







How Many Are There? Using DNA & Statistics to Estimate Population Size

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Motivation 1: Ferret Abundance

- In most areas, possums are maintenance host of wildlife TB
- Can ferrets maintain TB?



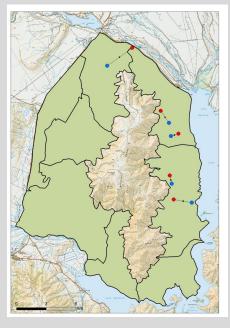






Motivation 1: Ferret Abundance

- Central Otago few possums but still TB in ferrets
- What is ferret density?





Motivation 2: Pig Abundance

- What happens if we detect TB in spill-over hosts?
- Even if possums are free of TB it may persist in other long-lived animals (pigs/deer)





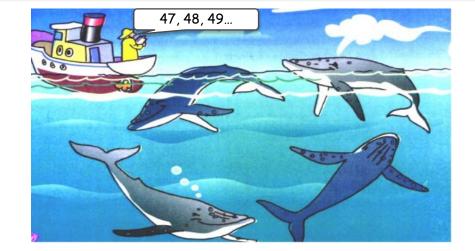
 Need to know population size to help determine scale of potential issue

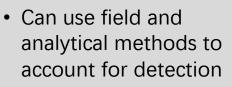




How many are there?

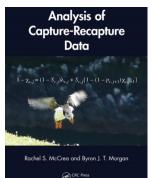
- Figuring out the size of a population is hard!
 - Counted all individuals?
 - Counted each individual only once?





– E.g. Mark-recapture



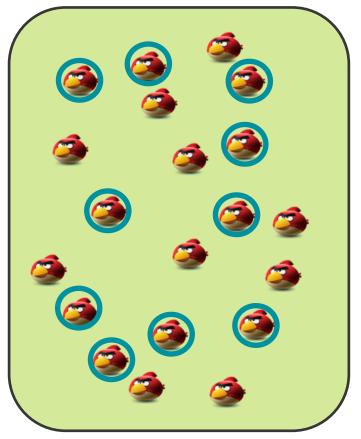




- Requires 2+ samples
- Sample 1: Catch *M* animals, mark them, then let them go.

Sample 1: *M* =10 marked animals





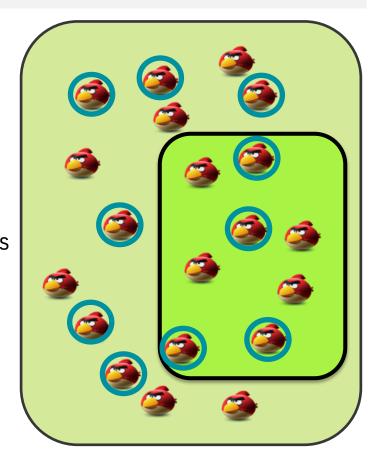
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- Requires 2+ samples
- Sample 1: Catch *M* animals, mark them, then let them go
- Sample 2: Size n; m will be marked previously



Sample 1: *M* =10 marked animals

Sample 2: n = 8 animals m = 4 have marks



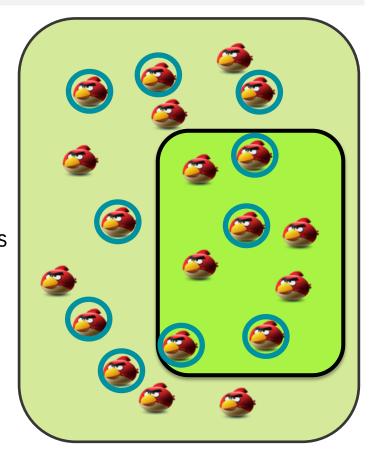
 Proportion of sample 2 with marks *should* equal proportion of population with marks

 $\frac{M}{N} = \frac{m}{n}$



Sample 1: *M* =10 marked animals

Sample 2: n = 8 animals m = 4 have marks



 Proportion of sample 2 with marks *should* equal proportion of population with marks

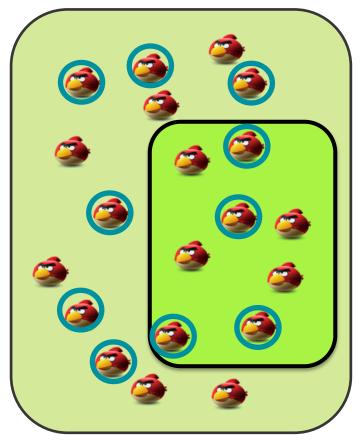
 $\widehat{N} = \frac{n}{m}M$



Sample 1: *M* =10 marked animals

Sample 2: n = 8 animals m = 4 have marks

$$\widehat{N} = \frac{8}{4}10 = 20$$



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Estimating Pest Mammal Abundance

Often we use relative abundance

- Wax tag/chew-card index
- Trap catch index
- Camera index
- A higher index = more animals... (hopefully)



