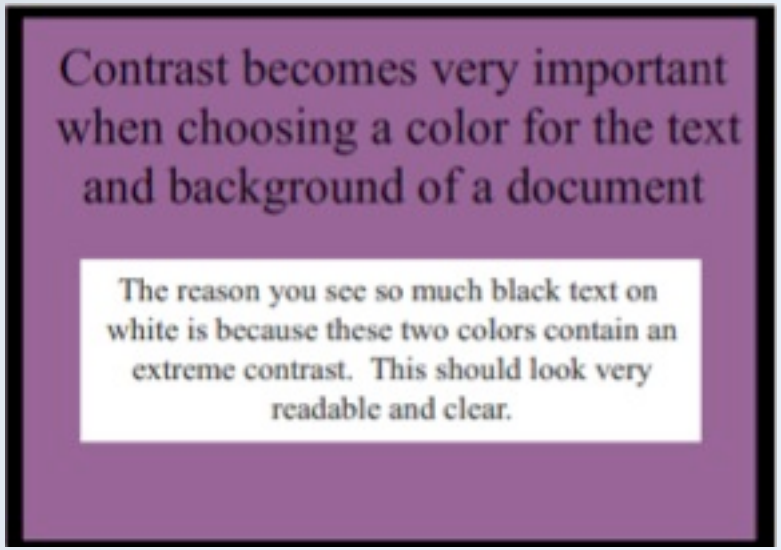
Original data available from www.crimelab.com

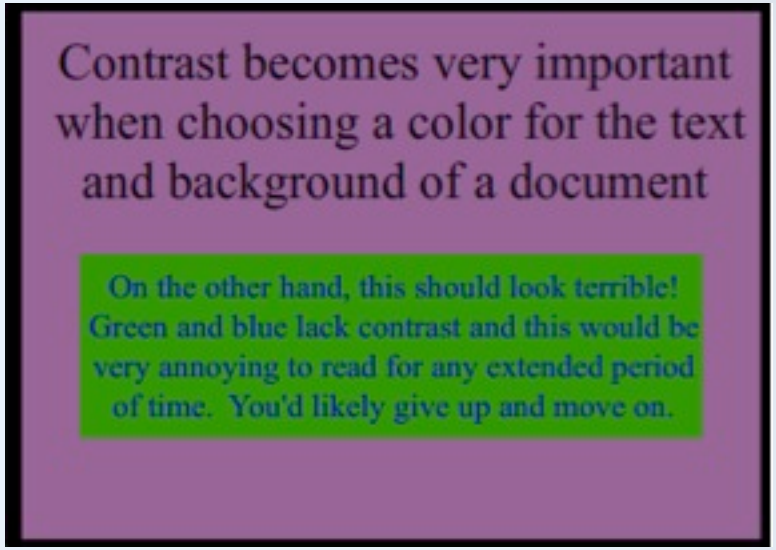
Source: *The LACS Training Blog*. 2012. <http://lacstrainingblog.com/2012/04/26/presentations-tips-for-effective-powerpoint-design/>.

