

Introducción a \LaTeX , Overleaf y Mendeley

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Basado en las notas originales de Dr John D. Lees-Miller

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Guía de L^AT_EX

¿Qué es L^AT_EX?



- ▶ Es un sistema de composición de texto a base de comandos TeX, que tiene funciones y paquetes
- ▶ Todo empieza con un archivo .tex que se compila y genera un archivo PDF

The screenshot shows a LaTeX editor interface. On the left, the 'Source' view displays the LaTeX code for a document titled 'Modeling SNP ascertainment bias...'. The code includes a preamble with `\usepackage{-11pt}` and `\section{Introduction}`. The main text describes the goals of the `HapMap` project and the challenges of SNP ascertainment bias. It mentions that SNPs were selected to increase the power of association tests and that the approach used to identify variants for these SNPs arrays may adversely affect the quality of such inferences. The code also includes a paragraph about SNPs found in a small sample of individuals from selected populations and their frequency in other populations.

On the right, the 'Preview' view shows the rendered PDF document. The title is 'Modeling SNP array ascertainment with Approximate Bayesian Computation for demographic inference'. The authors are 'Conrado D. Quinto-Cordero', 'August E. Weissen', 'Joseph C. Watkins', and 'Michael F. Hammer'. The abstract states: 'Single nucleotide polymorphisms (SNPs) in commercial genotyping arrays have often been discovered by sampling a small number of chromosomes from a group of selected populations. This form of non-random ascertainment skews patterns of nucleotide diversity and can affect population genetic inferences. In addition, the effects of ascertainment bias become stronger the more divergent the population of interest is to those in the discovery panel. Most attempts to correct for this bias suffer from uncertainty in the exact discovery protocols for most commercial arrays. In this work, we propose a demographic inference pipeline that explicitly models the SNP discovery protocol in an Approximate Bayesian Computation (ABC) framework. We simulated genomic regions according to a demographic model incorporating parameters for the divergence of three well-identified populations: the Yoruba, Han Chinese and CEU Europeans, and simulated the SNP distribution of a commercial array by varying the number of sampled chromosomes and the allele frequency cut-off in the given regions. We then calculated site frequency spectra and haplotype based summary statistics obtained from both the ascertained and genomic data and inferred both ascertainment and demographic parameters of the models. We also implemented our pipeline to study the admixture process between European and Native American populations that gave rise to the present-day Mexican population. In particular, our estimate of the time of admixture in Mexico is closer to the historical dates than those in works which did not consider ascertainment bias. Our inference framework is applicable to studies when only SNP array data of the populations of interest are available and will improve to accuracy of demographic model inference.'

The 'KEYWORDS' section lists: 'SNP array, Demographic inference, Approximate Bayesian Computation, Demographic modeling'.

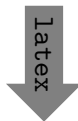
¿Por qué usar L^AT_EX?

- ▶ Puedes incluir:
 - ▶ Cajas de texto
 - ▶ Figuras
 - ▶ Tablas
 - ▶ Tablas de contenido
 - ▶ Secciones y subsecciones
 - ▶ Listas
 - ▶ Citas y bibliografía
 - ▶ Ecuaciones matemáticas
- ▶ Se puede extender con facilidad
 - ▶ Paquetes para publicaciones científicas, presentaciones, hojas de cálculos, ...

¿Cómo trabaja L^AT_EX?

- ▶ Escribe tu documento en texto plano con **comandos** que describen su estructura y significado.
- ▶ El programa latex procesa el texto y comandos para producir un documento en formato PDF.

La lluvia en `\textbf{España}` cae `\emph{principalmente}` en la llanura.



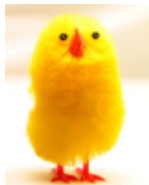
La lluvia en **España** cae *principalmente* sobre la llanura.

