

# Creating and Delivering a Winning Poster

Dr. Robert M. Ramirez  
rramirez@sfsu.edu  
Associate Dean,  
College of Science & Engineering

# Purpose of a poster.

*To communicate/publicize your information to others*

- ▶ Research or experimental results.
- ▶ Report a study.
- ▶ Outcome of a project.
- ▶ The characteristics of your organization.
- ▶ Clear & Effective

*Presenter must be*

- ▶ Knowledgeable
- ▶ Enthusiastic

# Purpose of a poster

- ▶ Communicate or publicize your research to others.
- ▶ Short, concise, but complete “story.”

Describes ...

- ... The question that is asked or the “gap” in our knowledge.
- ... the means by which you addressed this.
- ... your results that must “persuade” us.
- ... your conclusion & why it is significant.

# Vertical or "portrait"

# Types of Posters

# Horizontal or "Landscape"

## Three problems of speciation via unidirectional CI ... and why it might still happen

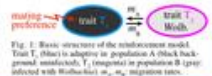
Matthias Flor<sup>1</sup>, Arndt Telschow<sup>1,2</sup>, Yutaka Kobayashi<sup>2</sup>, Jack Werren<sup>3</sup>, Peter Hammerstein<sup>1</sup>  
<sup>1</sup>Institute for Theoretical Biology, Humboldt University, Berlin, Germany; <sup>2</sup>Center for Ecological Research, Kyoto University, Kyoto, Japan; <sup>3</sup>Department of Biology, University of Rochester, New York, USA

### Introduction

If infected and uninfected host populations occur parapatrically, unidirectional cytoplasmic incompatibility (CI) constitutes a postmating isolation barrier between the populations. However, in order for CI to promote speciation, three problems must be overcome: (1) the infection polymorphism of neighboring host populations must be stable, (2) gene flow must not eliminate differences between diverging populations, and (3) runaway selection of female mating preference and male trait must be avoided to establish pre-mating isolation. We investigate these issues theoretically in a two-population model.

### Reinforcement model

Servedio (2000) developed a two-population model for reinforcement based on nuclear incompatibilities (NI). She showed that a male trait under local selection can be used as a cue for female mating preference under certain parameter conditions. In fig. 1, this model is depicted with NI replaced by CI.



### 1 Stability of CI patterns

A basic requirement for a reinforcement process to take place is that the postzygotic isolation barrier between populations be stable in face of migration. Following previous modeling efforts of Wolbachia dynamics (e.g. Fine, 1978), we use parameters for the vertical transmission efficiency,  $\tau$ , and the level of cytoplasmic incompatibility,  $i$ . A complete description of the model can be found in Flor et al. (2007) or Telschow et al. (2008). In a two-population scenario, the stability of an infection polymorphism between an uninfected population A and an infected population B (see fig. 1) can then be described by critical migration rates. Such a CI pattern is stable if CI is strong enough,  $i > 4(1-\tau)$ , and if the migration rates are below asymmetrical critical thresholds:

$$m_A < \frac{4\tau(1+i-2\sqrt{i})}{\sqrt{i_A} + \sqrt{i_B} - 4(1+i)}$$

$$m_B < \frac{4\tau(1+i-2\sqrt{i})}{\sqrt{i_A} + \sqrt{i_B} - 4(1+i)}$$

E.g. if  $i_A=0.9$  and  $i_B=0.87$  (values from Jenike et al. 2006), then  $m_A=50,000$  and  $m_B=50,148$ . Thus, parameter regions exist where patchy infection patterns are stable.

### 2 Gene flow reduction

Does a stable CI pattern allow genetic divergence between host populations? Telschow et al. (2002) introduced the effective migration rate as a measure of gene flow at weakly selected loci. For a mainland-island population structure (i.e. migration only in one direction), the effective migration rate can be determined by considering the matriline of migrants (which transmit the Wolbachia infection). For small migration rates, this approach can also be applied to the two-population scenario considered here. Gene flow reduction is symmetric because in one direction (infected → uninfected population) only the male half of the migrants' matriline suffers from CI whereas in the other direction (uninfected → infected population) it is only the female half that pays the cost of CI. Telschow et al. (2008) demonstrated that in this case the effective migration can be approximated by

$$m_{eff} \approx \frac{2-i_A-i_B}{2-i}$$

E.g. if  $i_A=0.9$  and  $i_B=0.87$  then gene flow is reduced by 80%. This enables better local adaptation and in turn stronger reinforcement than in a compatible scenario where CI is absent (due to either Wolbachia extinction or spread).

