## Writing an Effective Abstract



## Plan

- What is a scientific abstract ?
- Why abstract is important
- Elements of an effective abstract
- Tips





•Wrap up

### What is a scientific abstract

An abstract is a <u>condensed version</u> of a full scientific paper, thesis, review, conference proceeding, or any in-depth analysis of a particular subject.



### Four C's of An Effective Abstract

•Complete : it covers the major parts of the research project

•**Concise** — it contains no excess wordiness or unnecessary information.

•**Clear** — it is readable, well organized, and not too jargon-laden.

•**Cohesive** — it flows smoothly between the parts.



## Don't trust the dictionary

#### • ab·stract (ăb-străkt', ăb'străkt').

adj.

- Considered apart from concrete existence
- Not applied or practical; theoretical
- Difficult to understand; abstruse

## •Your next abstract should not be abstract (difficult to understand).

![](_page_4_Picture_7.jpeg)

### **Components of an effective Abstract**

- •Title
- •Authors
- Problem/Objective
- •Methods
- •Results
- •Conclusions

Briefly summarize (often 150-300 words)

![](_page_5_Picture_8.jpeg)

### Title

- •Describe your most important result/the major thing you found or did
- •Keep it relatively short
- •Avoid all abbreviations and technical jargon

#### **Possible titles – What is your best option ?**

- A. Genetic of Breast Cancer identifies risk factor
- B. GWAS of Breast Cancer in Africa
- C. First genome-wide association study of breast cancer in Africa identifies 10 novel loci

### Authors

- •Your name should go first if you are presenting (ideally you did most of the analysis)
- •Your supervisor should generally be an author (usually your main supervisor as last author)
- •Additional people who have worked on the project should be authors be sure to talk to your supervisor!
- •It is important you don't omit key individuals (data providers and collaborators on the work, etc)

### Problem/Objective (Background)

- •What is the BIG problem your research might solve ?
- •What practical or scientific gap is your project filling?
- •You will generally need a little background/intro to explain the objective
- •The objective should catch people's attention very important!
- •1-2 sentences
- Assume reviewer(s) are not the most knowledgeable in the field

### Example of a Background/Objective

#### Background

Chronic kidney disease (CKD) is a leading cause of morbidity and mortality worldwide with an estimate of over 850 million people with some form of kidney disease. This figure is about double the number of people who live with diabetes (422 million) and 20 times more than the prevalence of cancer worldwide (42 million) 3 or of people living with AIDS/HIV (36.7 million). CKD is at least three times more frequent in Africa, which has limited resources, than in developed countries. With rapidly increasing urbanisation, trends towards unhealthy diets, obesity and increases in metabolic risk factors, and as part of a broader epidemiological transition from infectious to non-infectious diseases, the projected increase in the prevalence of CKD may be even greater in Africa compared to developed countries. Genome-wide association studies (GWAS) of kidney function have uncovered hundreds of loci, primarily in populations of European ancestry. We have undertaken the first continental African GWAS of estimated glomerular filtration rate (eGFR), a measure of kidney function used to define CKD.

![](_page_9_Picture_3.jpeg)

## Example of a Background/Objective (compress further if required)

#### Background

Chronic kidney disease (CKD) is a leading cause of morbidity and mortality worldwide with estimate of over 850 million people with some form of kidney disease. This figure is about double the number of people who live with diabetes (422 million) and 20 times more than the prevalence of cancer worldwide (42 million) or of people living with AIDS/HIV (36.7 million). CKD is at least three times more frequent in Africa, which has limited resources, than in developed countries. With rapidly increasing urbanisation, trends towards unhealthy diets, obesity and increases in metabolic risk factors, and as part of a broader epidemiological transition from infectious to non-infectious diseases, the projected increase in the prevalence of CKD may be even greater in Africa compared to developed countries. Genome-wide association studies (GWAS) of kidney function have uncovered hundreds of loci, primarily in populations of European ancestry. We have undertaken the first continental African GWAS of estimated glomerular filtration rate (eGFR), a measure of kidney function used to define chronic kidney disease (CKD).