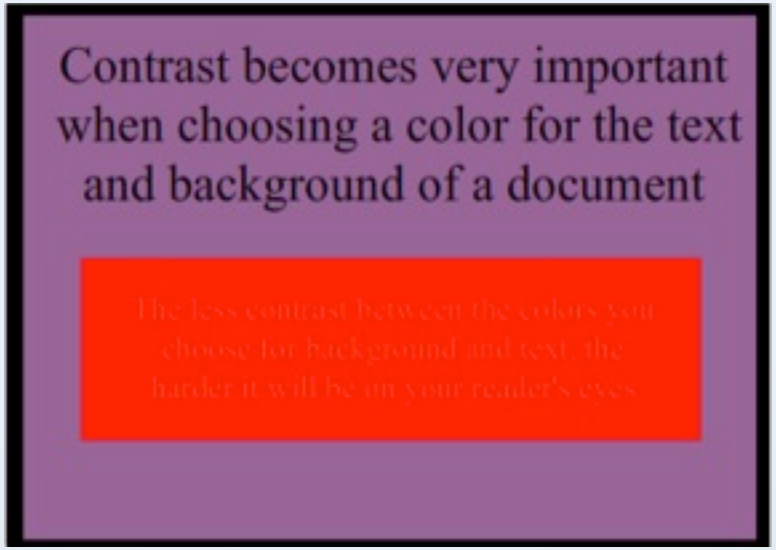
Alignment


Left Align
Stunningmesh is the best place for those persons who wanted to become Graphic/Web Designers. Here you will learn Graphic/Web Designing from the scratch. Even those persons who don't have enough knowledge about Computer, So some basic knowledge would be enough for you.
Right Align
Stunningmesh is the best place for those persons who wanted to become Graphic/Web Designers. Here you will learn Graphic/Web Designing from the scratch. Even those persons who don't have enough knowledge about Computer, So some basic knowledge would be enough for you.
Center Align
Stunningmesh is the best place for those persons who wanted to become Graphic/Web Designers. Here you will learn Graphic/Web Designing from the scratch. Even those persons who don't have enough knowledge about Computer, So some basic knowledge would be enough for you.
Justify
Stunningmesh is the best place for those persons who wanted to become Graphic/Web Designers. Here you will learn Graphic/Web Designing from the scratch. Even those persons who don't have enough knowledge about Computer, So some basic knowledge would be enough for you.

Contrast and Color







Importance of Font

Fonts to Avoid

Don't use any fonts that are hard to read. This includes:

- *cursive fonts,*
- **really wide fonts,**
- really narrow fonts,
- **fonts with really thick letters, and**
- Fonts that are too interesting

Look the Part

- Arrive early and stay late
- Dress professionally
- Check your details
- Verify technology
- Plan for small “failure”
- Engage through smiling
- Invite questions

Finish with Grace

- Summarize
- Pose question(s)
- Use “factoid,” polling data, usages, to close
- Leave audience with value, relevance
- Avoid abrupt stopping
- Adjust dynamics for group or individual

Factoid

- 30 million PowerPoint presentations are made each day worldwide
- How many are successful?

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FORMULATION AND OPTIMIZATION OF TRIGLYCERIDE-BASED ELASTOMERS, RUBBERS, AND ENGINEERING POLYMERS

John J. LaScala and Richard P. Wool

University of Delaware . Center for Composite Materials . Department of Chemical Engineering

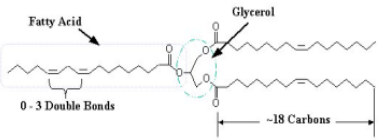
Objective

The objective of this work is to optimize the properties of triglyceride-based polymers. To do this we need understand how triglyceride-based polymers are affected by:

- The number and location of unsaturation sites.
- Different comonomers.
- The concentration of comonomer in the resin.

Chemical Structure of Plant Oils

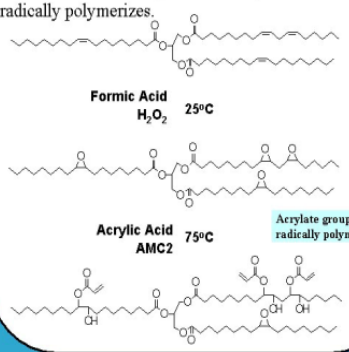
Refined plant oils contain more than 99% triglycerides



Level of Unsaturation	Location of Double Bonds
• 0-9 per Triglyceride • 2.1 DB/TG in Lard • 6.6 DB/TG in Linseed Oil	• 1st double bond on C9 • 2nd double bond on C12 • 3rd double bond on C15

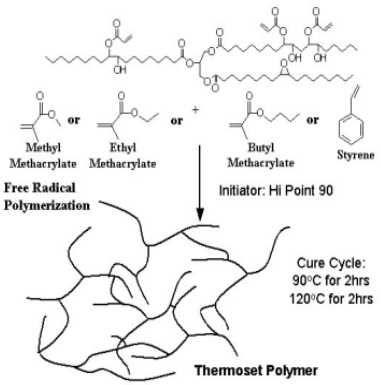
Monomer Synthesis

Unmodified triglycerides do not readily polymerize. However, the unsaturation sites of the triglycerides can be used to add vinyl functionality that free radically polymerizes.



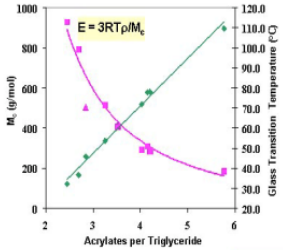
Polymer Synthesis

Triglyceride-based polymers can be formed with or without various comonomers.



