

# Maps



SHEEPCRC

# Genetic Maps

- Order and location of markers assigned to chromosome on the basis of linkage analysis
- Distance measured in Morgans (M)



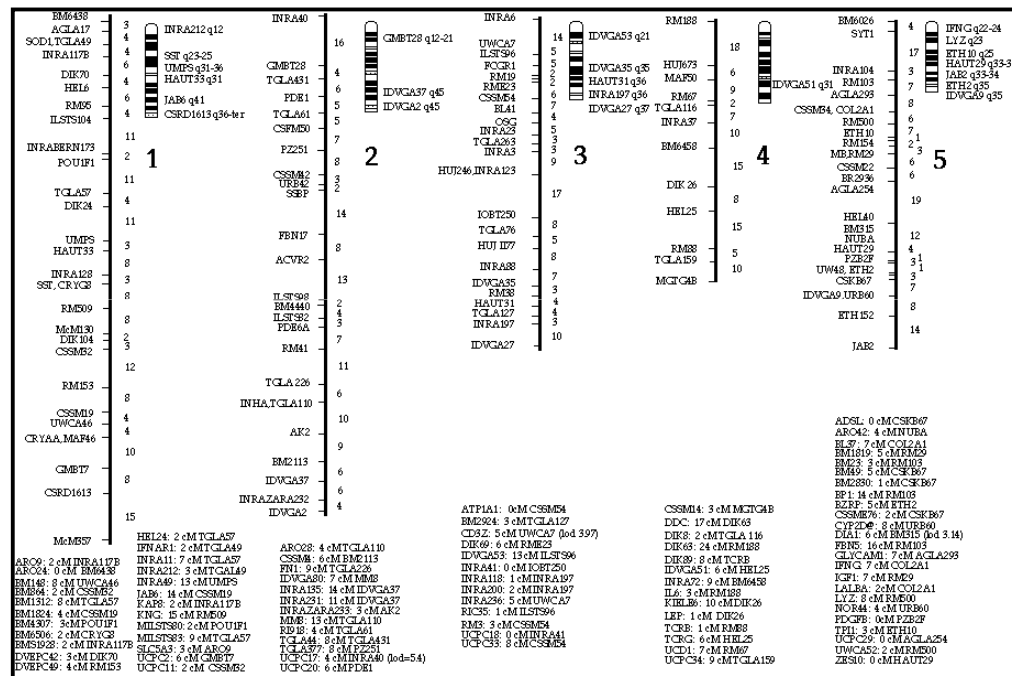
# Physical Maps

- Actual structure of genetic material
- At highest level DNA sequence
- Distance measured in  $10^6$ bp (Mbp)
- Genetic and physical maps are usually 'linked' together



# Example of a map

- Cattle chromosomes 1-5, from Cattle Genome Database hosted at the Queensland Biosciences Precinct: <http://www.cgd.csiro.au>



# Genetic maps

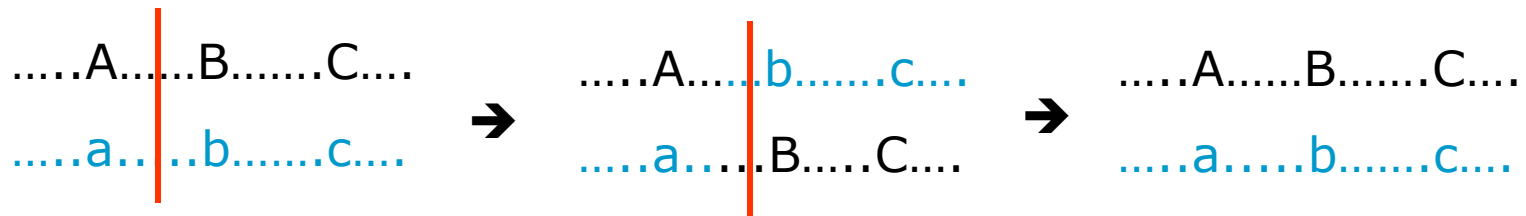
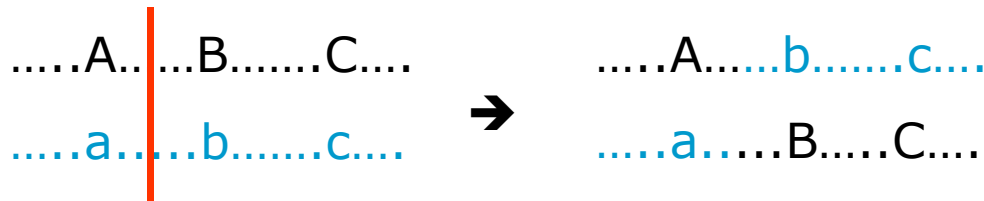
- Map distance is determined from the number of observed recombination events
- $1\text{cM} = 1$  recombination event per 100 meiosis (*simple mapping function*)