Más ejemplos de comandos y sus salidas. . .

```
\begin{itemize}
\item T\'e
\item Leche
\item Galletas
\end{itemize}
```

- ▶ Té
- ▶ Leche
- ▶ Galletas

```
\begin{figure}
\includegraphics{chick.png}
\end{figure}
```



```
\begin{equation}
\alpha + \beta + 1
\end{equation}
```

$$\alpha + \beta + 1 \quad (1)$$

Imagen de http://www.andy-roberts.net/writing/latex/importing_images

- ▶ Un documento \LaTeX simple:

```
\documentclass{article}
\begin{document}
Hello World! % your content goes here...
\end{document}
```

- ▶ Los comandos empiezan con una *barra invertida* \backslash .
- ▶ Todo documento comienza con un comando \backslash `documentclass`.
- ▶ El *argumento* en llaves $\{ \}$ le dice a \LaTeX que tipo de documento estamos creando: en este ejemplo, `article`.
- ▶ Un signo de porcentaje $\%$ comienza un *comentario* — \LaTeX ignorará el resto de la línea.

Tipos de documentos

- ▶ article
- ▶ report (tesis, libros pequeños)
- ▶ book
- ▶ letter
- ▶ beamer (presentaciones)

Todos se definen con `\documentclass{}`.

`\documentclass` también acepta argumentos opcionales.

- ▶ `\documentclass[12pt,twocolumn]{article}`
hace al texto más grande (12pt) y lo coloca en dos columnas.

Tipografía de Texto

- ▶ Escribe tu texto entre `\begin{document}` y `\end{document}`.
- ▶ En su mayoría, puedes escribir texto normalmente (a excepción de algunos caracteres especiales)
- ▶ Para escribir comillas, usa el acento invertido ``` y el apóstrofo `'`.

Comillas simple: ``texto'`.

Comillas simple: `'texto'`.

Comillas dobles: ```texto''`.

Comillas dobles: `"texto"`.

- ▶ Algunos caracteres comunes tienen significados especiales en \LaTeX :

`%` Signo de porcentaje

`#` Signo numeral

`&` Ampersand

`$` Signo pesos

- ▶ Para que alguno de estos caracteres aparezcan en el archivo de salida, se tienen que preceder con una barra invertida .

`\$ \% \& \# !`

`$ \% \& \# !`

Cambio del formato y tamaño de texto

`\textbf{Hello World!}`

```
\textit{Hello World!} \\
```

```
\underline{Hello World!} \\ \\
```

```
\tiny{Hello World!} \\ \\ \\
```

```
\footnotesize{Hello World!}
```

`\LARGE{Hello World!}`

Hello World!

Hello World!

Hello World!

Hello World!

Hello World! Hello
World!

*¿Qué pasa con el espacio entre las frases?

Tipografía Matemática: Signo pesos

- ▶ Los signos pesos $\$$ se usan para marcar contenido matemático dentro del texto.

% no tan bueno:

Sean a y b distintos números enteros positivos, y que $c = a - b + 1$.

Sean a y b distintos números enteros positivos, y que $c = a - b + 1$.

% mucho mejor:

Sean a y b distintos números enteros positivos, y que $c = a - b + 1$.

Sean a y b distintos números enteros positivos, y que $c = a - b + 1$.

- ▶ Utiliza siempre los signos de pesos en pares — uno para comenzar el contenido matemático, y uno para terminarlo.
- ▶ \LaTeX maneja el espacio automáticamente; por lo que ignorará los que hayamos puesto.

Sea $y = mx + b \dots$

Sea $y = mx + b \dots$

Sea $y = mx + b \dots$

Sea $y = mx + b \dots$

Paquetes

- ▶ Los *paquetes* son librerías de comandos y entornos adicionales. Hay miles de paquetes de libre acceso.
- ▶ Todos los comandos y entornos que hemos utilizado hasta el momento se encuentran integrados en L^AT_EX.
- ▶ Para cargar un paquete, usamos el comando `\usepackage` al inicio del documento.
- ▶ Ejemplo: `amsmath` desde la American Mathematical Society.

```
\documentclass{article}
\usepackage{amsmath} % pre\ 'ambulo
\begin{document}
% ahora podemos usar los comandos desde el
% paquete amsmath...
\end{document}
```

- ▶ Puedes hacer documentos estructurados, con página de título y autor (`\maketitle`, `\title`, `\author`)
- ▶ También puedes incluir secciones, subsecciones, subsubseccion (`\section`, `\subsection`, `\subsubsection`) y las numera automáticamente.
- ▶ Con `\tableofcontents`, se puede crear una tabla de contenido numerada con todas las secciones.