Effect of Oil Type

A number of distinct oils were used to make polymers. These oils ranged from 2.8 (olive oil) to 6.6 (linseed oil) unsaturation sites per triglyceride. In the first experiment, the unsaturation sites were 90% acrylated. In the second experiment, the oils were acrylated to different extents. The oils were polymerized with styrene in a 7:1 ratio.

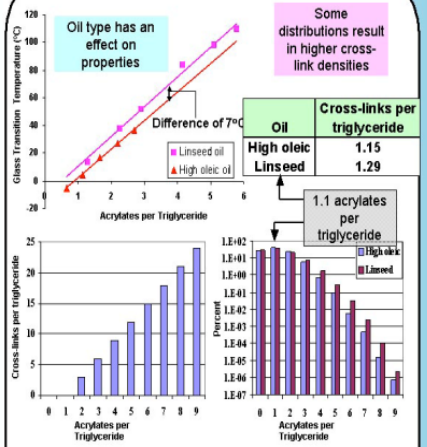


90% acrylation

Molecular weight between cross-links (M_c) decreases as the level of acrylation increases. This also causes increases in T_g.

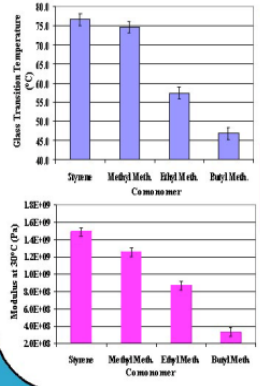
Further increase properties by increasing acrylation level

Oils acrylated to different extents



Effect of Comonomer Type

When made into linear polymers, the glass transition temperatures of styrene (100°C), methyl methacrylate (104°C), ethyl methacrylate (65°C), and butyl methacrylate (20°C) are essentially the only difference among these polymers. This experiment examined how these different comonomers affect the properties of triglyceride-based polymers.



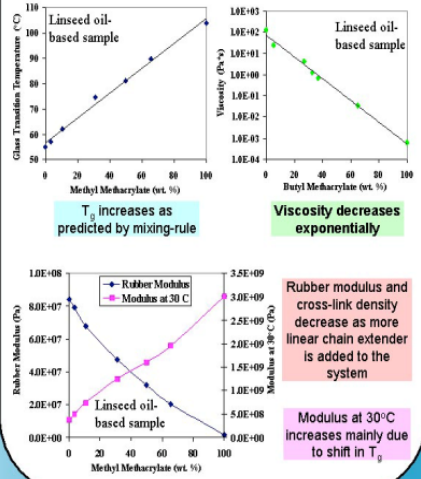
T_g change among comonomers is smaller than expected because of cross-linking

90% acrylated soybean oil with 7 moles of comonomer per mole of triglyceride

Modulus changes mainly because of shifting in T_g

Effect of Comonomer Content

Polymers were made from 90% acrylated oils using different amounts of the four comonomers.



T_g increases as predicted by mixing-rule

Viscosity decreases exponentially

Rubber modulus and cross-link density decrease as more linear chain extender is added to the system

Modulus at 30°C increases mainly due to shift in T_g

Conclusions

- Level of acrylation is the largest controlling factor of properties.
- Distribution of acrylates has a minor affect on properties.
- Increasing comonomer content improves properties even though cross-link density decreases.
- Different comonomers can be used to alter the polymer properties.
- Properties range from rigid and strong to flexible and soft.

Acknowledgements

- Josh Wendschlag
- Wool Research Group
- Garland Fussell
- Center for Composite Materials
- National Science Foundation

Creating a consensus homology model of CFTR from existing models to better define three-dimensional structure and function

Ethan J. Speir[1], Stephen Harvey[1] and Nael McCarty[2]
[1]Georgia Institute of Technology, School of Biology
[2]Emory University, Department of Pediatrics

Background

CFTR and cystic fibrosis

The cystic fibrosis transmembrane conductance regulator (CFTR) is a 1480-residue protein that functions as an ion channel by allowing Cl^- ions to flow out of the cell, a movement that is osmotically accompanied by water. A member of the ATP-binding cassette (ABC) transporter family, this protein has become the focus of recent research due to its role in the pathophysiology of cystic fibrosis. Individuals that are homozygous for defective or absent CFTRs have many chronic maladies with major organs, especially the lungs. This is because the reduced Cl^- export results in thickened mucus that aggregates in the lungs, which can lead to lung infection, lung damage, and early death.