# Map distance versus r

## ■ Only odd number of crossover events are observed

- $r$  = probability of an odd-number of cross-over events
- $1-r$  = probability of an even number of cross-over events, including zero



# Mapping functions

- Mapping functions predict the number of crossover events from observed recombination events
- Also account for interference (where a recombination event in one region affects the likelihood of a recombination event in a closely aligned region)



# Different Mapping functions

## ■ Haldane

- assumes no interference (crossovers occur randomly and independently over the entire chromosome )
- $M = -(\ln(1-2r))/2$

## ■ Kosambi

- assumes moderate interference (i.e. some crossover interference at adjacent sites)
- $M = \frac{1}{4} \ln (1+2r/1-2r)$

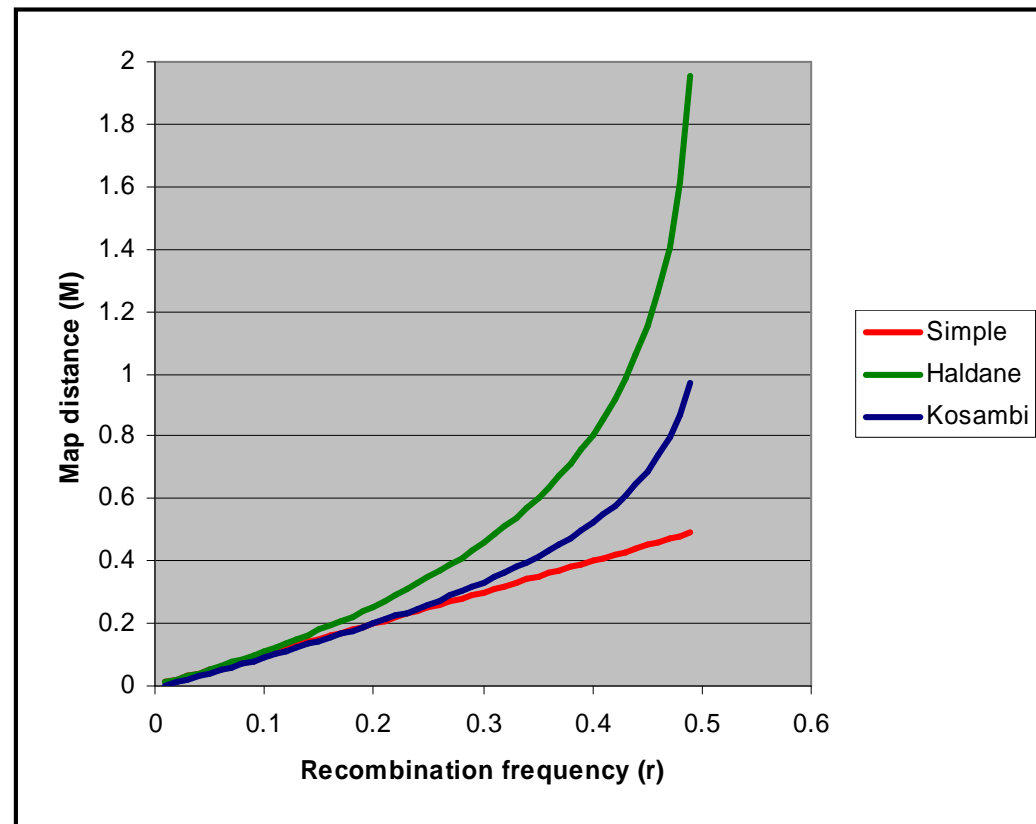
## ■ Simple

- assumes complete interference
- $r = M$





# Comparison of mapping functions



# Construction of linkage maps

- Simple example is 3 point testcross
- (see lecture notes)