### 3 Runaway selection

Previous models have revealed that the spread of a female mating preference can offset the selection disadvantage of the preferred trait in the divergent population (unpublished data). Thus, infection at the trait and preference loci and hence pre-mating isolation cannot evolve (Fig. 2a).

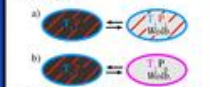


Fig. 2: Runaway selection and reinforcement. (a) If female mating preference is not costly then a runaway preference allele,  $P^*$ , sweeps both populations (depicted by red background) along with the preferred trait,  $T$  (mating selection). However, if by mating preference a costly trait divergence arises at both trait and preference loci (reinforcement), Wolbachia females carry allele  $P^*$  and an  $i$  allele.

However, if mating preference is costly for females — e.g. because of lost time or an increased risk of predation due to the rejection of unwanted mates — then this runaway selection process is prevented, and pre-mating isolation is established (Fig. 2b). Preliminary computer simulations of our model suggest that this occurs under a broad range of parameter values (unpublished data).

### Conclusions & Outlook

Our model shows that stable unidirectional CI may suffice to start reinforcement processes if female mating preference involves a cost. However, because critical migration rates will often be rather low, it seems likely that Wolbachia most efficiently promotes speciation in combination with other postzygotic isolation barriers that increase the stability of CI patterns. Jenike et al. (2006) found asymmetric mating preferences in a system of two closely related *Drosophila* species — one infected with Wolbachia, the other one uninfected — that hybridize in nature (Fig. 3). We want to further study the role that Wolbachia-induced unidirectional cytoplasmic incompatibility plays in host speciation by extending our model to incorporate both geographic characteristics and the hybrid male sterility present in this real system.

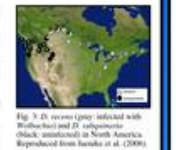


Fig. 3: *D. melanogaster* (top) infected with Wolbachia and *D. obscura* (bottom) uninfected hybridize in nature (Fig. 3). We want to further study the role that Wolbachia-induced unidirectional cytoplasmic incompatibility plays in host speciation by extending our model to incorporate both geographic characteristics and the hybrid male sterility present in this real system.

### Acknowledgements

This work was partly supported by NSF EF-0326063, the Deutsche Forschungsgemeinschaft (SFB 013), and the grant of Biochemistry Research of 114 Century OOE (A14).

### References

Flax, P.J.M., 1978. Dynamics of a symbiont-dependent cytoplasmic incompatibility in relation to migration. *J. Invertebr. Pathol.* 31: 19-24.  
 Flor, M., Hammerstein, P. & Telschow, A., 2007. Wolbachia-induced unidirectional CI and the stability of infection polymorphism in parapatric host populations. *J. Evol. Biol.* 20: 160-169.  
 Jenike, J., Dyer, K.A., Condit, C. & Malm, M.S., 2006. Asymmetrical reinforcement and Wolbachia infection in *Drosophila*. *PLoS Biol.* 4: 1812-1822.  
 Servedio, M.F., 2000. Reinforcement and the genetics of nonrandom mating. *Evolution* 54: 21-29.  
 Telschow, A., Hammerstein, P., Werren, J.H., 2002. The effect of Wolbachia on genetic divergence between populations: Male flies with two-way migration. *Am. Nat.* 160: 554-565.  
 Telschow, A., Flor, M., Kobayashi, Y., Hammerstein, P. & Werren, J.H., 2008. Wolbachia-induced unidirectional CI and speciation. *Molecular Biology and Evolution* 25: 870-879.

### 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 microbes, human microbiota, and pathogen populations. However, very little is known about the biological functionality governing these communities, how individual (unresolved) 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 microbes? How does the human oral or gut microbiota contribute to disease? What functional variation is significant in a pathogen population?

Here, we present preliminary work using large scale experimental data integration and network mining to characterize novel microbial and metagenomic communities by correlating 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.

#### 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 first that functional networks predicted using unsupervised techniques can be nearly as accurate as supervised Bayesian data integration.

#### 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 Cana Consortium hyperbaric 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.

#### Methods

We begin by applying Bayesian heterogeneous data integration developed for HMF (Huttenhower, 2005) and HEMIP (Huttenhower, 2005) to microbial experimental datasets. Previously, these methods relied on prior knowledge regarding functionally related genes (e.g. 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.

#### 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 process, for example, ranks the most functionally associated pathways in 87 *E. coli* datasets.