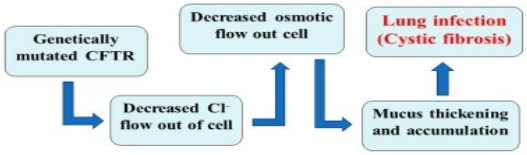
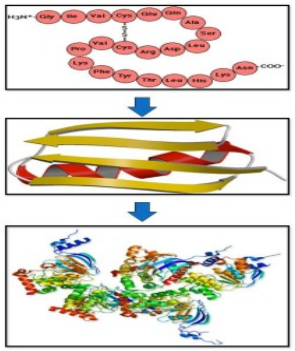


Figure I. Summary of the pathophysiology of Cystic fibrosis

Protein structure

When attempting to determine protein function, it is first necessary to understand protein structure as "structure determines function". This structure is hierarchal and has four distinct levels.



Primary structure: linear sequence of amino acid residues

Secondary structure: formation of local sub-structures resulting from residue interactions

Tertiary structure: formation of global 3D structure

Quaternary structure: assembly of separate protein subunits

Figure II. Depiction of the hierarchy of protein structure

Introduction

Determining protein structure

X-ray crystallography is the ideal method for determining 3D structure of protein. However, CFTR along with many other transmembrane proteins, is too fragile to be crystallized, therefore necessitating alternative structure prediction methods such as homology modeling. This method compares the primary amino acid sequence of a given 'target' protein to the known structure of a homologous 'template' protein through alignment in order to create an atomic-resolution model of the 'target' protein.

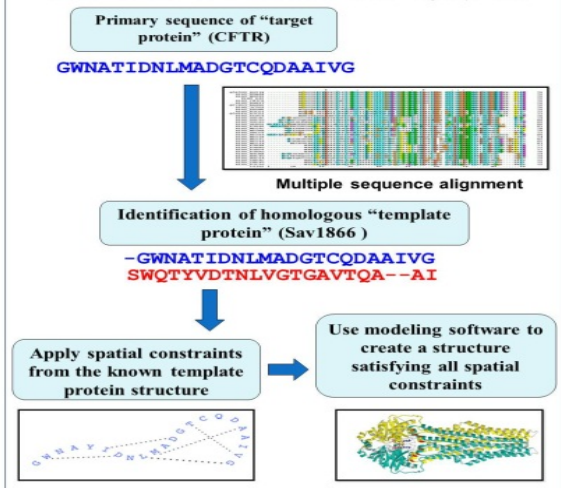


Figure III. Summary of the homology model construction process

Significance

Because "structure determines function" of a protein, a more defined and accurate model of CFTR three-dimensional structure could give insight to the open state of the protein. This would enable development of appropriate drugs that effectively lock CFTR in the open state, thereby increasing Cl^- secretion and potentially assuaging or even curing cystic fibrosis. As this disease currently affects 30,000 Americans, the potential for this research to improve the human condition is clear.

Creating a consensus homology model

Existing homology models

Currently, there exist several homology models for CFTR. Two models that will be considered are those produced by the laboratories of Dr. John Riordan and Drs. Dave Dawson and Mark Sansom. Both models are based on Sav1866.

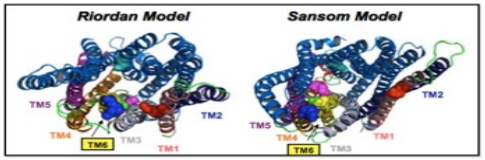


Figure IV. A comparison of the Riordan and Sansom homology models for CFTR

Neither of these models is completely consonant with the predictions gathered from experimentation.