# Construction of linkage maps

- In practice genetic maps are often constructed from complex pedigrees
  - First need to determine parental phase, such that gametes can be classed as recombinant or non-recombinant
  - Typically use a maximum likelihood approach



# Construction of linkage maps

- Identification of recombinant gametes is easier if
  - linkage phase of parents is known
    - Sire AaBb x Dam AABB → 9 AABB, 1 AaBB, 1 AABb, 9 AaBb
    - Sire thus gave gametes in frequency 0.45 AB, 0.05 aB, 0.05 Ab, 0.45ab
    - Most likely phase is AB ab
  - haplotype of gametes transmitted from parents to offspring is known
    - AaBb x AABB → AaBb, sire gave ab dam gave AB
    - AaBb x AaBb → AaBb, cannot determine transmitted haplotypes



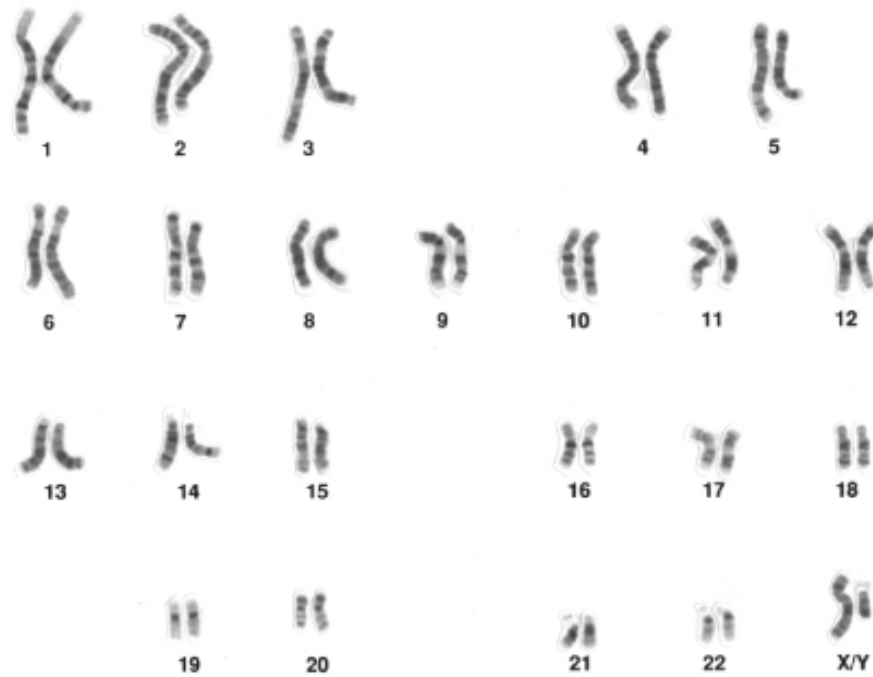
# Physical maps

## – Cytogenetic maps

- banding pattern observed under light microscopy of stained chromosomes
- low resolution (only estimates of the number of bp)



