

# From Genes to Kin: Dissecting Relatedness & Kinship in R

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LIVING CONSERVATION

# Overview



- What is relatedness ( $r$ )?
- Why estimating  $r$ ?
- Properties of  $r$
- Methods for estimating  $r$ 
  - ✓ Pedigree based methods
  - ✓ Marker based methods
- Issues with current marker based methods
  - ✓ Reference allele frequency and small sample sizes
  - ✓ Prior assumption of unrelatedness
  - ✓ Speed for large genomic data
  - ✓ Linkage and linkage disequilibrium in large genomic data
  - ✓ Negative estimates
  - ✓ Subdivided populations
  - ✓ Admixed populations
- Conclusions

# What is *RELATEDNESS* ?



## Genealogical definition

- It measures the degree that 2 individuals are genetically related due to **recent** common ancestors (CA)
- It is determined by the number of CAs, and the numbers of generations linking the 2 individuals to each CA
- Implicit reference population (unrelated and non-inbred):  $r$  is a **relative** measure

## Genomic definition

- It can also be measured by the proportion of alleles shared between individuals that are **IBD**
- Genes IBD are copies of the same gene of a **recent** ancestor (different from IIS)
- Implicit reference population (NO genes IBD within and between individuals):  $r$  is a **relative** measure

# What is *RELATEDNESS* – Cont 1



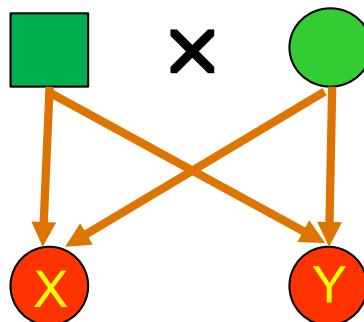
- Relatedness ( $r$ ): continuous quantity ( $0 \sim 1$ )

Relatives	Relationships ( $x, y$ )	$r_{xy}$
0 degree (?)	Monozygotic twins $x=y$	1
1st degree	Parent-Offspring Fullsibs	0.5
2ed degree	Halfsibs Avuncular Grandparents-Grandchildren Double First Cousins	0.25
3rd degree	First cousins Great Grandparents-Great Grandchildren Great Uncles/Aunts	0.125
...	...	...
$\infty$ degree (?)	Unrelated	0

# What is *RELATEDNESS* – Cont 2

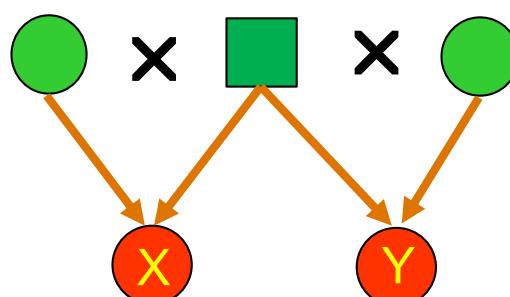


- Frequently  $r$  is measured by **coancestry coefficient** or **kinship coefficient**  $\theta$ : the probability that two homologous genes, one taken at random from each individual, are IBD



$$\theta_{FS} = 0.25$$

$$r_{FS} = 0.5$$



$$\theta_{HS} = 0.125$$

$$r_{HS} = 0.25$$

- The relationship between  $r$  and  $\theta$

$$r_{xy} = \frac{2\theta_{xy}}{\sqrt{2(1+F_x)(1+F_y)}}$$

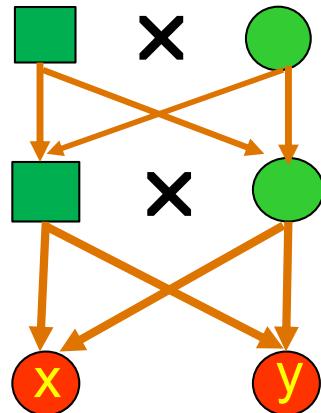
$r_{xy} = 2\theta_{xy}$ , ONLY when  $F_x = F_y = 0$

$r_{xy} < 2\theta_{xy}$ , when  $F_x > 0$  or  $F_y > 0$

# What is *RELATEDNESS* – Cont 3



- Fullsibs whose parents are fullsibs (FSFS)



- $\theta_{xy} = 0.375$
- $F_x = 0.25$
- $F_y = 0.25$
- $r_{xy} = \frac{2\theta_{xy}}{\sqrt{2(1+F_x)(1+F_y)}} = 0.6$
- $r_{xy} = 2\theta_{xy} = 0.75$

- Completely inbred twins

- $\theta_{xy} = 1$
- $F_x = 1$
- $F_y = 1$
- $r_{xy} = \frac{2\theta_{xy}}{\sqrt{2(1+F_x)(1+F_y)}} = 1$

- $r_{xy} = 2\theta_{xy} = 2$

# Why estimating $r$ ?



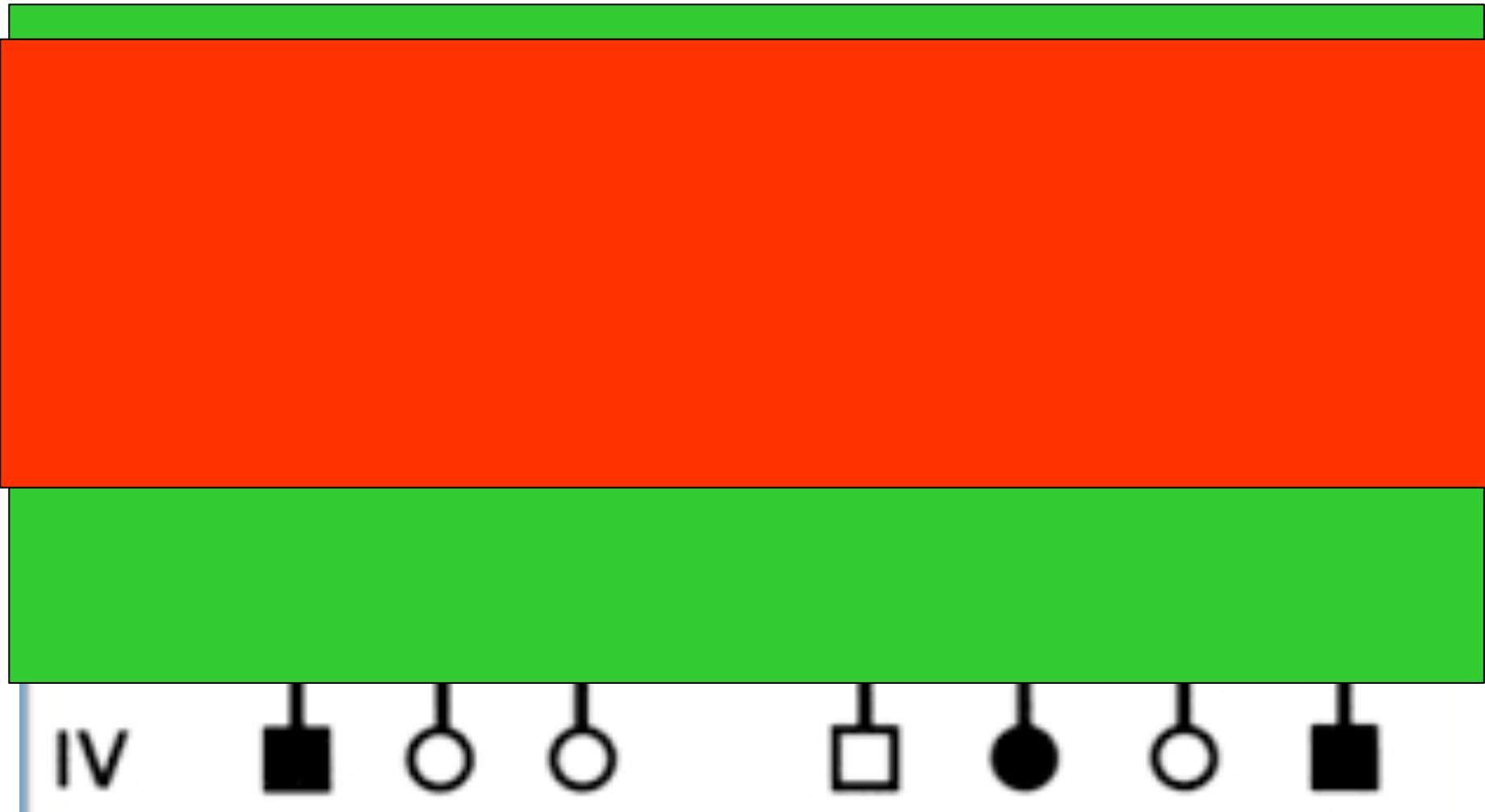
- Marriage & inheritance laws are partially determined by  $r$
- Forensics (for example, identifying bodies or body parts)
- Family reunion, pedigree reconstruction
- QTL mapping of disease genes
- Crop & domestic animal breeding:  $h^2$
- Conservation of engendered species: select unrelated individuals for reintroduction; for reproduction to maximize genetic diversity
- Evolutionary biology hypothesis about mate choice, kin selection, inbreeding depression
- ...