- ▶ Usa el paquete babel
- ▶ Añade en el preámbulo del documento de L^AT_EX:
 - ▶ `\usepackage[spanish]{babel}`

- ▶ Las figuras y tablas se etiquetan (`\label`) y se pueden referenciar en el documento (`\ref`) fácilmente
- ▶ Como estas se referencian por su nombre, no importan si cambia su orden de aparición en el documento, su número se actualiza automáticamente.

- ▶ Overleaf es un sitio web para escribir documentos en \LaTeX .
- ▶ Este “compila” tu texto \LaTeX automáticamente para que veas el resultado.

Click aquí para abrir el documento de ejemplo en **Overleaf**

Para un mejor resultado, use Google Chrome o una versión actualizada de FireFox.

Errores de manejo

- ▶ \LaTeX puede confundirse cuando está intentando compilar el documento y no habrá archivo de salida.
- ▶ Por ejemplo, si escribes `\emph` como `\meph`, \LaTeX se detendrá con un mensaje de error “undefined control sequence”, ya que “meph” no es un comando reconocido.

Indicaciones sobre Errores

1. Corregirlos a medida que se vayan presentando — si lo que acabas de escribir causa un error, empieza a depurar por ahí.
2. Si hay múltiples errores, comienza por el primero — La causa de muchos puede estar al inicio (básicamente como en cualquier otro lenguaje de programación).
3. En el peor de los casos, pregunta a Google.

Errores en Overleaf

The screenshot shows the Overleaf web editor interface. On the left, the 'Source' tab is active, displaying LaTeX code. On the right, two error messages are shown in a sidebar.

Source Code:

```
17 description={an example}}
18
19 \newacronym{abc}{ABC}{a sample acronym}
20
21 \begin{document}
22
23 \maketitle
24
25 \begin{abstract}
26 This is a \gls{sample} document. Modified: \pdfcreationdate{.
27 \end{abstract}
28
29 \section{Sample Section}
30 \label{sec:sample}
31
32 This is an example\index{example} section with a
   citation~\cite{sample} and \gls{abc}
33
34 \section{Another Section}
35 \label{sec:another}
36
37 This is another section with a cross-reference to
38 section \ref{sec:sample}.
```

Errors:

- Undefined control sequence.** (main.tex, line 26)
The compiler is having trouble understanding a command you have used. Check that the command is spelled correctly. If the command is part of a package, make sure you have included the package in your preamble using `\usepackage{...}`.
[Learn more](#)
- Citation 'smple' on page 1 undefined on Input line 32.** (main.tex, line 32)
You have cited something which is not included in your bibliography. Make sure that the citation (`\cite{...}`) has a

Overleaf templates

- ▶ Vamos a **Overleaf-Templates**
- ▶ Ventajas:
 - ▶ Amplia selección de tipos de documentos y plantillas
 - ▶ Envío directo de los artículos a las revistas
 - ▶ Colaboración entre varias personas en el mismo proyecto
 - ▶ Revisión gramatical en inglés
 - ▶ Chat en línea con los colaboradores, entre otras.

The screenshot displays the Overleaf web editor interface. On the left, a file explorer shows a project named 'GSA-journal-te...' with files like 'genetics.bst', 'gsajnl.cls', and 'references.bib'. The main editor area shows a LaTeX document titled 'Modeling SNP array ascertainment with Approximate Bayesian Computation for demographic inference'. The document content includes a title, authors (Garcés B. García-García, August B. Wimmer, Joseph E. Huddell, and Michael P. Hassler), affiliations, an abstract, and a keywords section. The abstract discusses the challenges of SNP array ascertainment and the proposed model. The keywords section lists 'Ascertainment bias', 'SNP array', 'Demographic inference', 'Approximate Bayesian Computation', and 'Demographic modeling'.