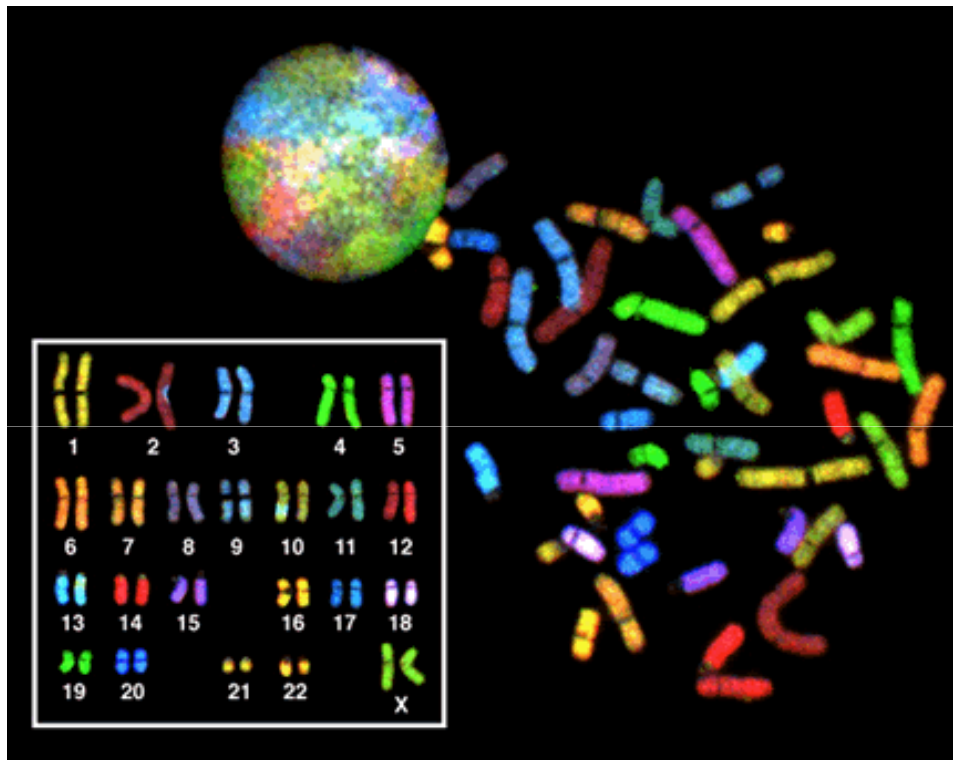
# Human Karyotype



Talking glossary of genetics, 2008



# Human Karyotype



Talking glossary of genetics, 2008



# Physical maps

- Radiation hybrid
  - Use breaks induced by radiation to determine the distance between two markers





# Physical maps continued

- Sequence tag sites (STS)
  - STS are short, unique DNA sequences with known location
- Sequence maps
  - ‘the ultimate’
  - now available for a number of livestock species



NC\_000001.9 - Homo sapiens chromosome 1, reference assembly, complete sequence :: NCBI Sequence - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/projects/sviewer/Tid=NC\_000001.9&v=11961297..11997811

Links: Google Nature VEJA Yahoo

NC\_000001.9 - Homo sapiens chromosome 1, ref...

NCBI Home PubMed GenBank BLAST Sequence Viewer 2.0.β

Homo sapiens chromosome 1, reference assembly, complete sequence gi|89161185|ref|NC\_000001.9|NC\_000001.9  
Accession NC\_000001.9

Shift Origin 0 Search for Theme NCBI Overview

Position 11,96M..12,00M Theme NCBI Details

11,965 K 11,970 K 11,975 K 11,980 K 11,985 K 11,990 K 11,995 K

Main Features:

Alignments:  
- mRNA product mapping alignment

Contact | Copyright | Disclaimer | Privacy | Accessibility  
National Center for Biotechnology Information, US National Library of Medicine  
8600 Rockville Pike, Rockville, MD USA 20894

Logos: National Center for Human Genome Research, NLM, USA.gov

Last update: Thu, 17 Jul 2008 Rev. 17374

Internet | Protected Mode: Off 100%



# Relationship between genetic and physical distance

- No universal relationship
  - Comparison of human genetic and sequence based physical maps, Yu et al. “Recombination rates varied greatly along each chromosome, from 0 to at least 9 centiMorgans per megabase”
- Various depending on
  - species
  - chromosomal region: crossovers often suppressed at centromeres, telomeres
  - Sex: female mammals usually have greater map distances than males, no crossover in male *Drosophila*