Expected feature	Riordan model	Sansom model
Pore open at both ends	No	No
S341 at narrowest point of pore	Yes	No
T338 and S341 facing into pore	Not quite	No
R334 at outer mouth	Yes	Yes
K95 facing pore	Yes	No
Wide cytoplasmic vestibule	No	No
Kink in TM6 at V350	No	Yes
R352 and D993 facing each other	Not quite	No
R347 and D924 facing each other	Yes	No
C343 in TM6 inaccessible to MTS	Yes	No

Table I. A comparison of the Riordan and Sansom homology models to physiological experimental data

It is important to note that all current models represent the closed state of CFTR. If an open state model that agrees with experimental data can be created, this could then be used for appropriate drug development. I aim to create a consensus homology model using VMD software and data from these two models, a third model (Callebaut), as well as crystal structures from Sav1866 and homologous proteins. Molecular dynamic simulations (up to 20 ns) will then be performed on the model using NAMD and SYBYL software packages.

Acknowledgements

This project would not be possible without the expertise and mentorship of Dr. Stephen Harvey and Dr. Nael McCarty.

Most current computational analysis techniques for newly sequenced microbes and metagenomes rely on orthology and manual annotation.

We're investigating ways to augment these methods using large scale functional network integration to improve microbial community characterization.

Functional Genomic Data Integration for Microbial and Metagenomic Characterization

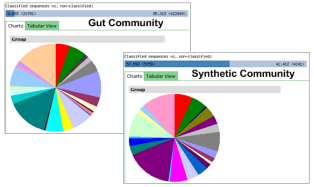
Curtis Huttenhower

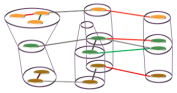
Department of Biostatistics, Harvard School of Public Health

Motivation

Next-generation sequencing is beginning to provide assays for several types of microbial communities, including environmental microbiomes, human microflora, and pathogen populations. However, very little is known about the biological functionality governing these communities, how individual (potentially uncultured) microorganisms function, how multiple species interact in a system, or how they interact with their host or environment. While high-throughput techniques provide an abundance of data, translating this data into useful biological knowledge and testable hypotheses remains a computational and experimental challenge. How can we transfer functional information from model systems to novel microbiomes? How does the human oral or gut microflora contribute to disease? What functional variation is significant in a pathogen population?

Current annotation methods rely on sequence similarity and curated pathways. Here, functional profiles have been generated for a human gut community and a synthetic five-organism community. The profiles are influenced by the structure of prior knowledge, and <5% of the microfloral community (and ~50% of the synthetic community) are characterized using sequence-based annotation.

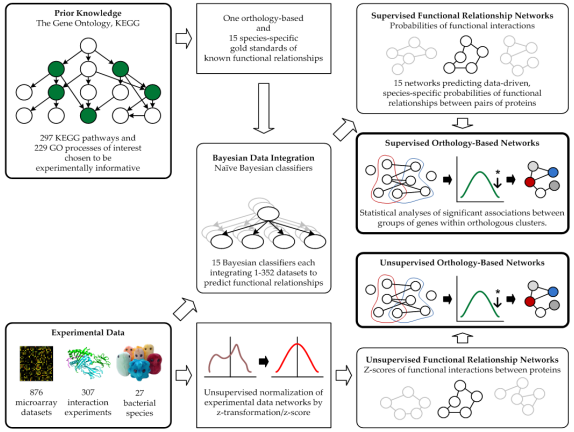




Here, we present preliminary work using large scale experimental data integration and network mining to characterize newly sequenced microbes and microbial communities. By combining sequence orthology with functional data and network models, we hope to provide more robust cross-species transfer of functional information and more comprehensively descriptive systems for microbial communities and metagenomes.

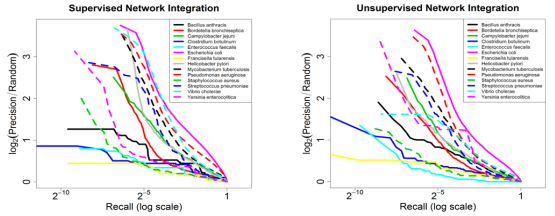
Methods

We begin by applying Bayesian heterogeneous data integration developed for MEFIT (Huttenhower, 2006) and HEFalMp (Huttenhower, 2009) to microbial experimental datasets. Previously, these methods relied on prior knowledge regarding functionally related genes (i.e. genes that participate in the same biological processes). Since such information is not typically available for newly sequenced organisms and communities, we are also developing unsupervised data integration methods that achieve comparable predictive accuracy. Each integration produces one supervised or unsupervised predicted functional interaction network per species, which can be mapped either to the originating organism's genome or to orthologous clusters.