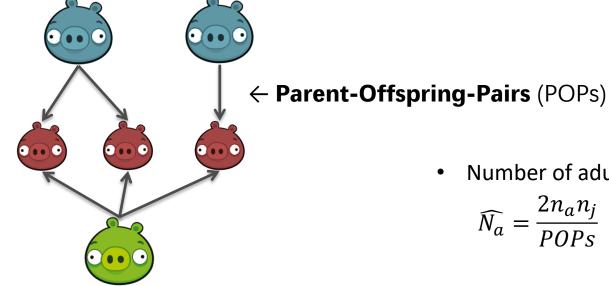
 Current methods are difficult for ferrets and pigs





• Offspring carry the 'marks' of each parent in their DNA





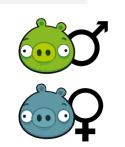
Number of adults in population

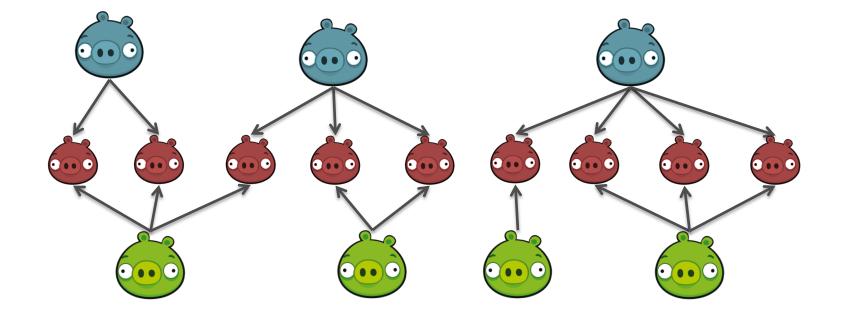
$$\widehat{N_a} = \frac{2n_a n_j}{POPs}$$

• Full sample...

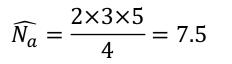
$$\widehat{N_a} = \frac{2n_a n_j}{POPs}$$

 $\widehat{N_a} = \frac{2 \times 7 \times 9}{18} = 7$

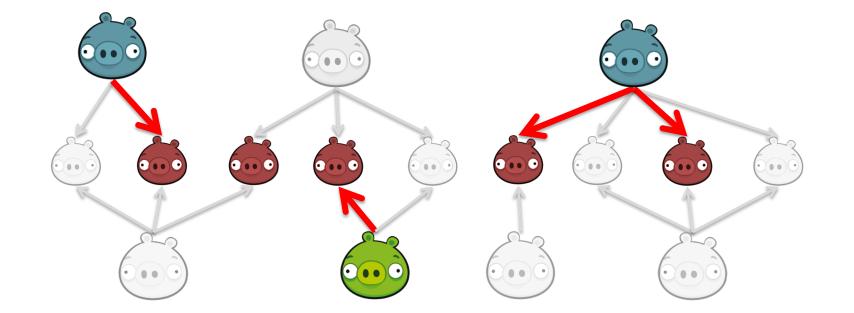




• Partial sample



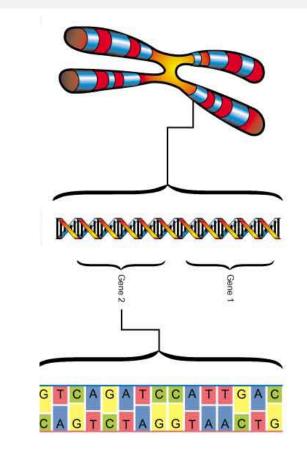




• Each cell nucleus contains **chromosomes**

 Each chromosome has 1000s of **genes**

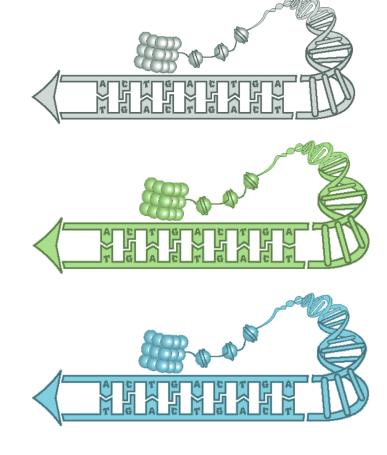
- Each gene is a chain of coded information made up of building blocks
 - A/G/T/C



 The different 'choices' at for a gene are called alleles

Eye-colour

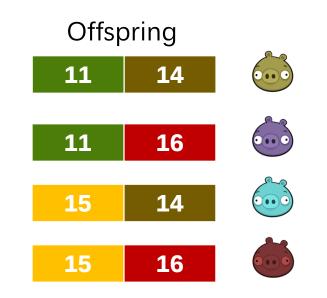
• Choices are grey, green, blue, brown, etc