# Properties of $r$



- Pedigree- or marker-based probability (IBD)  
definition:  $r$  is a probability with values in  $[0,1]$
- It is a relative quantity, relative to a reference population
- In the reference population, no genes are IBD (all individuals are outbred,  $F=0$ , and unrelated,  $r = 0$ )
- The reference population is artificial (arbitrary), but determines  $r$

# Properties of $r$ – Cont 1



# Properties of $r$ – Cont 2

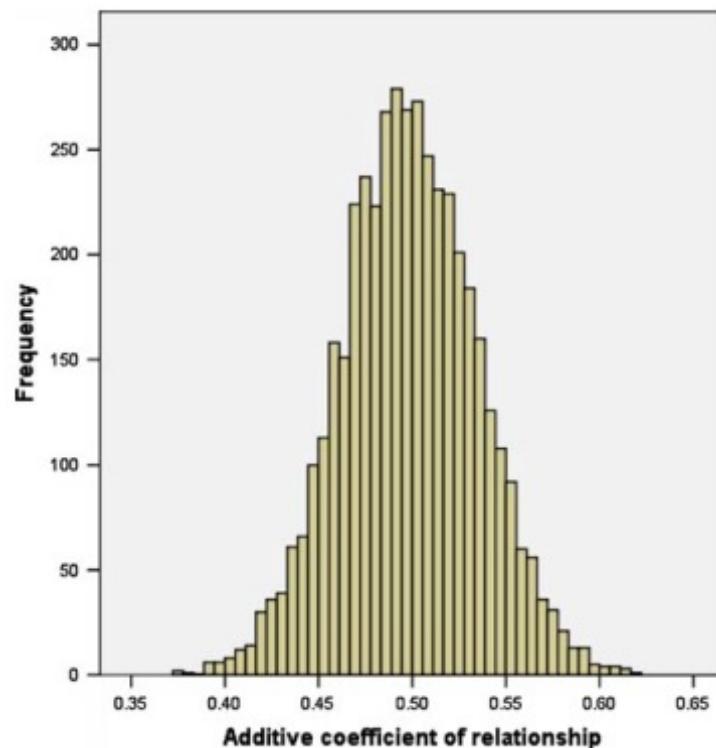


- In certain conditions,  $r$  can be meaningfully negative (hybrids, immigrants)
- Pedigree analysis gives the expected relatedness (e.g.  $r_{FS} = 0.5$ )
- Actual (realized) relatedness varies around the expected value due to Mendelian segregation

# Properties of $r$ – Cont 3



- ➤ The variance depends on the relationship (pedigree) and the genome size ( $L$ , genetic map length)
  - For human autosomes ( $k=22$ ,  $L=35M$ ), the variance of the actual (realized)  $r$  for full sibs is  $V(r_{FS}) \approx \frac{1}{16L} - \frac{22}{(8L)^2} \approx 0.0015$ ,  $SD(r_{FS}) \approx 0.039$ ,  $CV(r_{FS}) \approx 0.078$



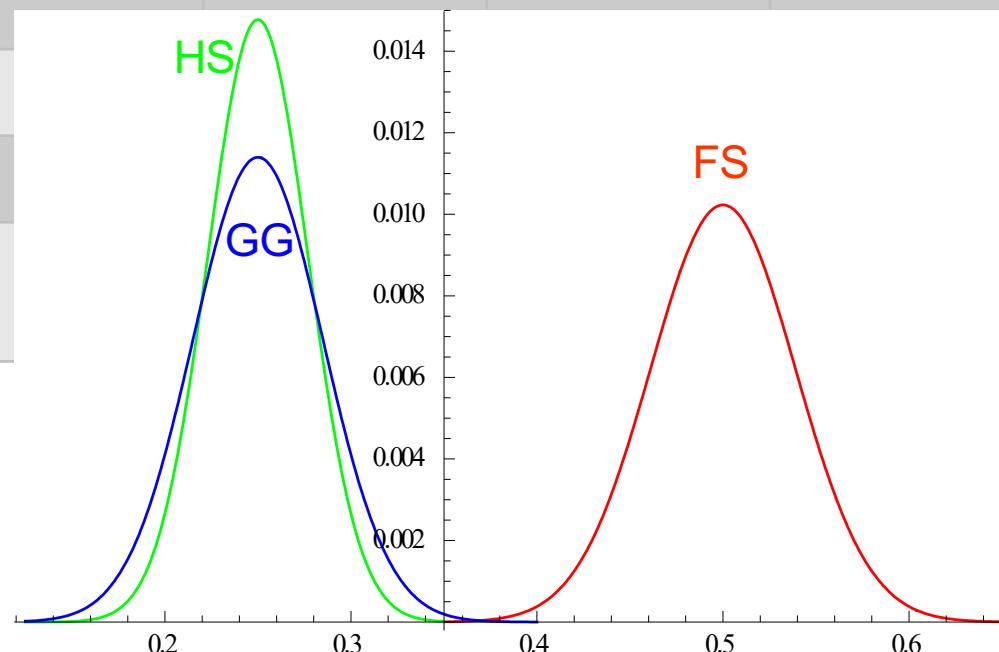
Empirical distribution of genomic  $r$  from 4401 pairs of fullsibs  
(Visscher et al. 2006)

Mean( $r$ ) = 0.498  
SD( $r$ ) = 0.036

# Properties of $r$ – Cont 4



Relationship	Single locus			Genomic (human)	
	$E(r)$	$V(r)$	$SD(r)$	$V(r)$	$SD(r)$
Parent-Offspring	1/2	0	0	0	0
Fullsibs	1/2	0.12500	0.354	0.00147	0.039
Halfsibs	1/4	0.06250	0.250	0.00075	0.027
Grandparent-Grandchild	1/4	0.06250	0.250	0.00122	0.035
Uncle-niece				0.025	
First cousin				0.021	
Double first cousin				0.030	