Modeling SNP array ascertainment with Approximate Bayesian Computation for demographic inference

Garcés B. García-García¹, August B. Wimmer², Joseph E. Huddell³ and Michael P. Hassler^{1,4}

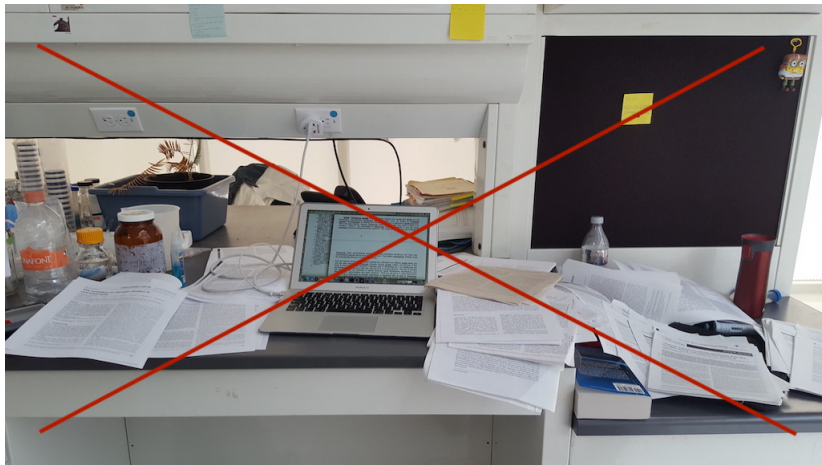
¹National Laboratory of Genetics for Biomedical Research (LNBIO), CONICET-UNC, Córdoba, Argentina; ²Center for Human Identification, University of North Texas Health Science Center, Texas, U.S.A.; ³Department of Mathematics, University of Arizona, Tucson, Arizona, U.S.A.; ⁴RISE, Department of Biotechnology, University of Arizona, Tucson, Arizona, U.S.A.

ABSTRACT

Single nucleotide polymorphisms (SNPs) in commercial genotyping arrays have often been discovered by sampling a small number of chromosomes from a group of selected populations. This form of non-random ascertainment biases patterns of nucleotide diversity and can affect population genetic inferences. In addition, the effects of ascertainment bias become stronger the more divergent the population of interest is to those in the discovery panel. Most attempts to correct for this bias suffer from uncertainty in the exact discovery protocols for most commercial arrays. In this work, we propose a demographic inference pipeline that explicitly models the SNP discovery protocol in an Approximate Bayesian Computation (ABC) framework. We simulated genetic regions according to a demographic model incorporating parameters for the divergence of three well-characterized populations: the Yoruba, Han Chinese and CEU (European), and simulated the SNP distribution of a commercial array by varying the number of sampled chromosomes and the allele frequency cut-off in the given regions. We then calculated allele frequency spectra and haplotypes based summary statistics obtained from both the ascertained and genomic data and inferred both ascertainment and demographic parameters of the models. We also implemented our pipeline to study the admixture process between European and Native American populations that gave rise to the present-day Mexican population. In particular, our estimate of the time of admixture in Mexico is closer to the historical dates than those of works which did not consider ascertainment bias. Our inference framework is applicable to studies when only SNP array data of the populations of interest are available and will improve to accuracy of demographic model inference.

KEYWORDS Ascertainment bias, SNP array, Demographic inference, Approximate Bayesian Computation, Demographic modeling

L^AT_EX te facilita la vida!



- ▶ Las referencias tienen que estar en un archivo .bib en el formato 'bibtex':

```
@Article{Jacobson1999,  
  author = {Van Jacobson},  
  title = {Towards the Analysis of Massive Multiplayer Online  
          Role-Playing Games},  
  journal = {Journal of Ubiquitous Information},  
  Month = jun,  
  Year = 1999,  
  Volume = 6,  
  Pages = {75--83}}  
  
@InProceedings{Brooks1997,  
  author = {Fredrick P. Brooks and John Kubiatawicz and  
          Christos Papadimitriou},  
  title = {A Methodology for the Study of the  
          Location-Identity Split},  
  booktitle = {Proceedings of OOPSLA},  
  Month = jun,  
  Year = 1997}
```

- ▶ Cada entrada en el archivo .bib tiene una *clave* para ser citado en el documento.