![](_page_10_Picture_3.jpeg)

### Methods

- Procedure or approach to the project.
- •How did you go about finding your results?
- What steps were taken to carry out the project?
  Include study design
  - •Study population (#, age, M,F, inclusion criteria)
  - •What was measured
- •Don't go into too much detail!

![](_page_11_Picture_7.jpeg)

![](_page_11_Picture_8.jpeg)

### **Example of Method in an Abstract**

#### Method

We conducted GWAS of eGFR in 3288 East Africans from the Uganda General Population Cohort (GPC) and replicated in 8224 African Americans from the Women's Health Initiative. Loci attaining genome-wide significant evidence for association ( $p<5x10^{-8}$ ) were followed up with Bayesian fine-mapping to localise potential causal variants. The predictive power of a genetic risk score (GRS) constructed from previously reported trans-ancestry eGFR lead SNPs was evaluated in the Uganda GPC.

![](_page_12_Picture_3.jpeg)

### Results

- A description of your data and observations enough detail to make it clear
- As a result of your procedure, what was found or created?
- Main finding of the study in words
- Give real numbers as well as significance
- Still try to avoid jargon
- NEVER predict your results!!!

![](_page_13_Picture_7.jpeg)

### Example of Results in an Abstract

#### • Findings

We identified and validated two eGFR loci. At the *GATM* locus, the association signal (lead SNP rs2433603, p=1.0x10<sup>-8</sup>) in the Uganda GPC GWAS was distinct from previously reported signals at this locus. At the *HBB* locus, the association signal (lead SNP rs141845179, p=3.0x10<sup>-8</sup>) has been previously reported. The lead SNP at the *HBB* locus accounted for 88% of the posterior probability of causality after fine-mapping, but did not colocalise with kidney expression quantitative trait loci. The trans-ancestry GRS of eGFR was not significantly predictive into the Ugandan population.

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### **Conclusions/Significance**

•What are the larger implications of your work?

•What is the bigger picture?

•Work on incorporating these implications into your very last sentence

![](_page_15_Picture_4.jpeg)

## Example of Interpretation/conclusion in an Abstract

"These results demonstrate the value of performing GWAS in continental Africans, providing a rich genomic resource to larger consortia for further discovery and fine-mapping. The study emphasizes that additional large-scale efforts in Africa are warranted to gain further insight into the genetic architecture of CKD"

![](_page_16_Picture_2.jpeg)

#### Abstract

#### Background

Genome-wide association studies (GWAS) of kidney function have uncovered hundreds of loci, primarily in populations of European ancestry. We have undertaken the first continental African GWAS of estimated glomerular filtration rate (eGFR), a measure of kidney function used to define chronic kidney disease (CKD).

#### Method

We conducted GWAS of eGFR in 3288 East Africans from the Uganda General Population Cohort (GPC) and replicated in 8224 African Americans from the Women's Health Initiative. Loci attaining genome-wide significant evidence for association (p<5x10<sup>-8</sup>) were followed up with Bayesian fine-mapping to localise potential causal variants. The predictive power of a genetic risk score (GRS) constructed from previously reported trans-ancestry eGFR lead SNPs was evaluated in the Uganda GPC.

#### Findings

We identified and validated two eGFR loci. At the *GATM* locus, the association signal (lead SNP rs2433603, p= $1.0x10^{-8}$ ) in the Uganda GPC GWAS was distinct from previously reported signals at this locus. At the *HBB* locus, the association signal (lead SNP rs141845179, p= $3.0x10^{-9}$ ) has been previously reported. The lead SNP at the *HBB* locus accounted for 88% of the posterior probability of causality after fine-mapping, but did not colocalise with kidney expression quantitative trait loci. The trans-ancestry GRS of eGFR was not significantly predictive into the Ugandan population.