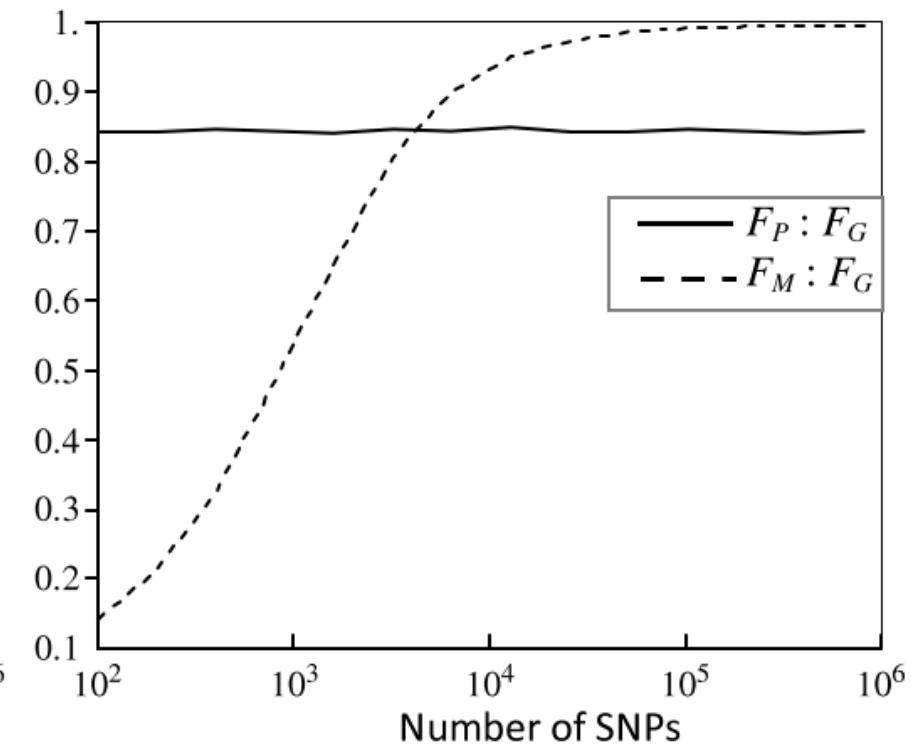
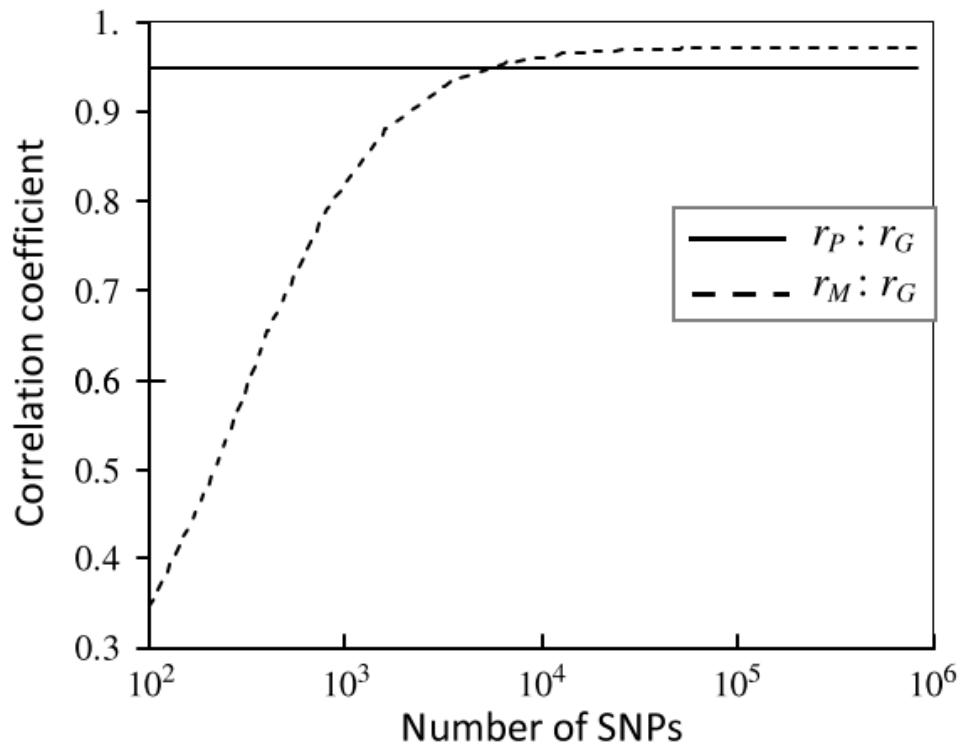
# Properties of $r$ – Cont 5



- Marker relatedness:  $r$  estimates from and for a particular set of markers. With many markers taken at random from the genome, average marker relatedness is close to the actual genomic relatedness
- Marker relatedness and pedigree relatedness, which is better as an estimator of the actual genomic relatedness?

Wang, J. 2016. Pedigrees or markers: Which are better in estimating relatedness and inbreeding coefficient? Theoretical Population Biology 107: 4-13.

# Properties of $r$ – Cont 6

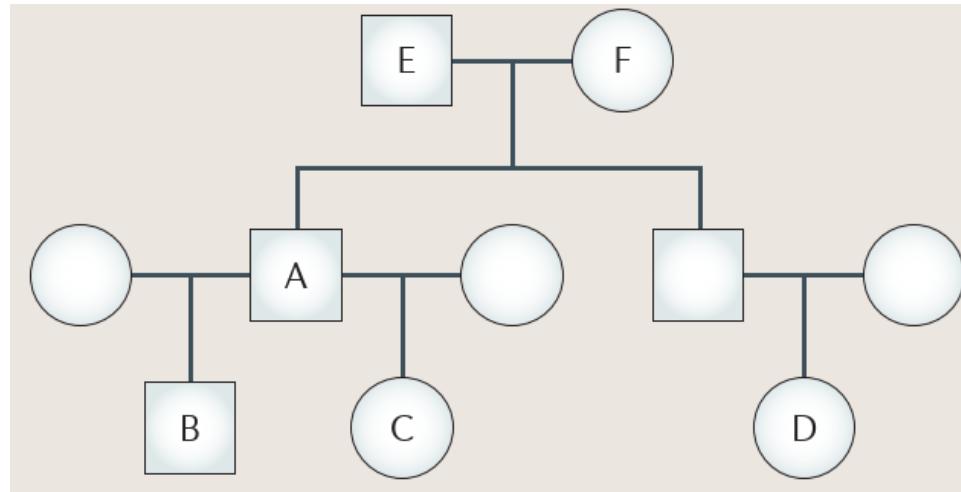


parameters are  $N = 64$ ,  $G = 8$ ,  $L = 32$  M, and  $L_{IBD} = 10^4$

# Methods for estimating $r$



- Estimating from pedigree (Wright's path analysis)



$$\checkmark \theta_{BC} = \sum_A \frac{1+F_A}{2^n} = \frac{1+0}{2^3} = 0.125$$

- Problems with pedigree-based  $r$ 
  - Expected values
  - Pedigree usually unavailable, incomplete, erroneous, too shallow
  - Expensive and time-consuming to get a decent pedigree

# Methods for estimating $r$ –Cont 1



- Marker-based estimators

- Many advantages (fast, cheap, more accurate?)
- Many estimators are developed, based on allele frequency moments
- Rely on the statistical framework linking the observed genotypes (i.e. IIS) to the probabilities of IBD & the frequencies of the alleles in the genotypes
- Estimating inbreeding coefficient,  $F$

The simplest example: individual genotype at a diallelic locus (A, a)

$$F_Z = \theta_{xy},$$

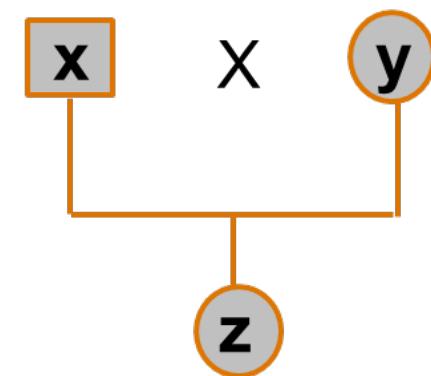
$$\Pr(G_Z = AA) = F_Z P_A + (1 - F_Z) P_A^2,$$

$$\Pr(G_Z = aa) = F_Z P_a + (1 - F_Z) P_a^2,$$

$$\Pr(G_Z = Aa) = 2(1 - F_Z)P_A P_a,$$

**PREDICTION** of genotypes given IBD coefficients

**ESTIMATION** of IBD coefficients ( $F$ ) given observed genotypes



# Methods for estimating $r$ –Cont 2



- Given  $G_Z = AA$ , we have  $1 = F_Z P_A + (1 - F_Z)P_A^2$ ,  $F_Z = \frac{1/P_A - P_A}{1 - P_A}$ ;
- Given  $G_Z = aa$ , we have  $1 = F_Z P_a + (1 - F_Z)P_a^2$ ,  $F_Z = \frac{1/P_a - P_a}{1 - P_a}$ ;
- Given  $G_Z = Aa$ , we have  $1 = 2(1 - F_Z)P_a P_A$ ,  $F_Z = 1 - \frac{0.5}{1 - P_a P_A}$ .
- Estimates of  $F_Z$  from a single locus are extremely variable, usually out of the legitimate range of [0,1] (in the probability or IBD definition of  $F$ ) or [-1,1] (in the correlation definition of  $F$ )
- The actual  $F_Z = 0$  or  $1$  at a locus, with probabilities  $1 - F_Z$  and  $F_Z$  respectively
- If  $P_A = 0.1$  and  $P_a = 0.9$ , we have  $\hat{F}_Z = 11, 2.1, -4.6$  with observed genotypes AA, aa, and Aa respectively
- Unbiased (at least in the ideal conditions)
- Consistent (estimate variance decline with an increasing #loci)
- Because of linkage, even genome-wide markers still give estimation errors
- Allele frequencies are usually unknown, but are estimated from the same genotypes

