# Ancestry Informative Markers in the Skin Microbiome for Human Identification

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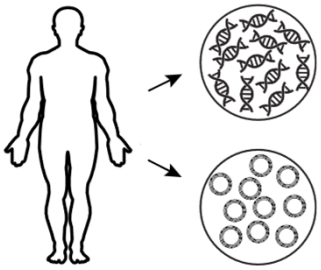
## Current methods in human identification

hsc



Nuclear DNA
- High discriminatory power
- Touch samples – low quantity
- Degradation – low quality

Mitochondrial DNA
- High quantity
- Low discriminatory power
- Maternally inherited

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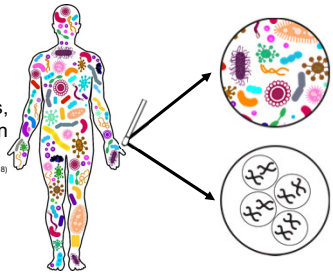
## Skin microbiome is another source of DNA

hsc

Skin swabbing only contained DNA equivalent to 4 diploid cells, but enough microbial information for accurate attribution
(Schmedes et al. 2018)



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## Skin microbiome stable up to 3 years

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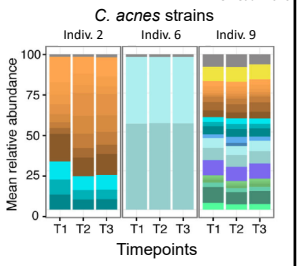
Oh et al. 2016

- Shotgun sequence data
- Short time intervals (1-2 months)
  and long-time intervals (1-2 years)
- No substantial change
  in community composition

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## Targeted genome sequencing panel

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- Using Oh et al. 2016 data, Schmedes et al. 2018 identified stable microorganisms
  - *Cutibacterium acnes* was highly abundant
- 286 markers (ranging from family, genus, and species level resolution)

hidSkinplex

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## Ancestry informative markers (AIMs)

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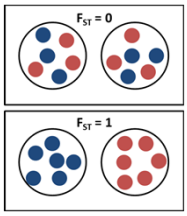
## Wright's index of fixation ($F_{ST}$)

- A measure of the difference in genetic structure between two populations

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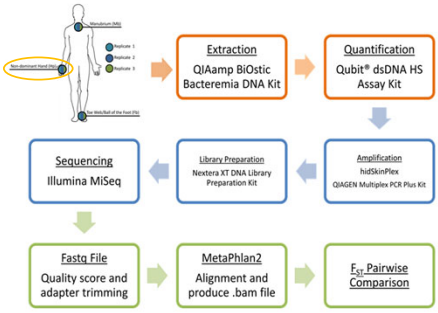
## Analysis workflow

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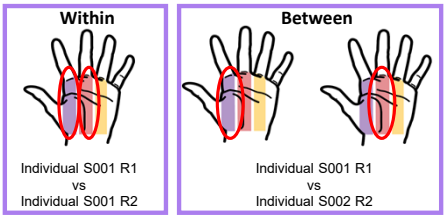
$F_{ST}$ Comparisons between all sample pairs

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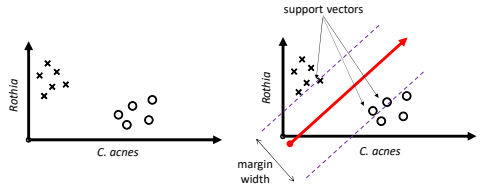
## What is support vector machine?

hsc

Classification method that finds a boundary to distinctly classify data points

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## SNPs for classification

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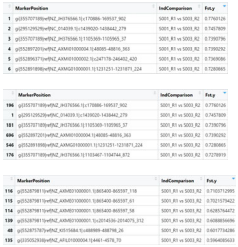
- **Highest-ranking $F_{ST}$**
  Overall
  500, 1,000, or 2,000
- **Diversity**
  Per Marker
  5, 10, or 25
- **Common highest-ranking SNPs**
  Selected
  50 to 2,000



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## Parameters

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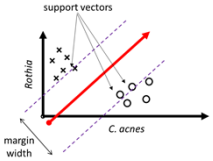
- Number of SNPs
- Minimum reads at each SNP
- Cost of SVM (helps determine optimal boundary)

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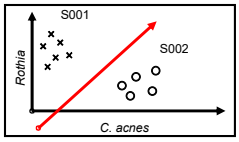
## SVM for hidSkinPlex




| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.82 | 1 |
| S002 | 0.18 | 0 |

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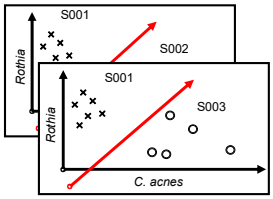
## SVM for hidSkinPlex




| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.82 | 1 |
| S002 | 0.18 | 0 |
| S001 | 0.75 | 1 |
| S003 | 0.25 | 0 |