#### 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.

#### Conclusions & Outlook

Our model shows that stable unidirectional CI may suffice to start reinforcement processes if female mating preference involves a cost. However, because critical migration rates will often be rather low, it seems likely that Wolbachia most efficiently promotes speciation in combination with other postzygotic isolation barriers that increase the stability of CI patterns. Jenike et al. (2006) found asymmetric mating preferences in a system of two closely related *Drosophila* species — one infected with Wolbachia, the other one uninfected — that hybridize in nature (Fig. 3). We want to further study the role that Wolbachia-induced unidirectional cytoplasmic incompatibility plays in host speciation by extending our model to incorporate both geographic characteristics and the hybrid male sterility present in this real system.

#### 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, functional ontologies (GO/KEGG/MP), 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>

3 Column poster is the most common

# Before starting...

- ▶ Know your intended audience.
- ▶ Decide upon the “basic message”.
- ▶ Gather your information, graphs, tables, photos, etc.
- ▶ Allocate the correct amount of space.
- ▶ Allocate **TIME** to design the poster; this is especially true if there are several partners.
- ▶ Pre-sketch a layout.
- ▶ Be clear in your ideas and simple in your presentation.

# Who is the audience?

- ▶ Are they people in your own specialty?
  - Then you can use some jargon (i.e. words used in your profession) & some shortcuts.
- ▶ Are they people in a related field?
  - Then use less jargon, but you can assume they have basic knowledge.
- ▶ Are they people in an unrelated field?
  - Then use basic, simple language & terms.



# What is the message?

- ▶ State the main point(s) and conclusions succinctly.  
A short but informative title + an effective abstract & introduction.
- ▶ All other points should relate to the main title.
- ▶ You do not have to include everything. Other corollary findings can be summarized as “bullet points”.

# Be strategic !

- ▶ How to present your data?  
*Tables are better than written text.*  
*Figures are better than tables.*
- ▶ Use short, informative statements.
- ▶ This is not a publication ... you don't have to present a graph or table for everything!
- ▶ Use graphs/tables for most important data.
- ▶ Check spelling and grammar.



## Banner :

Concise Title, Author(s),  
Affiliation (legible @ 20 ft)

## Methods:

What did you do? (How?). Enough detail to ascertain validity (Correct method? Reproducible?)

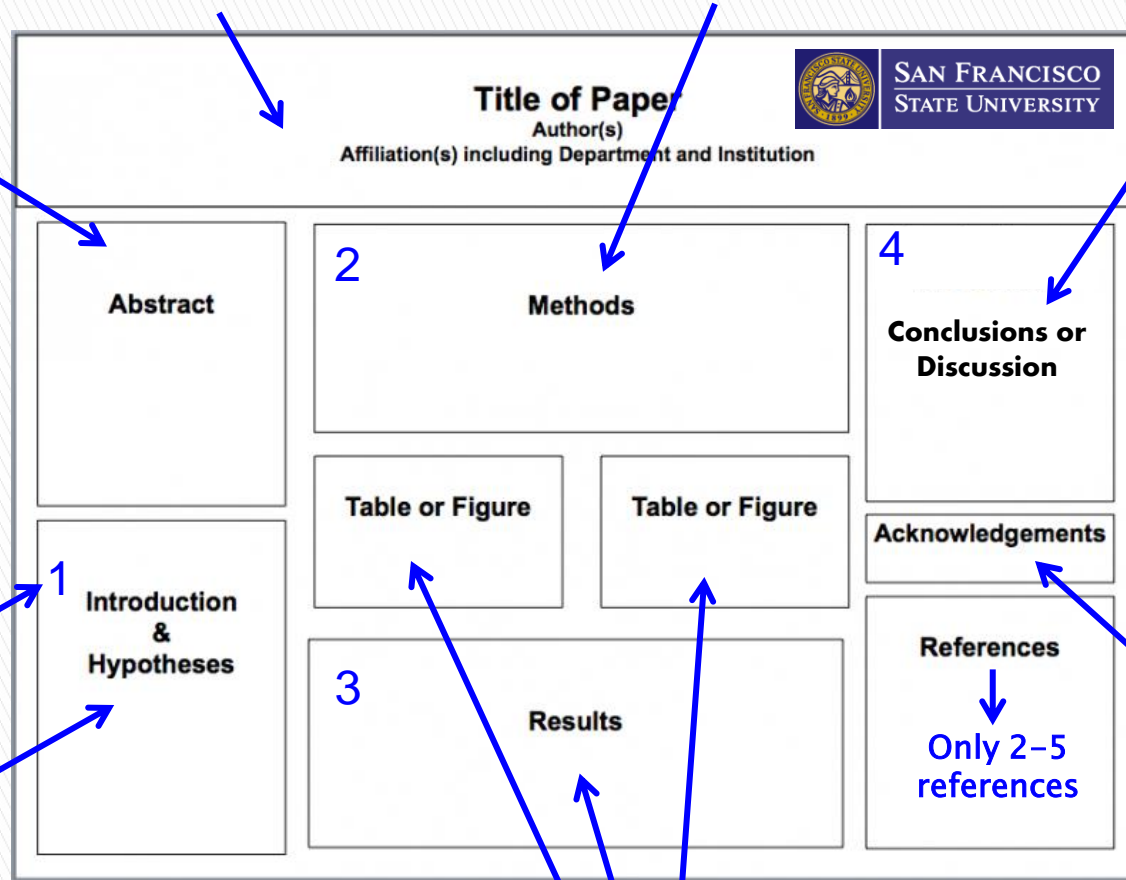
## Abstract:

- Hypothesis or objectives
- Short methods & Results.
- Conclusions or significance.

Use numbers to guide your audience

## Introduction:

- Essential background information.
- Why is this problem being researched?
- What is your objective or questions?
- What is your hypothesis?



## Discussion:

- What do your results “mean”? (don’t repeat results). Address any contradictions.
- How does this support your hypothesis?

## Acknowledge:

Grant agency or special assistance.

## Results:

What did you observe? (Outcome?).  
Arrange data (graphs or tables) in logical order. Enough data to support conclusions

# General Suggestions:

## LAYOUT

- ▶ Use numbered heading sub-titles so that audience reads the poster *in the order that you want.*
- ▶ Balance placement of text and graphics (symmetry).
- ▶ Don't CRAM! Use white spaces between sections.
- ▶ Follow normal flow of reading: Top to bottom, left to right.
- ▶ Use Left-justification alignment of text.

# General Suggestions:

## Text and Font

- ▶ Use a simple font (sans serif) throughout.

- ▶ Examples:

Sans Serif = Arial (simple)

Serif = Times New Roman (less simple)

- ▶ Use key words and phrases. Omit unnecessary words or language.
- ▶ Use large font size: 18 point for smallest text, 24 point for regular text, 28 point for subtitles, 48 point for main title in banner (smaller font for authors and affiliation).

# General Suggestions:

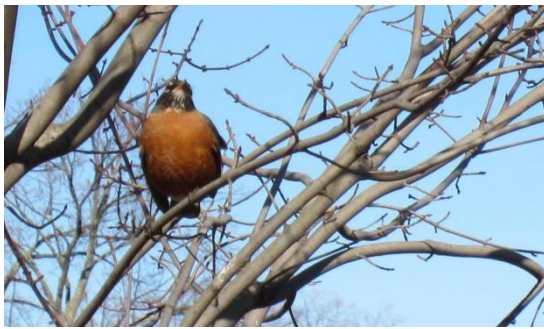
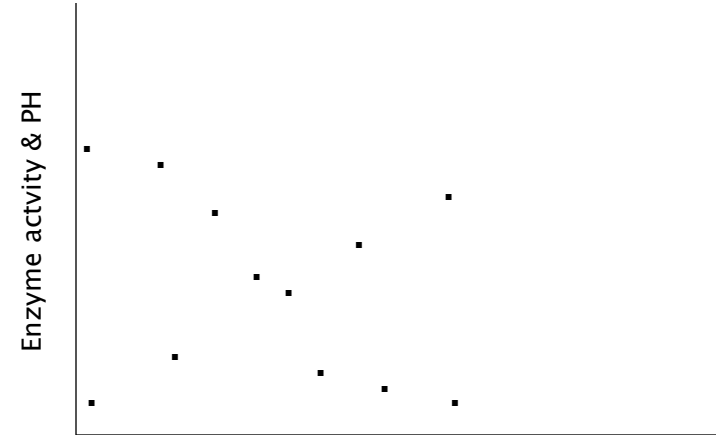
## Photos, figures and tables

- ▶ Should be clear, self-explanatory, uncomplicated, and sufficiently large.
- ▶ Tables and figures must have titles.
- ▶ Tables: columns and rows should have titles.
- ▶ Graphs: horizontal and vertical axes should be labeled. Symbols for each condition (●, ◆, ○, △) should be robust (visible at 3-4 feet). Line on graph should be “tagged” with a label.
- ▶ Photos: Should be cropped & enlarged to clearly show your key point.