#### Interpretation

In the first GWAS of eGFR in continental Africa, we validated two previously reported loci at *GATM* and *HBB*. At the *GATM* locus, the association signal was distinct from that previously reported. These results demonstrate the value of performing GWAS in continental Africans, providing a rich genomic resource to larger consortia for further discovery and finemapping. The study emphasizes that additional large-scale efforts in Africa are warranted to gain further insight into the genetic architecture of CKD.

### •Complete

### •Concise

### •Clear

### •Cohesive

![](_page_17_Picture_13.jpeg)

### Same abstract but different format

Genome-wide association studies (GWAS) of kidney function have uncovered hundreds of loci, primarily in populations of European ancestry. We have undertaken the first continental African GWAS of estimated glomerular filtration rate (eGFR), a measure of kidney function used to define chronic kidney disease (CKD).

We conducted GWAS of eGFR in 3288 East Africans from the Uganda General Population Cohort (GPC) and replicated in 8224 African Americans from the Women's Health Initiative. Loci attaining genome-wide significant evidence for association (p<5x10<sup>-8</sup>) were followed up with Bayesian fine-mapping to localise potential causal variants. The predictive power of a genetic risk score (GRS) constructed from previously reported trans-ancestry eGFR lead SNPs was evaluated in the Uganda GPC.

We identified and validated two eGFR loci. At the *GATM* locus, the association signal (lead SNP rs2433603, p=1.0x10<sup>-8</sup>) in the Uganda GPC GWAS was distinct from previously reported signals at this locus. At the *HBB* locus, the association signal (lead SNP rs141845179, p=3.0x10<sup>-8</sup>) has been previously reported. The lead SNP at the *HBB* locus accounted for 88% of the posterior probability of causality after fine-mapping, but did not colocalise with kidney expression quantitative trait loci. The trans-ancestry GRS of eGFR was not significantly predictive into the Ugandan population.

In the first GWAS of eGFR in continental Africa, we validated two previously reported loci at *GATM* and *HBB*. At the *GATM* locus, the association signal was distinct from that previously reported. These results demonstrate the value of performing GWAS in continental Africans, providing a rich genomic resource to larger consortia for further discovery and fine-mapping. The study emphasizes that additional large-scale efforts in Africa are warranted to gain further insight into the genetic architecture of CKD.

![](_page_18_Picture_5.jpeg)

### What does an effective abstract do ?

- •Sparks interest in your project
- Provides a concise description of your research project
- States in a clear and simple way the main points of your project
- •Represents you
- •Could provide your next job
- •Makes you known in the field

![](_page_19_Picture_7.jpeg)

### Helpful Tips – 10 golden rules

- 1. Abstracts are short but time-consuming. Take your time, it might take you days even weeks
- 2. Look at examples of abstracts in your field
- 3. Write "long" and scale down if needed
- 4. Analyze one sentence at a time
- 5. Each sentence has purpose
- 6. Each sentence logically follows another
- 7. Use plain English wherever you can
- 8. Use active voice when you can
- 9. State only your most important conclusion(s)
- 10. Get your supervisor's approval

### Things to avoid in an abstract

- 1. Lengthy background information (readers peruse your abstract to learn about your current work, not the previous work of other researchers)
- 2. Citations
- 3. Details about routine laboratory procedures
- 4. Details about the statistical methods or software used (unless this is the focus of your study)
- Undefined abbreviations or acronyms (most journals will provide a lis of common abbreviations/acronyms that do not need to be defined; some journals do not allow the use of abbreviations/acronyms in the abstract)
- 6. Results or interpretations that are not discussed in the text

### 10 Breakout

![](_page_22_Picture_1.jpeg)