# Methods for estimating $r$ –Cont 3



- Estimating relatedness  $r$  or coancestry  $\theta$ 
  - Two diploid individuals, 4 alleles at a locus

Individual X's two genes (a,b):



Individual Y's two genes (c,d):



- 15 IBD states (coefficients) of the 4 alleles if their paternal & maternal origins are relevant
- 9 condensed IBD states (coefficients) of the 4 alleles if their paternal & maternal origins are irrelevant

# Methods for estimating $r$ –Cont 4



IBD State	$S_1$	$S_2$	$S_3$	$S_4$	$S_5$	$S_6$	$S_7$	$S_8$	$S_9$
IBD Config									
#non-IBD genes	1	2	2	3	2	3	2	3	4
IBD Prb	$\Delta_1$	$\Delta_2$	$\Delta_3$	$\Delta_4$	$\Delta_5$	$\Delta_6$	$\Delta_7$	$\Delta_8$	$\Delta_9$

$$\Delta_1 + \Delta_2 + \Delta_3 + \Delta_4 + \Delta_5 + \Delta_6 + \Delta_7 + \Delta_8 + \Delta_9 \equiv 1,$$

$$F_X = \Delta_1 + \Delta_2 + \Delta_3 + \Delta_4,$$

$$F_Y = \Delta_1 + \Delta_2 + \Delta_5 + \Delta_6,$$

$$\theta_{XY} = \Delta_1 + \frac{1}{2}(\Delta_3 + \Delta_5 + \Delta_7) + \frac{1}{4}\Delta_8$$

# Methods for estimating $r$ –Cont 5

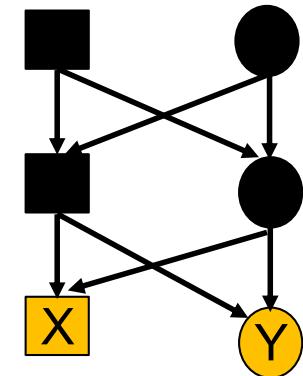


- NO INBREEDING

$$-\Delta_1 = \Delta_2 = \Delta_3 = \Delta_4 = \Delta_5 = \Delta_6 = 0; F_X = F_Y = 0$$

$$-\Delta_7 + \Delta_8 + \Delta_9 \equiv 1$$

IBD coefficients of some relationships



Kinship	$\Delta_1$	$\Delta_2$	$\Delta_3$	$\Delta_4$	$\Delta_5$	$\Delta_6$	$\Delta_7$	$\Delta_8$	$\Delta_9$	$\theta$
Parent-offspring	0	0	0	0	0	0	0	1	0	1/4
Fullsibs	0	0	0	0	0	0	1/4	1/2	1/4	1/4
Halfsibs	0	0	0	0	0	0	0	1/2	1/2	1/8
First cousins	0	0	0	0	0	0	0	1/4	3/4	1/16
Second cousins	0	0	0	0	0	0	0	1/16	15/16	1/64
Avuncular	0	0	0	0	0	0	0	1/2	1/2	1/8
FSFS	1/16	1/32	1/8	1/32	1/8	1/32	7/32	5/16	1/16	3/8

# Methods for estimating $r$ –Cont 6



IIS mode	Allelic state ( $i \neq j \neq k \neq l$ )	IBD modes								
		S <sub>1</sub>	S <sub>2</sub>	S <sub>3</sub>	S <sub>4</sub>	S <sub>5</sub>	S <sub>6</sub>	S <sub>7</sub>	S <sub>8</sub>	S <sub>9</sub>
S <sub>1</sub>	A <sub>i</sub> A <sub>i</sub> , A <sub>j</sub> A <sub>j</sub>	$p_i$	$p_i^2$	$p_i^2$	$p_i^3$	$p_i^2$	$p_i^3$	$p_i^2$	$p_i^3$	$p_i^4$
S <sub>2</sub>	A <sub>i</sub> A <sub>i</sub> , A <sub>j</sub> A <sub>j</sub>	0	$p_i p_j$	0	$p_i p_j^2$	0	$p_i^2 p_j$	0	0	$p_i^2 p_j^2$
S <sub>3</sub>	A <sub>i</sub> A <sub>i</sub> , A <sub>i</sub> A <sub>j</sub>	0	0	$p_i p_j$	$2p_i^2 p_j$	0	0	0	$p_i^2 p_j$	$2p_i^3 p_j$
S <sub>4</sub>	A <sub>i</sub> A <sub>i</sub> , A <sub>j</sub> A <sub>k</sub>	0	0	0	$2p_i p_j p_k$	0	0	0	0	$2p_i^2 p_j p_k$
S <sub>5</sub>	A <sub>i</sub> A <sub>j</sub> , A <sub>i</sub> A <sub>i</sub>	0	0	0	0	$p_i p_j$	$2p_i^2 p_j$	0	$p_i^2 p_j$	$2p_i^3 p_j$
S <sub>6</sub>	A <sub>j</sub> A <sub>k</sub> , A <sub>i</sub> A <sub>i</sub>	0	0	0	0	0	$2p_i p_j p_k$	0	0	$2p_i^2 p_j p_k$
S <sub>7</sub>	A <sub>i</sub> A <sub>j</sub> , A <sub>i</sub> A <sub>j</sub>	0	0	0	0	0	0	$2p_i p_j (p_i + p_j)$	$4p_i^2 p_j^2$	
S <sub>8</sub>	A <sub>i</sub> A <sub>j</sub> , A <sub>i</sub> A <sub>k</sub>	0	0	0	0	0	0	$p_i p_j p_k$	$4p_i^2 p_j p_k$	
S <sub>9</sub>	A <sub>i</sub> A <sub>j</sub> , A <sub>k</sub> A <sub>l</sub>	0	0	0	0	0	0	0	0	$4p_i p_j p_k p_l$

$$\Pr(A_i A_i, A_i A_i) = p_i \Delta_1 + p_i^2 \Delta_2 + p_i^2 \Delta_3 + p_i^3 \Delta_4 + p_i^2 \Delta_5 + p_i^3 \Delta_6 + p_i^2 \Delta_7 + p_i^3 \Delta_8 + p_i^4 \Delta_9$$

Prediction: given  $p$  &  $\Delta$ , compute genotype pair probabilities

Estimation: given observed genotype pair &  $p$ , estimate  $\Delta$

# Methods for estimating $r$ –Cont 7



- $r$  can also be estimated from genotype data
  - *Realized* values (for the particular markers)
  - Can be highly variable (due to Mendelian segregation) across loci ( $CV(r | PO) = 0$ ,  $CV(r | FS) = 0.71$ ), much higher with sampling variance
  - Estimation variance declines with an increasing #loci
  - Quality of  $r$  estimates determined by *the actual relationship, marker information, r estimators*
  - Many independent markers to produce better  $r$  than pedigree
  - Reference is the population in which allele frequencies are used in calculating  $r$
  - With reference = current population, mean  $\hat{r}$  tends to be 0, many  $\hat{r} < 0$
  - More appropriately,  $r$  should be defined as a correlation coefficient, legitimate range [-1,1]

# Methods for estimating $r$ –Cont 8

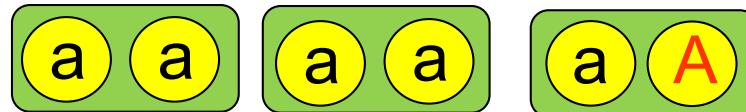


- Many marker-based  $r$  estimators developed
  - Ritland (1996, Genetical Research):  $\Delta_7, \Delta_8, \Delta_9, \theta, r$
  - Queller & Goodnight (1989, Evolution):  $\theta, r$
  - Lynch (1988, Mol Biol Evol) & Li et al. (1993, Human Heredity):  $\theta, r$
  - Wang (2002, Genetics; 2017, Heredity):  $\Delta_7, \Delta_8, \Delta_9, \theta, r$
  - Lynch & Ritland (1999, Genetics):  $\Delta_7, \Delta_8, \Delta_9, \theta, r$
  - Milligan (2003, Genetics):  $\Delta_7, \Delta_8, \Delta_9, \theta, r$
  - Wang (2007, Genetics Research):  $\Delta_1 \sim \Delta_9, F, \theta, r$  (**COANCESTRY**)
  - Wang (2022, MEE):  $\Delta_1 \sim \Delta_9, F, \theta, r$  (**EMIBD9**)
  - Manichaikul et al. (2010, Bioinformatics):  $\theta, r$  (**KING**)
  - Conomos et al. (2016, AJHG):  $\theta, r$  (**PC-Relate**)
  - .....