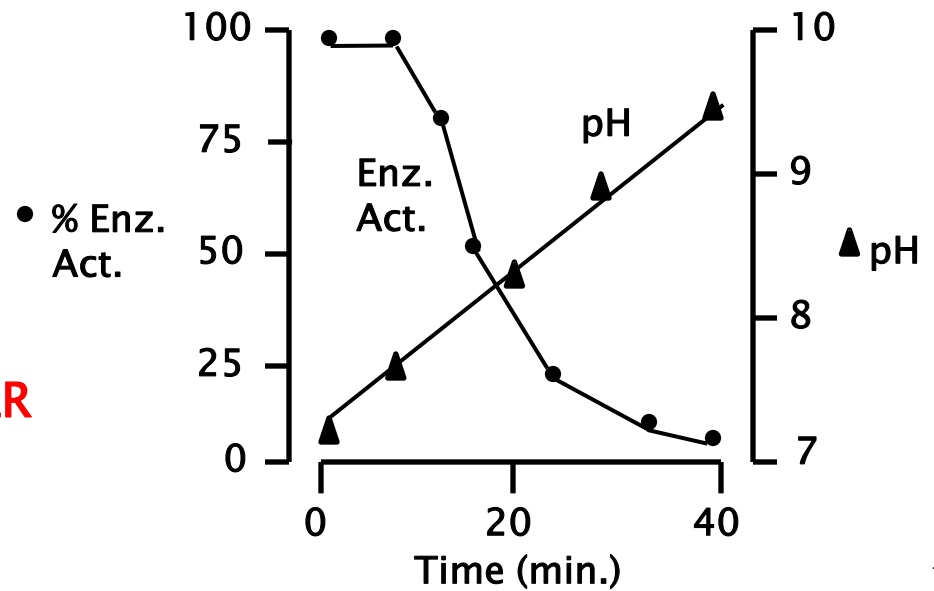
# General Suggestions: Photos & figures



**BAD**



**BETTER**



# General Suggestions:

## Color and Contrast

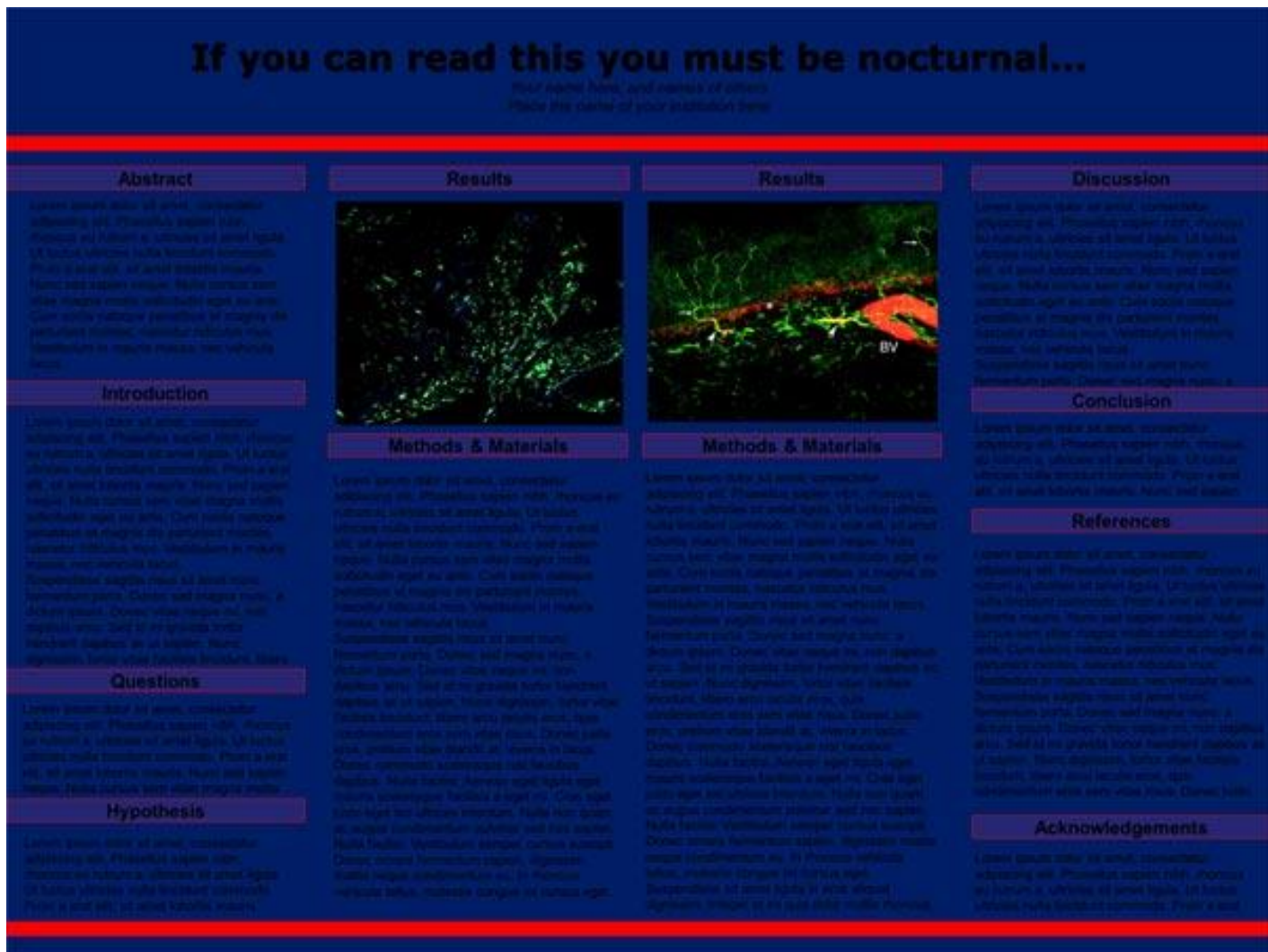
- ▶ Use a white background but a colored border line to draw attention to important parts of your poster.
- ▶ White background also saves ink.
- ▶ Use pleasing contrast to reduce eye strain.