![](_page_22_Picture_2.jpeg)

https://docs.google.com/document/d/1psVfNP4M-KBO3IXZ3HoLpJ04hPEqvx3Q/edit

### **Create an Hypothetical Abstract** (Hunger Problem)

- ✔ Approx. 700 million people go to bed hungry every night
- ✓ Say, you are interested in solving a bit of this hunger pandemic
- In your PhD/postdoc, you have developed a "powerful salt-like content" if a small content is added to a glass of water, it can make people not to be hungry for 3 days.
- ✓ This is really exciting for you, as you are contributing to knowledge
- ..but you were only to make a few content of your magic (scientific) discovery enough for the neighbouring around your university.
- .you are clear that your work is able to solve hunger problem in a small scale for a short time, but there are limitations (eg number of days)
- ✓ Write an abstract (150 to 250 word) on this your exciting work. Please provide background, method, finding and significant/conclusion.

![](_page_23_Picture_8.jpeg)

### Example 1

"Lafora disease (LD) is an autosomal recessive, fatal progressive myoclonus epilepsy caused by the abnormal buildup of insoluble glycogen, called Lafora bodies. Mutations in the gene encoding the protein laforin lead to LD. Laforin is a dual-specificity phosphatase with a carbohydrate-binding module. This enzyme is necessary for proper glycogen metabolism, but its role in the development of LD is not yet fully understood. In this study, we established a purification scheme to purify recombinant laforin and analyzed laforin to determine whether the monomer or dimer species is more physiologically relevant. Our ultimate goal is to crystallize laforin to determine its three-dimensional structure and use these insights to understand the enzyme. Human laforin is difficult to purify due to its tendency to be sequestered into inclusion bodies when expressed in E. coli. Therefore, we cloned the gene for laforin from the Gallus gallus (red rooster) genome into a bacterial expression vector and purified laforin from E. coli using a two-step purification procedure. We subjected monomeric Gallus gallus laforin to gel electrophoresis, mass spectrometry, dynamic light scattering, phosphatase and starch-binding assays. We conclude that laforin is present mainly as a monomer, remains monomeric, and has phosphatase and carbohydrate-binding activity comparable to human laforin. Therefore, Gallus gallus laforin is an appropriate model for human laforin, and any insights we gain from it can be directly applied to human laforin. With this information we can move forward in understanding the role of laforin in the body and eventually develop treatment options for LD."

![](_page_24_Picture_2.jpeg)

### Example 2

"Biomedical experiments often require the use of live or recently deceases tissue samples. However, these tissue samples do not always get used in the experimental process, and thus go to waste. A cost effective, efficient means of best preserving skeletal muscle tissue for biophysical research is the goal of the research. Cryopreservation, or significantly dropping the temperature of a sample to essentially stop all cell function, is believed to be the best means of storing specimens. Freezing tissue samples exists as an intricate and delicate process in order for samples to maintain structural integrity. A major barrier is the formation of ice within cells. Intracellular ice will expand when frozen, tearing the cellular structure apart. Therefore, rates of freezing, level of cryopreservants and tying muscles to capillary tubes were studied. Working in Dr. Kenneth Campbell's laboratory in the Department of Physiology with Senior Lab Technician Ben Lawson, a cryopreserving solution which appears to maintain the structure of the tissue sample was search for. Also, finding a means of insulating the specimen vials to control freezing rate was performed. The samples were determined effectively stored if mechanical assays of stored tissue had no significant difference in physical properties than recently excised tissue. Results suggest that a slow freezing rate with a high rate of thawing in high concentrations of cryopreservants and being tied to capillary tubes allows for the best structurally sound samples. Finding a method of preserving tissue samples allows decreases the amount of waste due to degraded muscle tissue."

![](_page_25_Picture_2.jpeg)

### SUMMARY

#### Abstract

#### Background

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#### Method

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### •Complete

•Concise

•Clear

Cohesive

![](_page_26_Picture_14.jpeg)

### Finally Finally Finally !!!

•An abstract is a condensed version of a full scientific paper

- •Your next abstract should not be abstract (difficult to understand).
- •Lets your next abstract SPEAK for you

# Thank you