Por ejemplo, Jacobson1999 es la clave para este artículo:

```
@Article{Jacobson1999,  
  author = {Van Jacobson},  
  ...  
}
```

- ▶ Es recomendable utilizar una clave basada en el nombre y año del artículo.
- ▶ \LaTeX formatea automáticamente las citas en el texto y genera una lista de referencias.

Bibliografía

- ▶ Utiliza el paquete natbib con los comandos `\citet`, `\citep`, `\citeyear` y `\citeauthor`.
- ▶ Las referencias bibliográficas se insertan con el comando `\bibliography`, y el estilo con `\bibliographystyle`.

```
\documentclass{article}
\usepackage{natbib}
\begin{document}

\citet{Brooks1997} muestra
que \ldots. Evidentemente todos
los n'umeros impares son primos
\citep{Jacobson1999}.

\bibliography{bib-exercise}
% Siendo `bib-exercise' el nombre
% de su archivo bib

\bibliographystyle{plainnat}
% Intente cambiar a abbrnat

\end{document}
```

Brooks et al. [1997] muestra que Evidentemente todos los números impares son primos [Jacobson, 1999].

References

Fredrick P. Brooks, John Kubiatorowicz, and Christos Papadimitriou. A methodology for the study of the location-identity split. In *Proceedings of OOPSLA*, June 1997.

Van Jacobson. Towards the analysis of massive multiplayer online role-playing games. *Journal of Ubiquitous Information*, 6:75–83, June 1999.

Ejemplos de estilo de bibliografía *natbib*

References

dinat

[Einstein 1905] EINSTEIN, Albert: Zur Elektrodynamik bewegter Körper. (German) [On the electrodynamics of moving bodies]. In: *Annalen der Physik* 322 (1905), Nr. 10, S. 891–921.

[Gossens u. a. 1993] GOOSSENS, Michel ; MITTELBACH, Frank ; SAMARDI, Alexander: *The L^AT_EX Companion*. Reading, Massachusetts : Addison-Wesley, 1993

[Knuth] KNUTH, Donald: *Knuth: Computers and Typesetting*. – URL: <http://www-cs-faculty.stanford.edu/~uno/abcde.html>

Items are cited: *The L^AT_EX Companion* book Gossens et al. (1993), the Einstein journal paper Einstein (1905), and The L^AT_EX related items are Gossens et al. (1993); Knuth.

References

humannat

Einstein, A.
1905. Zur Elektrodynamik bewegter Körper. (German) [On the electrodynamics of moving bodies]. *Annalen der Physik*, 322(10):891–921.

Goossens, M., F. Mittelbach, and A. Samarin
1993. *The L^AT_EX Companion*. Reading, Massachusetts: Addison-Wesley.

Knuth, D.
 . Knuth: Computers and typesetting.

Items are cited: *The L^AT_EX Companion* book Goossens et al. [1993], the Einstein journal paper Einstein [1905], and The L^AT_EX related items are Goossens et al. [1993], Knuth.

References

plainnat

Albert Einstein. Zur Elektrodynamik bewegter Körper. (German) [On the electrodynamics of moving bodies]. *Annalen der Physik*, 322(10):891–921, 1905. doi: <http://dx.doi.org/10.1002/andp.19053221004>.

Michel Goossens, Frank Mittelbach, and Alexander Samarin. *The L^AT_EX Companion*. Addison-Wesley, Reading, Massachusetts, 1993.

Donald Knuth. Knuth: Computers and typesetting. URL
<http://www-cs-faculty.stanford.edu/~uno/abcde.html>.

Items are cited: *The L^AT_EX Companion* book Goossens et al. [1993], the Einstein journal paper Einstein [1906], and The L^AT_EX related items are Goossens et al. [1993], Knuth.