# Australian Sheep Gene Mapping Website

The screenshot shows a web browser window titled "Australian Sheep Gene Mapping Web Site - Windows Internet Explorer". The address bar contains the URL <http://rubens.its.unimelb.edu.au/~jillm/jill.htm>. The browser's search bar contains the word "Google". The page content is as follows:

**Australian Sheep Gene Mapping Web Site**

Welcome to the Australian Gene Mapping Web Site. Please follow the links, to the left or below, to the page that interests you. Some recent pages that have been added to the site or elsewhere are shown below.

**Discrepancies between Virtual Sheep Genome and linkage map** 27<sup>th</sup> June 2007

**Sheep QTL database** 9<sup>th</sup> May 2007

**Sheep, cattle and human comparisons using CMap v0.14** 22<sup>nd</sup> April 2007  
*Note: CMap now contains VSG maps*

**Sheep, cattle and human comparisons using CMap v0.16** 22<sup>nd</sup> April 2007  
*Note: CMap now contains VSG maps*

**Current sex averaged, female, male distances for framework maps (v4.7)** 22<sup>nd</sup> March 2007  
*ascii tab delimited file*

**Search tool for sheep BES microsatellites in Virtual Sheep Genome map** 5<sup>th</sup> January 2007

**Current sex averaged, female, male distances for best position maps (v4.7)** 3<sup>rd</sup> December 2006  
*ascii tab delimited file*

**sheepGENOMICS - sheep BES aligned to cattle (v2) sequence map** 12<sup>th</sup> January 2006  
*New loci mapped to sheep chromosomes*

**Sheep BES microsatellites aligned to cattle sequence map - search by cattle Mb position** 2<sup>nd</sup> December 2005

**Sheep BAC end sequences from 12x BAC library deposited in NCBI Trace Archive, trimmed sequences in GenBank** 10<sup>th</sup> October 2005

*Bos taurus* version 2 assembly Ensembl, NCBI MapView 5<sup>th</sup> October 2005

**Diagram showing distribution and informativeness of markers on sheep map (v4.4)** 14<sup>th</sup> July 2005

**Predicted Sheep Map v 1.4 - Gene positions inferred from sheep-human comparisons** 5<sup>th</sup> July 2005

**Predicted Human Positions for Sheep GenBank Genomic Sequences** 1<sup>st</sup> February 2005

**Predicted Human Positions and Microsatellites for Sheep BAC Ends** 28<sup>th</sup> January 2005

**Locus Assignments for GenBank Sheep EST and RNA sequences** 22<sup>nd</sup> April 2004

**Latest Sheep versus Human Comparisons** 17<sup>th</sup> December 2003

**Sheep vs Cattle (MARC 2003) Comparisons** 16<sup>th</sup> October 2003

**Sheep vs Human comparisons (XIX International Congress of Genetics poster)** 5<sup>th</sup> July 2003



<http://rubens.its.unimelb.edu.au/~jillm/jill.htm>

**SHEEPCRC**

# Extract from Australian Sheep Map

## Sheep Best Positions Linkage Map Version 4.4

Chromosome	Sex Av cM	Female cM	Male cM	Locus Code	Marker
1	0.0	0.0	0.0	\RM309	<a href="#">RM309A</a>
1	14.2	6.6	22.5	\BMS2833	<a href="#">BMS2833</a>
1	16.7	10.1	24.4	\TGLA127	<a href="#">TGLA127</a>
1	16.7	10.1	24.4	\INRA197	<a href="#">INRA197</a>
1	16.7	10.1	24.4	\MCM46	<a href="#">MCM46</a>
1	19.0	12.5	26.6	<a href="#">PPT1</a>	<a href="#">PPT</a>
1	24.3	19.6	30.9	\EPCDV022	<a href="#">EPCDV22</a>



<http://rubens.its.unimelb.edu.au/~jillm/jill.htm>



**SHEEPCRC**