# Problems in estimating $r$



- Assume known allele frequencies (AF, reference)
- Estimate AF from the same genotype data
- Assume a large sample of  $N$  outbred unrelated individuals
- AF powers and products: biased estimation when  $N$  is small!



$$\hat{p}_A = \frac{1}{6} = 0.1667,$$

$$\hat{p}_A^2 = (\hat{p}_A)^2 = \frac{1}{36} = 0.0278, \text{ sampling with replacement}$$

$$\hat{p}_A^2 = \left(\frac{1}{6}\right) \left(\frac{1-1}{6-1}\right) = 0, \quad \text{sampling without replacement}$$

(Wang 2017, Heredity)

# Problems in estimating $r$ – Cont 1

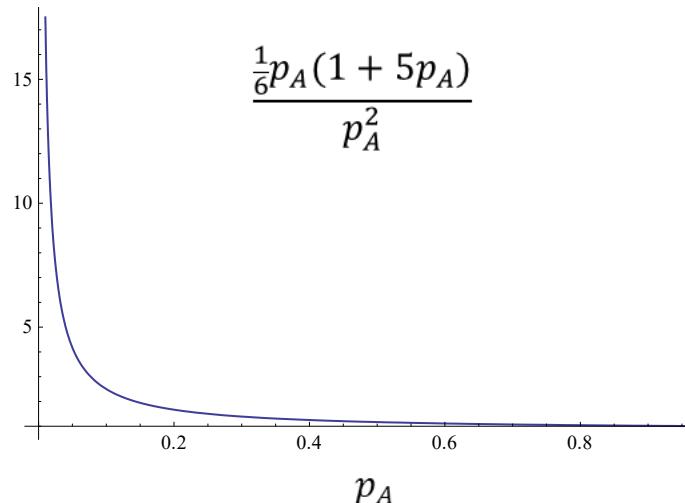


- Under binomial sampling with population allele frequency  $p_A$

$$E[\hat{p}_{A1}^2] = \sum_{n=0}^6 \frac{6!}{n!(6-n)!} p_A^n (1-p_A)^{6-n} \left(\frac{n}{6}\right)^2 = \frac{1}{6}p_A(1+5p_A) \geq p_A^2$$

$$E[\hat{p}_{A2}^2] = \sum_{n=0}^6 \frac{6!}{n!(6-n)!} p_A^n (1-p_A)^{6-n} \left(\frac{n}{6}\right) \left(\frac{n-1}{6-1}\right) = p_A^2$$

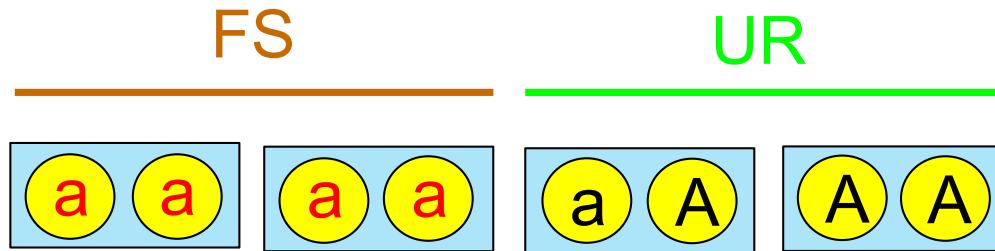
- $\hat{p}_{A1}^2$  (sampling with replacement) is overestimating!
- $\hat{p}_{A2}^2$  (sampling without replacement) is UNBIASED!



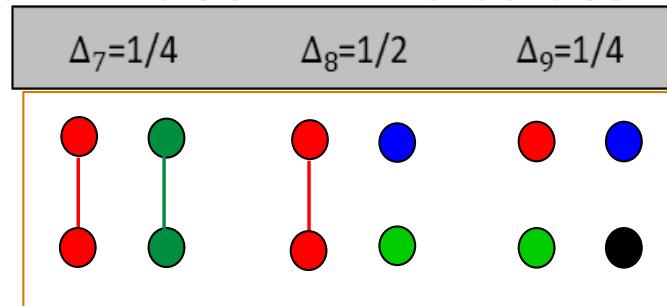
# Problems in estimating $r$ – Cont 2



- AF estimated with bias with inbred or/and related individuals!



- Assuming  $F = r = 0$ ,  $P_a = \frac{5}{8} = 0.625$
- AF estimated with bias with inbred or/and related individuals!



- Assuming  $F = 0$  but  $r > 0$  (FS),  $P_a = \frac{2\Delta_7+3\Delta_8+4\Delta_9+1}{2\Delta_7+3\Delta_8+4\Delta_9+4} = \frac{4}{7} = 0.571$

Wang 2022 (MEE)

# Problems in estimating $r$ – Cont 3



- Speed for large genomic data

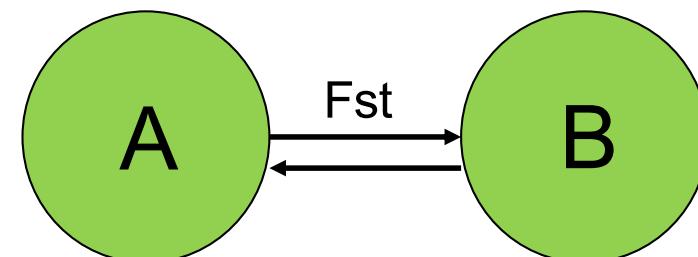
Computational time increases linearly with  $L$ , but quadratically with  $N$

Large genomic data poses a challenge even for a moment estimator. The UK biobank data: 0.5 million individuals, 59 million loci, 7375GB genotype data in .bed format.  $N(N - 1)/2 = 249,999,750,000$  pairs of individuals for  $r$  calculation, 145 days with 10k pairs per second

- Linkage and linkage disequilibrium in large genomic data
- Negative estimates

- Subdivided populations

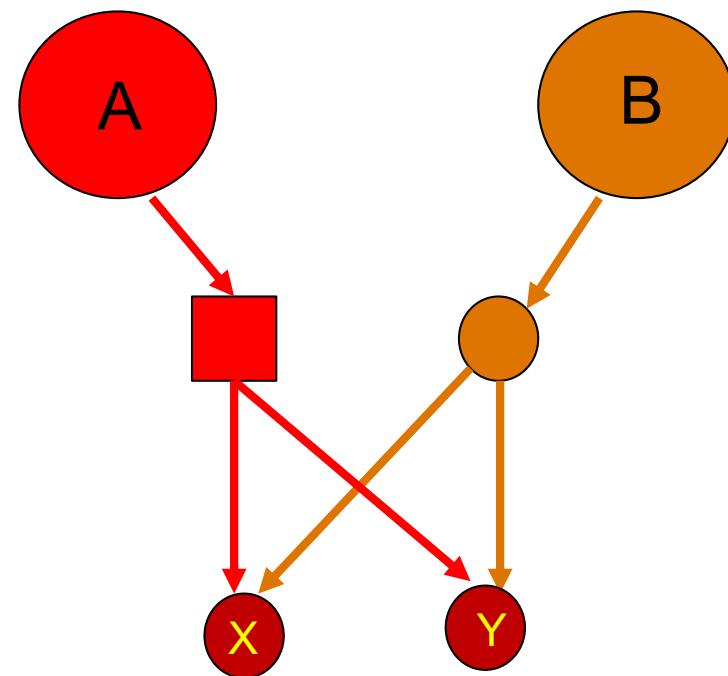
- Indirect method: use  $p$  of the entire population and  $Fst$  (Anderson & Weir, 2007, Genetics)
- Direct method: use  $p$  of the focal subpopulation (Wang 2011, Genetics)