References

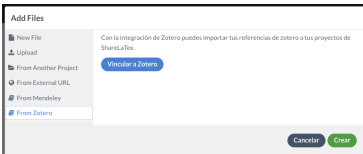
abrvnat

A. Einstein. Zur Elektrodynamik bewegter Körper. (German) [On the electrodynamics of moving bodies]. *Annalen der Physik*, 322(10):891–921, 1905. doi:<http://dx.doi.org/10.1002/andp.19053221004>.

M. Goossens, F. Mittelbach, and A. Samarin. *The L^AT_EX Companion*. Addison-Wesley, Reading, Massachusetts, 1993.

Gestor de referencias **Mendeley**

- ▶ Se puede usar de manera local y en línea ¹
- ▶ Ventajas:
 - ▶ Hacer anotaciones directamente en los artículos
 - ▶ Organizar las referencias por carpeta
 - ▶ Añadir artículos directamente sin necesidad de tener el archivo
 - ▶ Exportar las referencias en formato BibTeX (Formato más utilizado para construir bibliografías en \LaTeX)
 - ▶ Se puede sincronizar con **Overleaf**



¹Existen otros gestores de referencias como Papers, Zotero, Endnote.

Cómo usar Mendeley

The screenshot shows the Mendeley Desktop application window. On the left is a sidebar with navigation options like 'MY LIBRARY', 'GROUPS', and 'TRASH'. The main area displays a list of references with columns for Authors, Title, Year, Published in, and Added. The selected reference is 'Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across the Pacific' by V. Thomson, O. Lebrasseur, J. Austin et al., published in 2014 in the 'Proceedings of the National Academy of Sciences'.

Reference List:

Authors	Title	Year	Published in	Added
van Oven, Marnik; Brauer, Silke; Choi, Ying...	Human genetics of the Kula-Ring: Y-chromosome and mitochondrial DNA variation in the Measim...	2014	European Journal of Hu...	10/5/18
Delin, Frederick; Mylkes, Sean; Choi, Ying; Hughes...	Bringing Near and Remote Oceania: mtDNA and HVI variation in the Solomon Islands	2012	Molecular Biology and E...	10/5/18
Brewis, Alexandra A; Irwin, Geoffrey; Allen, J...	Patterns of colonisation and the "thrifty" genotype in Pacific prehistory	1986	Asia Pacific J Clin Nutr	10/12/18
Lipson, Mark; Charnot, Olivia; Mallick, Swapan...	Ancient genomes document multiple waves of migration in Southwest Asian prehistory	2018	Science	10/5/18
Duggan, Ana T.; Evans, Bethwyn; Friedlander, ...	Maternal history of Oceania from complete mtDNA genomes: Contrasting ancient diversity with rec...	2014	American Journal of Hu...	10/5/18
Montenegro, Álvaro; Callaghan, Richard T.; FL...	Using seafaring simulations and short-cut hop trajectories to model the prehistoric colonization ...	2016	Proceedings of the National ...	10/5/18
Hill, Catherine; Soares, Pedro; Marnik, Marni...	A mitochondrial strategy for island southeast Asia	2007	American Journal of Hu...	5/2/11
Kusuma, Pradistapati; Brucato, Nicolas; Cox...	Contrasting Linguistic and Genetic Origins of the Asian Source Populations of Malagasy	2018	Scientific Reports	10/5/18
Lipson, Mark; Skoglund, Pontus; Spriggs, Matthe...	Population Turnover in Remote Oceania Shortly after Initial Settlement	2018	Current Biology	10/5/18
Minister, Ryan L.; Hawley, Nicolas L.; Su, Chi Ting...	A thrifty variant in CERS6 strongly influences body mass index in Samoans	2016	Nature Genetics	10/5/18
Cox, Murray P.; Lafr, Maria Miriam	Y-chromosome diversity is inversely associated with language affiliation in paired Austronesian...	2016	American Journal of Hu...	10/5/18
Pooth, Christine; Niglicke, Kathrin; Colvener, Heidi...	Language continuity despite population replacement in Remote Oceania	2018	Nature Ecology and Evolution	10/5/18
Thomson, Vicki A.; Lebrasseur, Catherine Au...	Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across...	2014	Proceedings of the National ...	10/5/18
Chang, Chi-Shan; Liu, Hsiao-Li; Mancada, X...	A holistic picture of Austronesian migrations revealed by phylogeography of Pacific paper mul...	2015	Proceedings of the National ...	10/5/18
Bergstrom, Anders; Tyler-Smith, Chris	Human Genetics: Busy Highway Networks in Remote Oceania?	2018	Current Biology	10/5/18
Kel Lum, J.; Cann, Rebecca L.	mtDNA lineage analyses: Origins and migrations of Micronesians and Polynesians	2010	American Journal of Hu...	10/5/18
Soares, Pedro; Rito, Teresa; Tjebk, Jean M...	Ancient voyaging and polynesian origins	2011	American Journal of Hu...	10/5/18
Martinez-Camacho, A.; Tjebk, Jennifer J. S...	Global prevalence of putative haemochromatosis mutations.	1987	Journal of medical gene...	1/10/17
Wu, Lan Hai; Yan, Shi; Tan, Yi; Yan, Sheng...	Phylogeography of Y-chromosome haplogroup O1a2b1b1 reveals panethnic traces of Austrone...	2017	PLoS ONE	10/5/18
Shapiro, Gerhard P.; Taylor, Diana A.; M'Yer...	Genetic Evidence for Modifying Oceanic Boundaries Relative to Fiji	2016	Human Biology	10/5/18
Soares, Pedro A.; Tjebk, Jean A.; Rito, Teresa, C...	Resolving the ancestry of Austronesian-speaking populations	2016	Human Genetics	10/5/18
Censer, Chris A.; McElreath, Patricia A...	The Q2 Mitochondrial Haplogroup in Oceania	2012	PLoS ONE	10/5/18
Lum, J.; Kel, Cann, Rebecca L.; Martinson, J...	Mitochondrial and nuclear genetic relationships among Pacific Island and Asian populations.	1988	American Journal of Hu...	10/5/18