Good: This is a **good contrast** for a poster.

Poor: This is a **poor contrast** for a poster.



# Good or Bad?







# Good or Bad?

**Determining functional linkages between virulent genes of *Porphyromonas gingivalis***  
 Carmen Crawford and Gabriel Moreno-Hagelsieb  
 Department of Biology, Wilfrid Laurier University, Waterloo, ON

**Introduction**  
 Porphyromonas gingivalis is a gram-negative bacterium with a complex genome and a high degree of genetic diversity. It is a major pathogen in periodontitis, a chronic inflammatory disease of the supporting structures of the teeth. The virulence of P. gingivalis is determined by a set of virulence genes, including gingipains, fimbriae, and other surface-associated proteins.

**Open Genes**  
 We have identified a set of open reading frames (ORFs) that are highly conserved across different strains of P. gingivalis. These ORFs are located in the same genomic region as the known virulence genes and are therefore likely to be involved in virulence.

**Discussion**  
 There are many more virulent functioning genes than originally thought. The linkage network involves the linkage of many of the original known virulent genes.

**References**  
 Morelli, J.E., Chapman, C.G., Kelly, D.T., Paster, T., Hultine, E.M., Chen, J.A., ... et al. (2005) Comparative genomics of the oral pathogen Porphyromonas gingivalis. *Genome Research*, 15(11), 1881-1891.  
 Jorgensen, J.C., Collins-Walker, J., and Moreno-Hagelsieb, G. (2014) A comprehensive genome-wide analysis of the virulence genes of *Porphyromonas gingivalis*.

Gene	Accession	Length (bp)	GC (%)	ORF (%)	ORF Length (aa)	ORF Score
g1	U00001	13	77	58	4.3	14.89
g2	U00002	9	77	58	4.3	14.89
g3	U00003	97	79	12	11.1	21.1
g4	U00004	16	79	12	11.1	21.1
g5	U00005	1	8	1	1	4
g6	U00006	31	79	12	11.1	21.1
g7	U00007	31	79	12	11.1	21.1
g8	U00008	16	77	58	4.3	14.89

**Acknowledgments**  
 Dr. Gabriel Moreno-Hagelsieb  
 M.C. Blomberg  
 Andrew Munn

# Good or Bad?





# Bad or Good?

## Cooling Effects of Dirt Purge Holes on the Tips of Gas Turbine Blades



Eric Couch, Jesse Christophel, Erik Hohlfeld, and Karen Thole



Gas turbine engines run better at higher combustion temperatures

At higher combustion temperatures, these engines generate more power and use less fuel. However, these temperatures are restricted by melting temperatures of the turbine blades downstream of the combustor (see Figure 1).

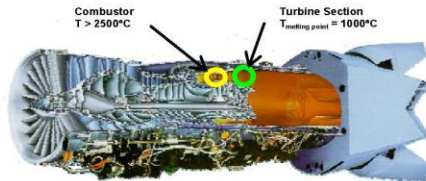


Figure 1. Pratt & Whitney F119 gas turbine engine.