- Admixed populations

## Individual specific allele frequencies

- ✓ Thornton et al. 2012, AJHG  
REAP
- ✓ Moltke & Albrechtsen 2014,  
Bioinformatics, RelateAdmix
- ✓ Conomos et al., 2016 AJHG,  
PC-Relate



# Conclusions (take home messages)



- Many marker-based estimators developed
- Precision increases with the use of genomic markers
- Marker-based  $r$  can be more accurate than pedigree-based  $r$
- More detailed IBD coefficients estimation possible
- $r$  is defined and measured relative to a reference population. Many issues are due to allele frequency estimation (small samples, related/inbred individuals, duplicated samples, population structure, ...)
- Missing data affect the precision of relatedness estimates
- Issues related to computational efficiency with large samples of individuals and loci

# The Bull Sharks of the Shark Reef Marine Reserve

## 'Kinship & Relatedness'

**Natasha Dominique Marosi**

Beqa Adventure Divers

University of Exeter

Fiji Shark Lab



# Beqa Adventure Divers

- Located in Viti Levu, Fiji
- Shark Diving specialists
- Beqa Lagoon – Soft Coral Capital
- Conservation Group running a Dive Shop



# Fiji



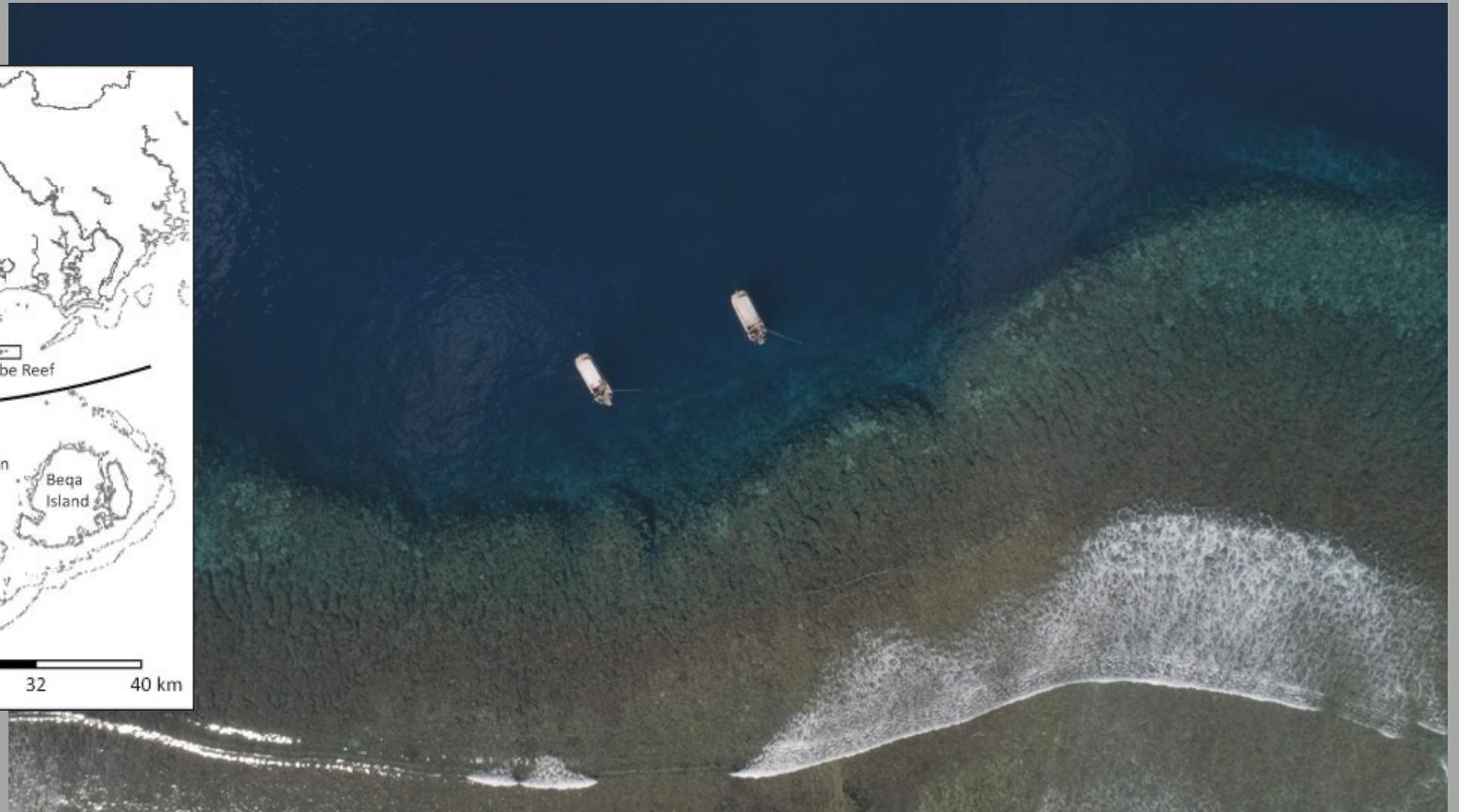
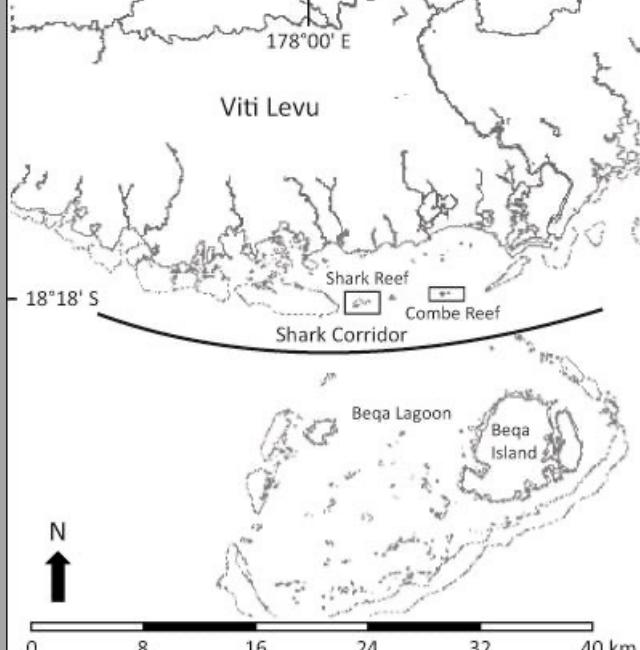
330 islands - Archipelago

Main Island Viti Levu

## Dive Sites Southern Coast Viti Levu



# The Shark Reef Marine Reserve, Viti Levu, Fiji



2004 - Marine Protected Area

2014 - Fiji's 1<sup>st</sup> National Marine Park

# Village of Galoa

Traditional owners of Shark Reef  
gave up fishing rights to SRMR



Village of Galoa receives in exchange  
Protected 'Fish Bank' yielding spillover  
In unprotected area

SRMR Marine Park levy  
\$25 per day per diver

Total Paid to date:  
\$375,000FJD





## Fisheries (Shark Reef Marine Reserve) (Serua) Regulations 2014

IN exercise of the powers conferred upon me by section 9 of the Fisheries Act (Cap. 158),  
I hereby make these Regulations—

### *Short title and commencement*

1. These Regulations may be cited as the Fisheries (Shark Reef Marine Reserve) (Serua) Regulations 2014 and shall come into force on the date of its publication in the *Gazette*.