Details for 'Using ancient DNA to study the origins and dispersal of ancestral Polynesian chickens across the Pacific':

- Type:** Journal Article
- Journal:** Proceedings of the National Academy of Sciences
- Year:** 2014
- Volume:** 111
- Issue:** 13
- Pages:** 4826-4831
- Abstract:** The human colonization of Remote Oceania remains one of the great feats of exploration in history, proceeding east from Asia across the vast expanse of the Pacific Ocean. Human commercial and domesticated species were widely transported as part of this dispersal, possibly as far as South America. We sequenced mitochondrial control region DNA from 123 modern and 22 ancient chicken specimens from Polynesia and Island Southeast Asia and used these together with Bayesian modeling methods to examine the human dispersal of chickens across this area. We show that specific techniques are essential to remove contaminating modern DNA from experiments, which appear to have impeded previous studies of Pacific chickens. In contrast to previous reports, we find that ancient specimens and a high proportion of the modern chickens possess a group of unique, closely related haplotypes found only in the Pacific. This group of haplotypes appears to represent the authentic f...
- Tags:**
- Author Keywords:**
- Citation Key:** Thomson2014
- URL:** <http://www.pnas.org/lookup/suppl/doi:10.1073/pnas.132...>
- Catalog IDs:** Arxiv ID: arXiv:1604.03974v2 DOI: 10.1073/pnas.1320417111

*La mayoría de los gestores de referencias pueden exportar al formato bibtext.

Cómo usar Mendeley

The screenshot shows the Mendeley Desktop application interface. At the top, there is a toolbar with icons for star, folder, and document, followed by an 'Edit Settings' button. Below this is a table of references. A right-click context menu is open over one of the entries, showing options like 'Update Details', 'Open File', 'Export...', and 'BibTeX Entry'.