Dirt purge holes on turbine blade tips allow for higher combustion temperatures

Harmful hot gases from the combustor leak across the gap between the blade tip and the shroud (see Figure 2). Dirt purge holes expel foreign particles from the blade tip so that film cooling holes are not blocked.

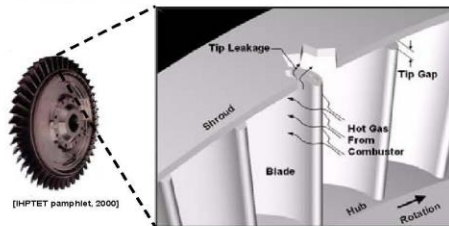


Figure 2. Flow at the tip region of a turbine blade.

The project goal was to find the film cooling effects of these dirt purge holes

To find the effects, we performed wind tunnel experiments with scaled turbine blades. The wind tunnel was low speed and low temperature, and the blades, shown in Figure 3, were scaled at 12 times their normal size. To measure temperatures on the blade tip, we used an infrared camera. Tip gap sizes and amount of coolant flow from the dirt purge holes were both varied.



Figure 3. Large-scale turbine blade in wind tunnel.

Temperature measurements were converted to dimensionless cooling effectiveness

$$\text{Effectiveness } \eta = \frac{T_{\infty} - T_{aw}}{T_{\infty} - T_c} \quad \text{where } \begin{matrix} T_{\infty} = \text{mainstream temperature} \\ T_c = \text{coolant temperature} \\ T_{aw} = \text{adiabatic wall temperature (on tip surface)} \end{matrix}$$

Cooling increased with blowing ratio

The effectiveness contours of Figure 4 show that cooling increased with blowing ratio.

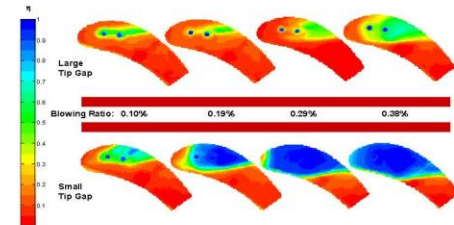


Figure 4. Measurements of film cooling effectiveness.

Tip size dramatically affected cooling

In Figure 5, the lateral averages of effectiveness plotted against the axial chord length show that tip size dramatically affected the cooling.

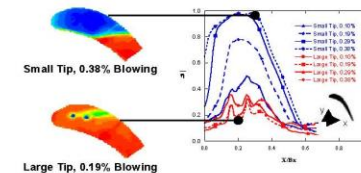


Figure 5. Laterally averaged effectiveness plotted against normalized axial chord.

In summary, dirt purge holes provide cooling to the tip surface

While intended to remove dirt from the blade, dirt purge holes also provide cooling to the tip surface. This cooling is enhanced with a small tip gap as the dirt purge floods the tip region near the leading edge with cool air.

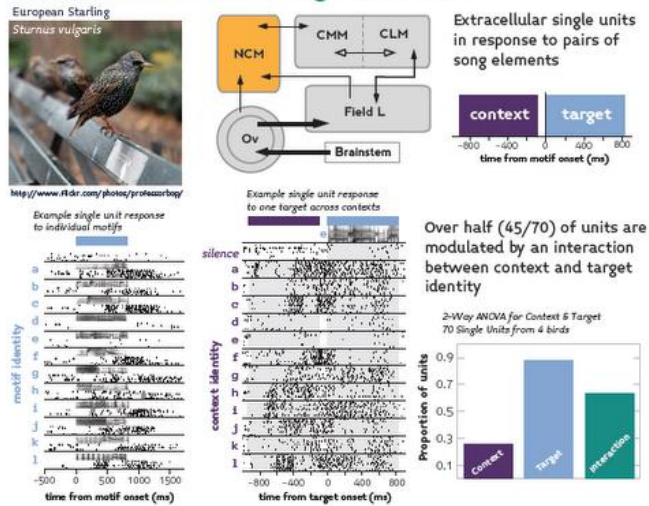
Acknowledgments

The sponsor for this project was Pratt & Whitney.