### *Interpretation*

2. In these Regulations, unless the context otherwise requires—

“Act” means the Fisheries Act (Cap. 158);

“Buffer Zone” means the Buffer Zone declared under regulation 4;

“Coastal Zone” for the purposes of these Regulations means the area within 2 kilometres inland from the high water mark and includes areas from the high water mark up to the Marine Reserve;



# THE FIJI SHARK LAB



Charitable Trust Designation filed October 2023

[www.fijisharklab.com](http://www.fijisharklab.com)

# Shark Diving Ecotourism

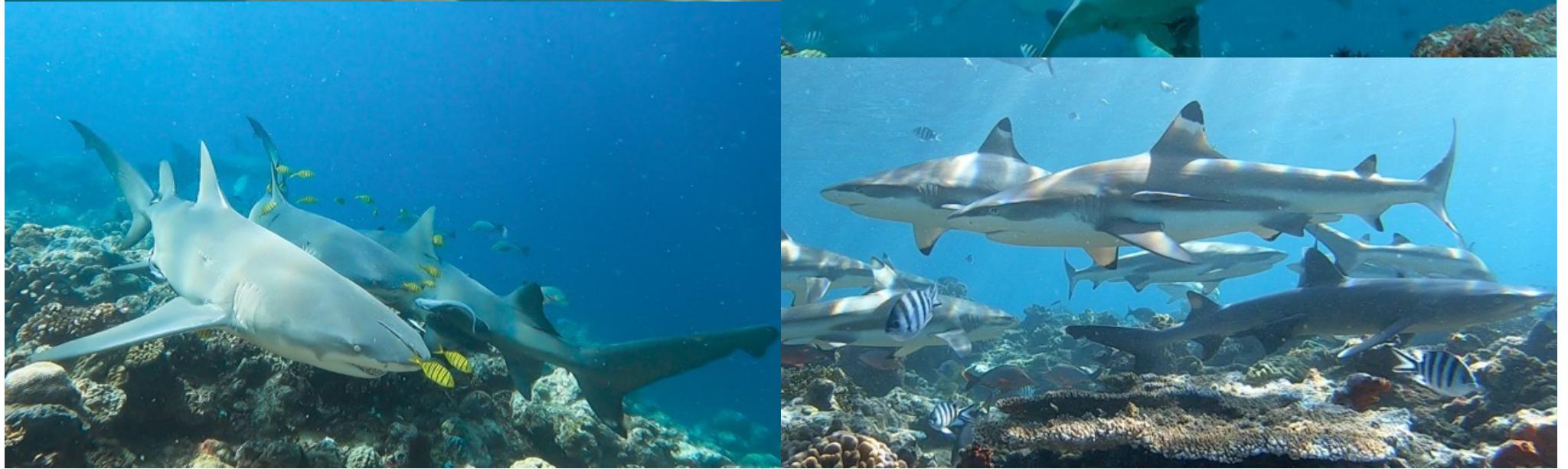


<https://www.elasmodiver.com>

Shark and Ray Dives around the World



- Shark Diving brings over \$42 million USD to Fiji every year (this figure is from a 2011 study *Vianna et. al* so the actual income has increased substantially \$\$\$ and is projected to be well over \$100 million)
- Not only dive shops profit, but also airlines, hotels, restaurants, activity centres, markets, shops and more from tourist dollars
- Sharks worth more alive than dead

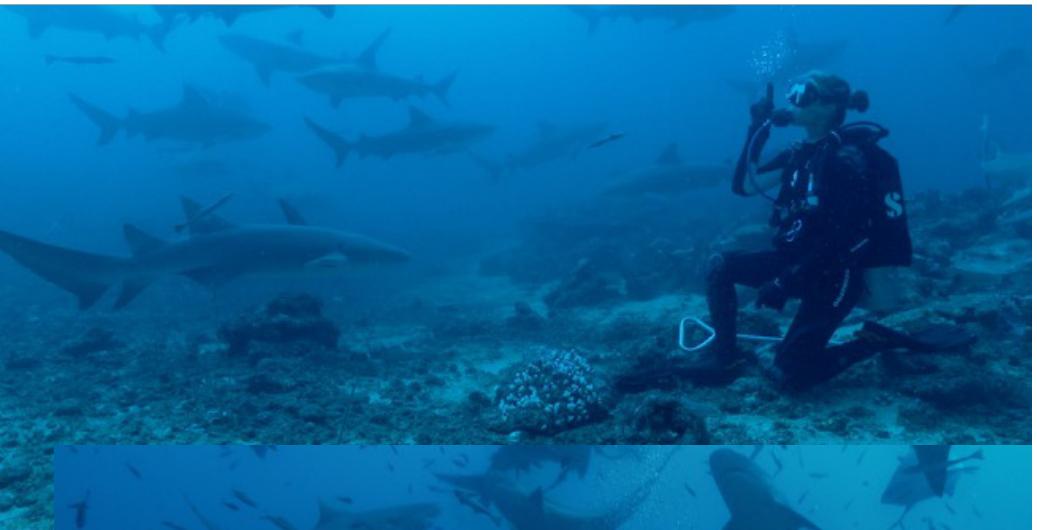












# Current Shark Research

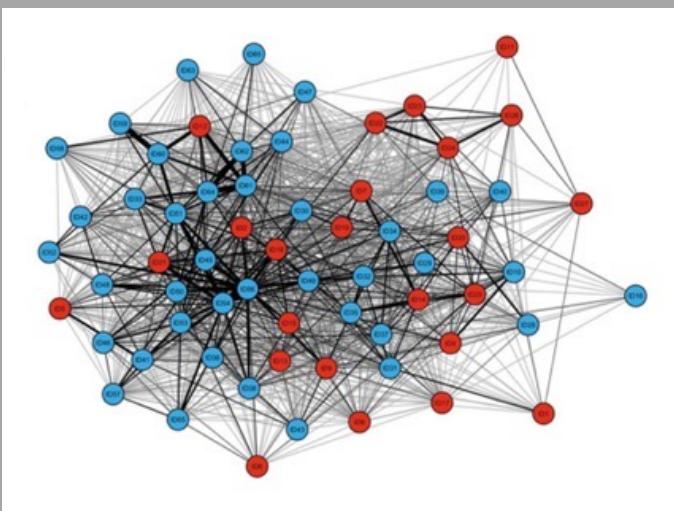
Sociality in the aggregation of bull sharks (*Carcharhinus leucas*) on the Shark Reef Marine Reserve

Associations | Personality  
Dominance-Hierarchy | Kinship



- Foundation laid from dive ectotourism and provisioning for over 20 years
- Unique opportunity to gain valuable information for use in management and conservation of the population

# Pilot Work: Bull Sharks May Have Preferred Associations



**Social Network Analysis** on presence/absence data spanning from 2003-2016

**Best fitting model** describing the temporal association pattern for these bull sharks was one of preferred companionships and casual acquaintances.

Bouveroux, T., Loiseau, N., Barnett, A., **Marosi, N.D.**, & Brunnenschweiler, J.M. Companions and Casual Acquaintances: The Nature of Associations Among Bull Sharks at a Shark Feeding Site in Fiji. *Front. Mar. Sci.* 8:678074 June 2021

## Social Interactions Are Complex

Need more than data on presence/ absence.



Observing directed interactions between individuals.