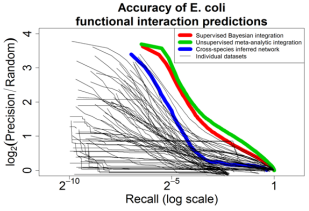
Evaluating integrated microbial data

A key question in analyzing environmental samples – which typically contain almost completely uncharacterized organisms – is the accuracy with which we can perform functional data integration in the absence of curated prior knowledge. Using cross-validation in characterized organisms, we find that **functional networks predicted using unsupervised techniques can be nearly as accurate as supervised Bayesian data integration**.



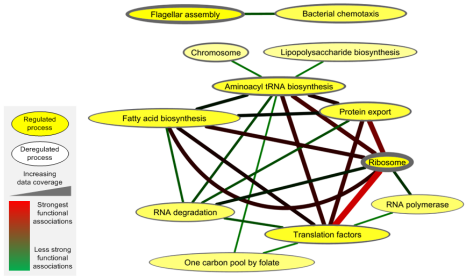
Cross-species knowledge transfer

A great deal of previous work has investigated transferring protein functional annotations between species, particularly in microbes. We find that functional interaction networks can also be accurately inferred by inter-species transfer, weighting experimental data from characterized organisms by either functional or phylogenetic similarity to the target. Here, **an *E. coli* functional network inferred from 14 other organisms (without any *E. coli* data) is of comparable accuracy and functional diversity to species-specific integrated networks.**



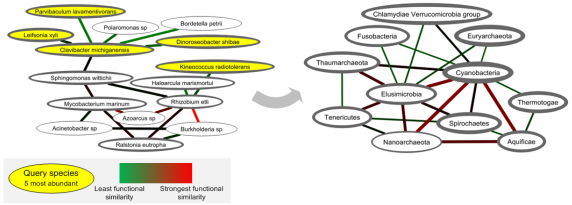
Functional mapping

The process of **functional mapping builds hierarchical networks by grouping genes and statistically summarizing their intra- and inter-group links as significance values.** This provides, for example, maps of the most functionally associated pathways in 87 *E. coli* datasets.

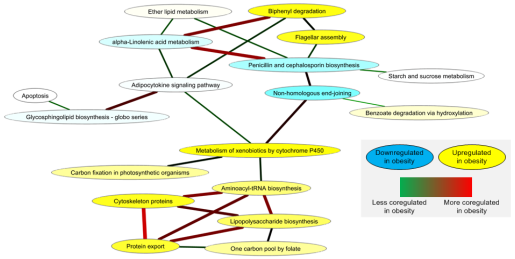


Microbiomes: a network perspective

Species-specific networks can be combined and functionally mapped to obtain a network perspective on the genes, pathways, organisms, and phyla present and interacting in a microbial community. Here, the Punta Cormorant hypersaline lagoon community from the Global Ocean Sampling project (Venter, 2004) has been mapped. All available microbial data was integrated into species-specific networks, which were combined with weights reflecting the phylogenetic and genetic distribution of the community's metagenome. Individual interactions were mapped through pathways into organisms, which were in turn mapped to phyla, resulting in a **single network summarizing millions of metagenomic reads and hundreds of genome-scale datasets.**



Functionally mapping multiple communities provides a way of comparing microbiomes both taxonomically and functionally. Below, two networks were constructed representing the aggregate of six lean and eleven overweight/obese gut microbiomes from (Turnbaugh, 2009). The network shown here includes the **pathways with the greatest increases and decreases in cohesiveness during obesity**, as well as their changes in coregulation and network neighborhood.



Computational Tools: The *Sleipnir* Library

The Sleipnir library for computational functional genomics provides a computational platform for rapidly analyzing and integrating very large collections of biological data.

- Over 60,000 lines of fully documented, open source C++ code for genomic analysis.
- Algorithms for data integration, microarray processing, functional ontology mining, Bayesian learning and inference, Support Vector Machines, and more.
- Data types for expression and interaction data, function catalogs (GO/KEGG/MIPS), clustering and similarity measures, and gene lists and identifiers.
- Efficient in runtime and memory usage, parallelizable, and up to hundreds of times faster than other data integration tools.

http://huttenhower.sph.harvard.edu