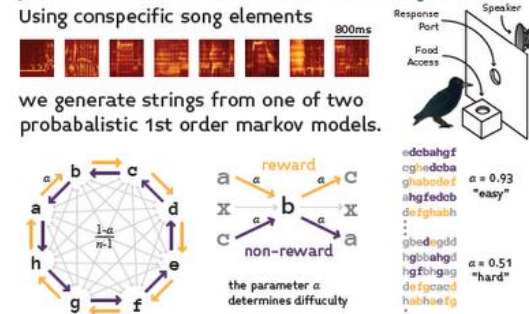
# Good or Bad?

## The neural representation of behaviorally relevant acoustical sequences

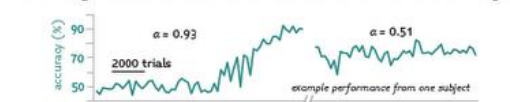
### Neurons in NCM are sensitive to temporal combinations of song elements



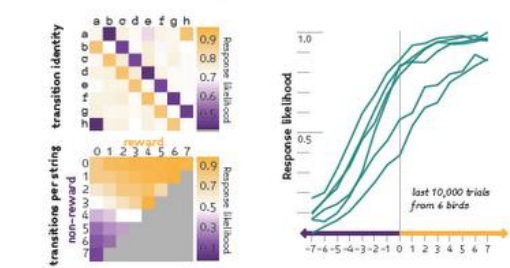
### Starlings can discriminate between probabilistic acoustical sequences



### Starlings learn to discriminate between these strings



### and differentially weight individual transitions.



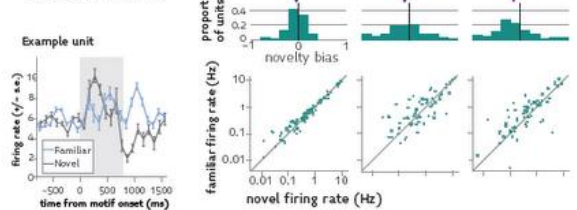
Justin T. Kiggins jkiggins@ucsd.edu  
Neurosciences Graduate Program, UC San Diego

Timothy Q. Gentner tgentner@ucsd.edu  
Department of Psychology, Neurosciences Graduate Program, Kavli Institute for Brain and Mind, UC San Diego



### Responses in NCM are biased by the familiarity of elements & sequences

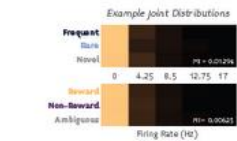
#### Offset responses are stronger for familiar motifs



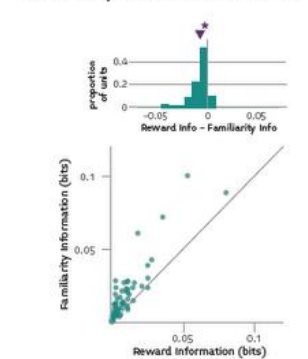
#### Familiarity Classification



#### Reward Classification



#### Responses to pairs of motifs have more information about familiarity than reward value





# 10 rules to make a bad poster

- ▶ Wait until the last minute to design your poster.
- ▶ Boring is best.
- ▶ Include political or sexually offensive statements.
- ▶ No results? Then use a lot of pictures.
- ▶ Use a font size that will require the use of a magnifying lens.
- ▶ Don't proofread; everybody else should "know" what your mistakes mean.
- ▶ Use 3000 words in your poster. Also provide armchair and some potato chips.
- ▶ Just show results, your audience doesn't need know anything else.
- ▶ Don't attend the poster session ... people know how to read on their own, anyway.
- ▶ Include "Spiderman" as the poster background.

# Good Visual Communication

Poster should ...

- ▶ Be informative.
- ▶ Be a conversation starter.
- ▶ Capture the attention of as many people as possible within 15 seconds.
- ▶ Be pleasing to the eye & “exciting”.
- ▶ Be succinct and well organized.
- ▶ Be readable from 3–6 feet.

# Poster preparation

## Poster size for :

Tri-fold poster = 48 in. length x 36 in. height.

Foam board = 60 in. length x 40 in height.

- ▶ First 50 posters = No charge.
- ▶ Prepare poster & send [final version](#) to:

*In Press Printing*

Details & account number to be announced.

# On the Showcase day...

- ▶ Prepare & rehearse a 2–3 minute presentation for the judges.
- ▶ Focus on the main point. Explain how your different data support the main point.
- ▶ Explain why your research is important or how it solves a problem or need.
- ▶ Limit technical language (“jargon”).
- ▶ Do you use a special technique? Then prepare a concise (3–4 sentence) explanation for it.
- ▶ Arrive early to set up. Bring your poster & tacks.
- ▶ Bring a 1–page version of poster (optional).
- ▶ Attend your poster from 12–3PM.