Star	Folder	Document	Authors	Title	Year	Published In	Added
★			van Oven, Mannis; Brauer, Silke; Choi, Ying...	Human genetics of the Kula Ring: Y-chromosome and mitochondrial DNA variation in the Massim e...	2014	European Journal of hu...	10/5/18
★			Defin, Frederick; Myles, Sean; Choi, Ying; Hughe...	Bridging Near and Remote Oceania: mtDNA and NRY variation in the Solomon Islands	2012	Molecular Biology and E...	10/5/18
★			Brewis, Alexandra A; Irwin, Geoffrey; Allen, J...	Patterns of colonisation and the "thrifty" genotype in Pacific prehistory	1995	Asia Pacific J Clin Nutr	10/12/18
★			Lipson, Mark; Cheronet, Olivia; Mallick, Swapan; ...	Ancient genomes document multiple waves of migration in Southeast Asian prehistory	2018	Science	10/5/18
★			Duggan, Ana T.; Evans, Bethwyn; Friedlaender, ...	Maternal history of oceania from complete mtDNA genomes: Contrasting ancient diversity with rece...	2014	American Journal of Hu...	10/5/18
★			Montenegro, Álvaro; Callaghan, Richard T.; Fl...	Using seafaring simulations and shortest-hop trajectories to model the prehistoric colonization ...	2016	Proceedings of the National ...	10/5/18
★			Hill, Catherine; Soares, Pedro; Mormina, Maru; ...	A mitochondrial stratigraphy for island southeast Asia.	2007	American journal of hu...	2/5/11
★			Kusuma, Pradiptajati; Brucato, Nicolas; Cox, ...	Contrasting Linguistic and Genetic Origins of the Asian Source Populations of Malagasy	2016	Scientific Reports	10/5/18
★			Lipson, Mark; Skoglund, Pontus; Spriggs, Matthe...	Population Turnover in Remote Oceania Shortly after Initial Settlement	2018	Current Biology	10/5/18
★			Minster, Ryan L.; Hawley, Nicola L.; Su, Chi Ting; ...	A thrifty variant in CREBRF strongly influences body mass index in Samoans	2016	Nature Genetics	10/5/18
★			Cox, Murray P.; Lahr, Marta Mirazón	Y-chromosome diversity is inversely associated with language affiliation in paired Austronesian- ...	2006	American Journal of Hu...	10/5/18
★			Posth, Cosimo; Nägele, Kathrin; Collier, Heidi; ...	Language continuity despite population replacement in Remote Oceania	2018	Nature Ecology and Evolution	10/5/18

The context menu options are:

- Update Details
- Related Documents
- Open File
- Open File Externally
- Open Containing Folder
- Rename Document Files...
- Merge Documents
- Mark As
- Copy As
- Export...
- Export PDF(s) with Sticky Notes...
- Select All
- Remove from Folder
- Delete Documents
- Formatted Citation
- LaTeX Citation Command
- BibTeX Entry

Cómo usar Mendeley

The screenshot shows the Mendeley Desktop application interface. At the top, there is a toolbar with 'OOVP' and 'Edit Settings' buttons. Below this is a table of references with columns for Authors, Title, Year, Published in, and Added. The table contains several entries, including 'Human genetics of the Kula Ring: Y-chromosome and mitochondrial DNA variation in the Massim o...', 'Bridging Near and Remote Oceania: mtDNA and NRY variation in the Solomon Islands', and 'Patterns of colonisation and the "thrifty" genotype in Pacific prehistory'.

A context menu is open over the selected row, showing options such as 'Update Details', 'Related Documents', 'Open File', 'Open File Externally', 'Open Containing Folder', 'Rename Document Files...', 'Merge Documents', 'Mark As', 'Copy As', 'Export...', 'Export PDF(s) with Sticky Notes...', 'Select All', 'Remove from Folder', and 'Delete Documents'.

Below the main table, there is a smaller table with the same columns, showing a subset of the references. A 'Save As' dialog box is open over this smaller table, with the filename 'My Collection.bib', the location 'Desktop', and the file type 'BibTeX (*.bib)'. The dialog box has 'Cancel' and 'Save' buttons.

- ▶ Esta presentación se hizo con beamer :)
- ▶ <https://hartwork.org/beamer-theme-matrix/>

► <https://www.ilovepdf.com/es>

https://www.overleaf.com/learn/latex/Main_Page