Lead follow behaviour



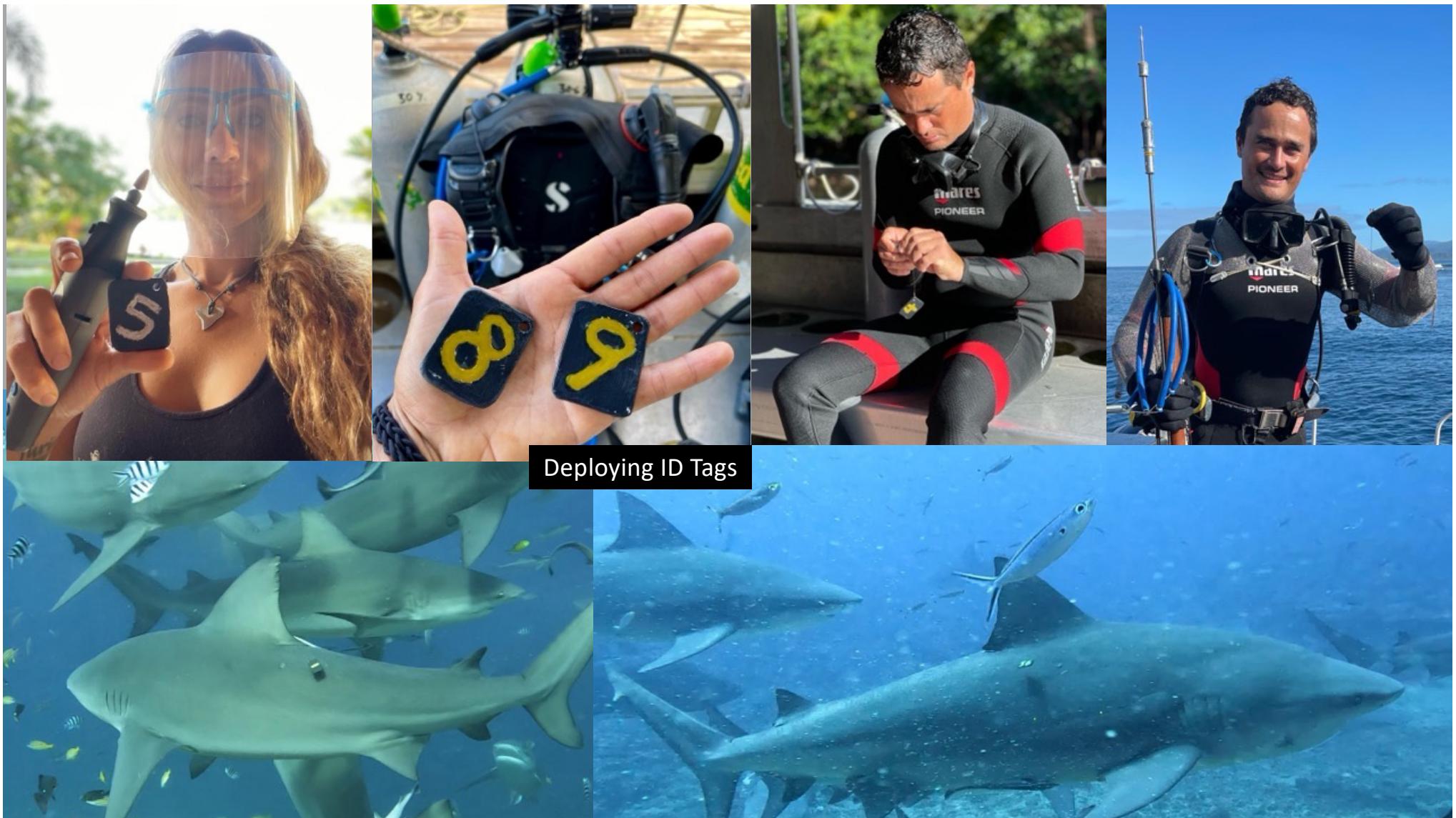
Parallel Swim

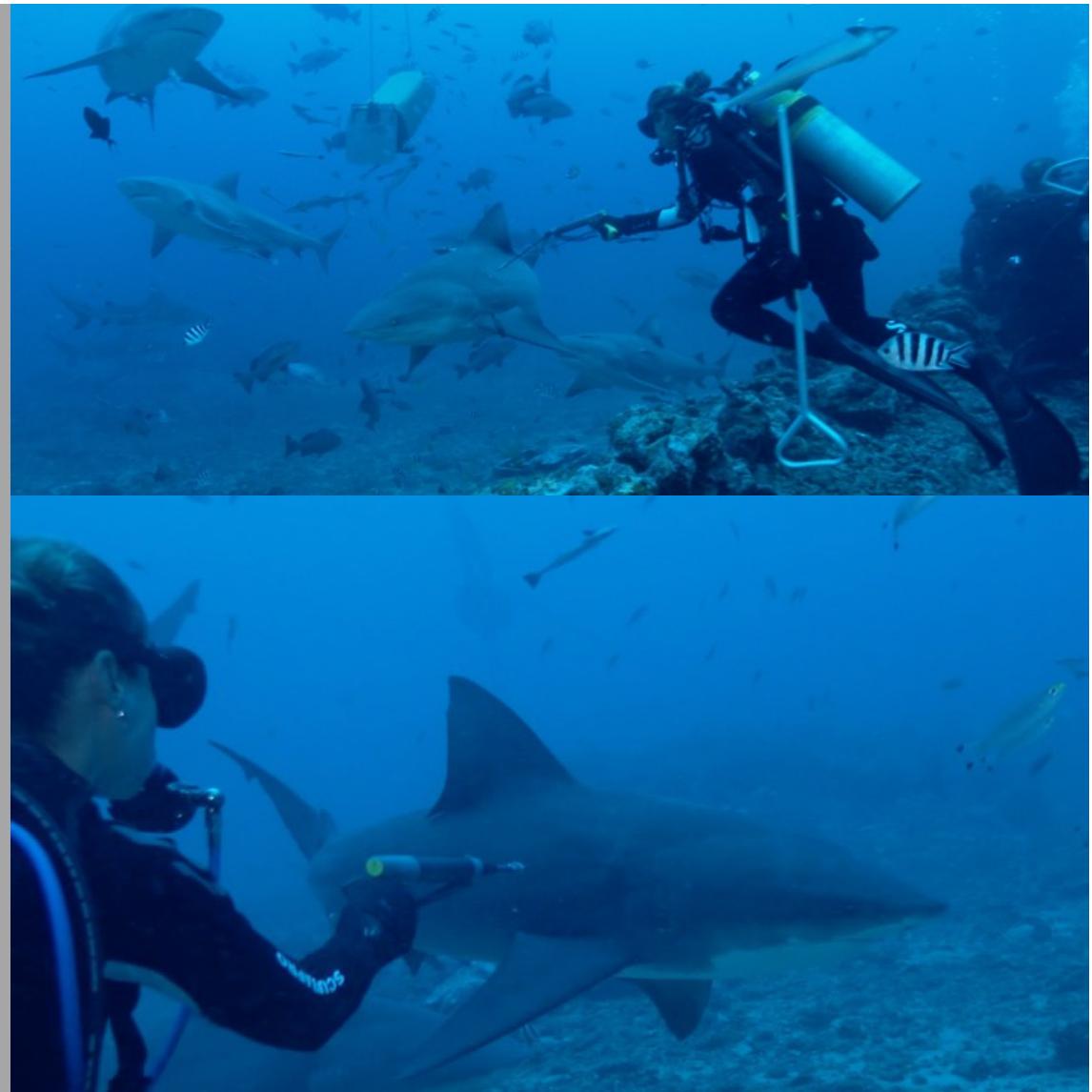
Lead follow behaviour

# Social Grouping

- Grouping and group living occurs all over the animal kingdom
- Well documented costs and benefits







Laser Photogrammetry  
Measuring Sharks





Deploying  
Camera Tags



# Research Questions:

1. What is the role of relatedness in driving association patterns?
2. Does relatedness predict the structure of the network?
3. Does kinship play a role in driving dominance interactions?
4. Is cooperation influenced by kinship?



## Kinship / Relatedness Analysis

*C. Leucas* samples n=188 individuals

Kinship and relatedness estimated using SNP

Sequencing provider DArT™ (Canberra) for genotyping

SNP filtering was performed using the R package *dartR* (Mijangos et al., 2022).

Software/Algorithm requested: Wangs CoAncestry, COLONY2, GCTA

Definitions simplified:

- Kinship - closer kin siblings/parents/close family
- Relatedness- levels of similarity across the whole population (2<sup>nd</sup> cousins, great grandparents)





# Significance

- Population genetically closed (Fiji) vulnerable to extirpation\*
- Yield valuable tools for use in future conservation work
- Insights to how kinship influences association patterns and rank
- Insights concerning threat of inbreeding

\*Refs: Glaus et al., 2020



**Operation Shark  
Pups**

## Gillnet Use in Rivers, Streams and Estuaries is Illegal

- No gillnets are to be used in rivers or streams or estuaries.
- Using gillnets in rivers is an offence under Fisheries Act CAP 158





- Shark Adoption Program
- Marine Park Scientific Database
- Change Perceptions about sharks
- Raise money for conservation

[www.myfijishark.com](http://www.myfijishark.com)

**Please adopt a shark!**



**[www.FijiSharkLab.com](http://www.FijiSharkLab.com)**

**Or come dive with us!**

**[www.fijisharkdive.com](http://www.fijisharkdive.com)**



A scuba diver in full gear, including a black wetsuit, a white tank with a blue logo, and a black buoyancy control device (BCD), is kneeling on a sandy ocean floor. The diver is holding a long-handled camera arm with a camera attached, pointing it towards a large shark swimming above them. The shark is a light-colored species, possibly a hammerhead or tiger shark. In the background, there are rocky outcrops and a school of small, silvery fish. The water is a deep blue.

**The End! Thank You!**