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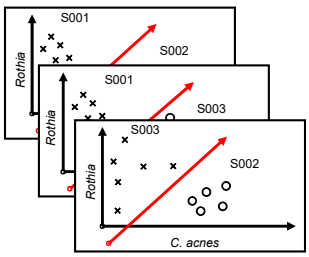
## SVM for hidSkinPlex




| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.82 | 1 |
| S002 | 0.18 | 0 |
| S001 | 0.75 | 1 |
| S003 | 0.25 | 0 |
| S002 | 0.37 | 0 |
| S003 | 0.63 | 1 |

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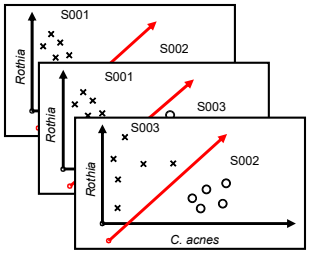
## SVM for hidSkinPlex




| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.82 | 1 |
| S002 | 0.18 | 0 |
| S001 | 0.75 | 1 |
| S003 | 0.25 | 0 |
| S002 | 0.37 | 0 |
| S003 | 0.63 | 1 |

| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.78 | 2 |
| S003 | 0.63 | 1 |
| S002 | 0.00 | 0 |

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## Accuracy of true positive

| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.79 | 25 |
| S002 | 0.67 | 21 |
| S003 | 0.00 | 0 |
| S004 | 0.67 | 20 |
| S005 | 0.69 | 15 |
| S006 | 0.69 | 12 |
| S007 | 0.73 | 24 |
| S008 | 0.65 | 16 |
| S009 | 0.71 | 3 |
| S010 | 0.61 | 4 |
| … | … | .. |

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## Accuracy of true positive

| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.79 | 25 |
| S002 | 0.67 | 21 |
| S003 | 0.00 | 0 |
| S004 | 0.67 | 20 |
| S005 | 0.69 | 15 |
| S006 | 0.69 | 12 |
| S007 | 0.73 | 24 |
| S008 | 0.65 | 16 |
| S009 | 0.71 | 3 |
| S010 | 0.61 | 4 |
| … | … | .. |

Descending order by votes

| Class | Confidence of Prediction | Vote |
|---|---|---|
| S001 | 0.79 | 25 |
| S007 | 0.73 | 24 |
| S028 | 0.76 | 23 |
| S038 | 0.70 | 22 |
| S002 | 0.67 | 21 |
| S004 | 0.67 | 20 |
| S029 | 0.65 | 19 |
| S033 | 0.69 | 18 |
| S035 | 0.69 | 17 |
| S008 | 0.65 | 16 |
| … | … | … |

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## Accuracy of true positive

| Class | Classification | Result |
|---|---|---|
| … | … | … |
| S027 R2 | S027 | True |
| S027 R3 | S027 | True |
| S028 R1 | S028 | True |
| S028 R2 | S028 | True |
| S028 R3 | S036 | False |
| S029 R1 | S029 | True |
| S029 R2 | S028 | False |
| S029 R3 | S029 | True |
| S030 R1 | S030 | True |
| … | … | .. |

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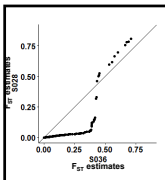


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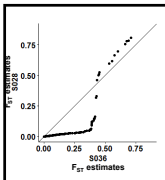


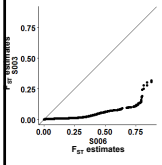


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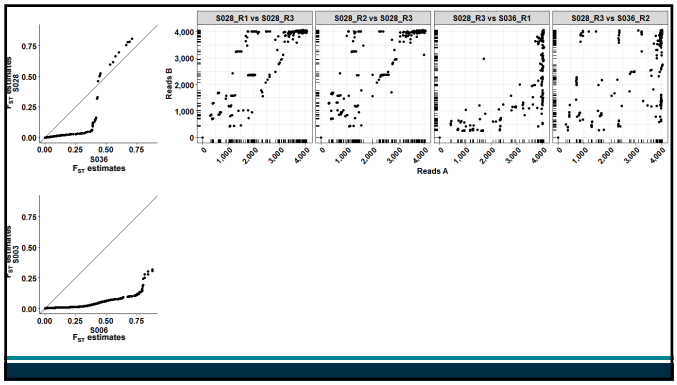


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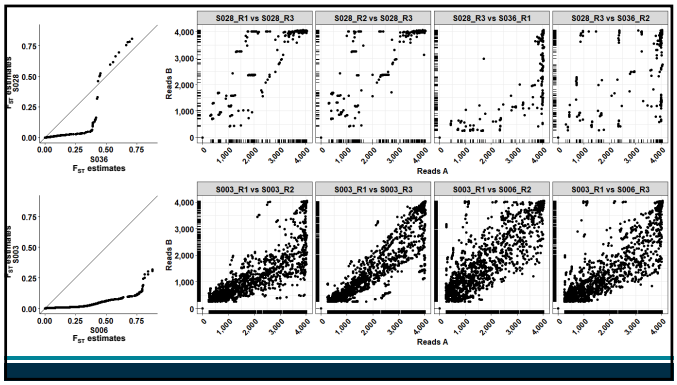


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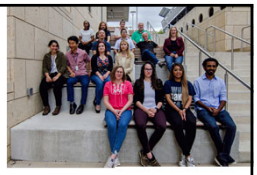

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