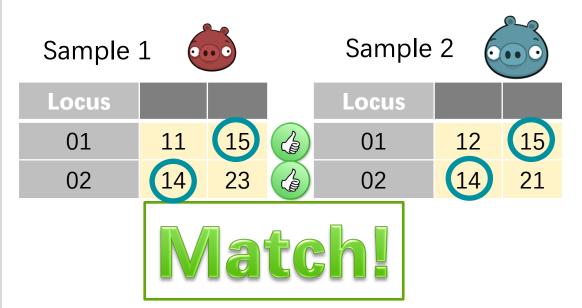
• Mammals have 'pairs' of chromosomes



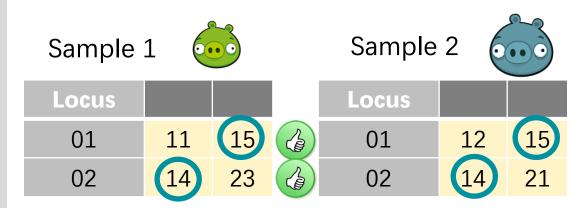
- Inherit one from mother, one from father
- Therefore offspring will have at least 1 match with each parent



• Parent-Offspring-Pairs have at least one allele in common at each locus



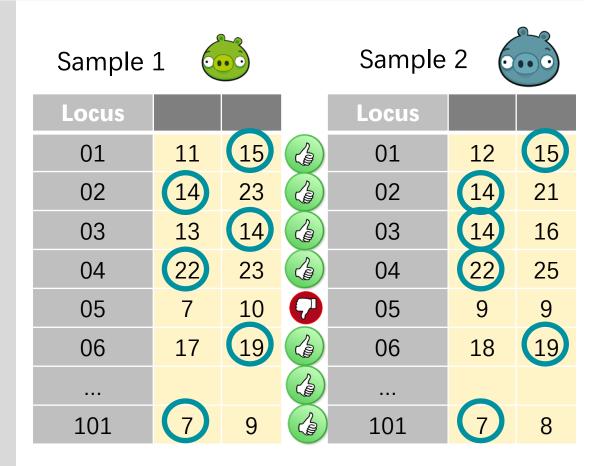
• But can have matching by chance



- But can have matching by chance
- So examine lots of loci to reduce chance of false positives.

Sample 1 💿			Sample 2			
Locus				Locus		
01	11	15	4	01	12	15
02	14	23	L	02	14	21
03	13	13	7	03	14	16
04	22	23	L	04	22	25
05	7	10	7	05	9	11
06	17	19	L	06	18	19
07	16	24	7	07	18	21
80	7	9	L	08	7	8

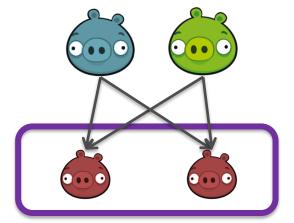
- Looking in lots of places can increase chance of false negatives
- Genotyping error
- Allelic dropout

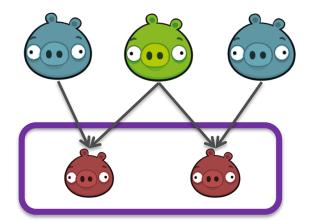


• Other relationships have different rates of matching

- Full-Siblings (two parents in common)
 - No matches on 25% of loci
 - One match on 50% of loci
 - Two matches on 25% of loci

- Half-Siblings (one parent in common)
 - No matches on 50% of loci
 - One match on 50% of loci





• Complicated if multiple generations in sample

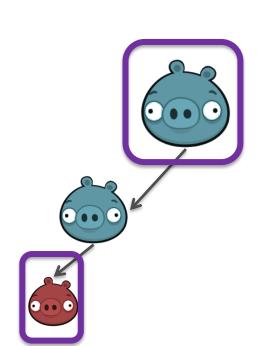
• Half-Siblings (one parent in common)

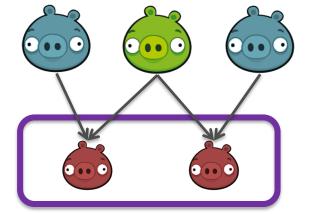
• Grandparents/grand-child

No matches on 50% of loci One match on 50% of loci

Need:

- Age data
- Population dynamics model







OSPRI Funded Project

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• Ferrets (Central Otago)



• Pigs (Hauhungaroa)





- Time sampling to have juvenile and adult cohort only
 - Lots of Parent-Offspring-Pairs
 - Age structure of adults known
- In-breeding means difficulty of genetic matching

- Under-sampling of juveniles
 - OSPRI want older animals during TB surveys
- Parent may be dead need to include population dynamics

Summary: Close-Kin Mark-Recapture

- It works!
 - Demonstrated on whitesharks & bluefin- tuna
- Well suited to pest species
 - Can collect data using dead animals
- Potentially cost effective
 - Only one sample
 - Cheaper DNA methods
 - Better matching
- Issues of in-breeding

