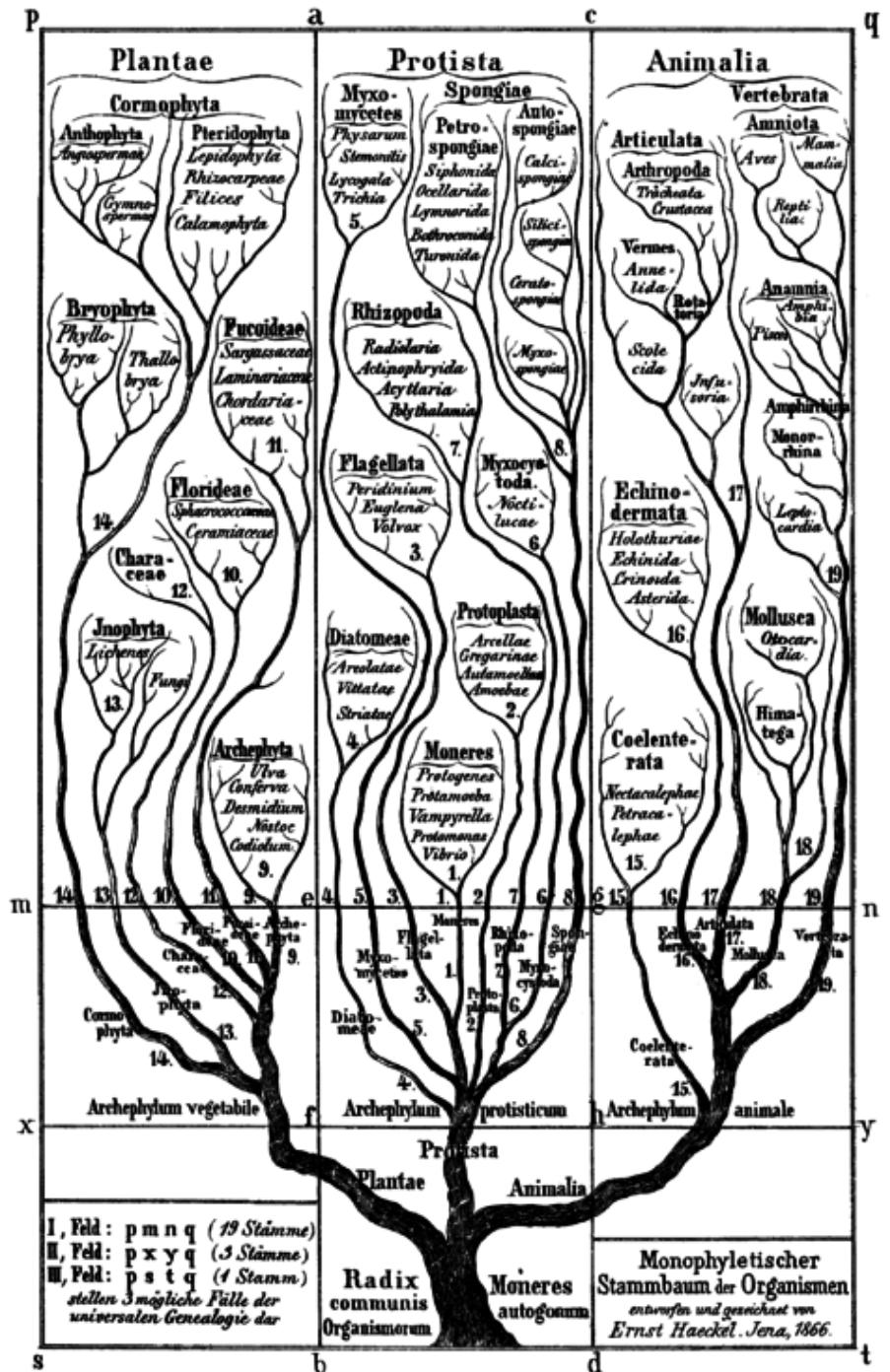


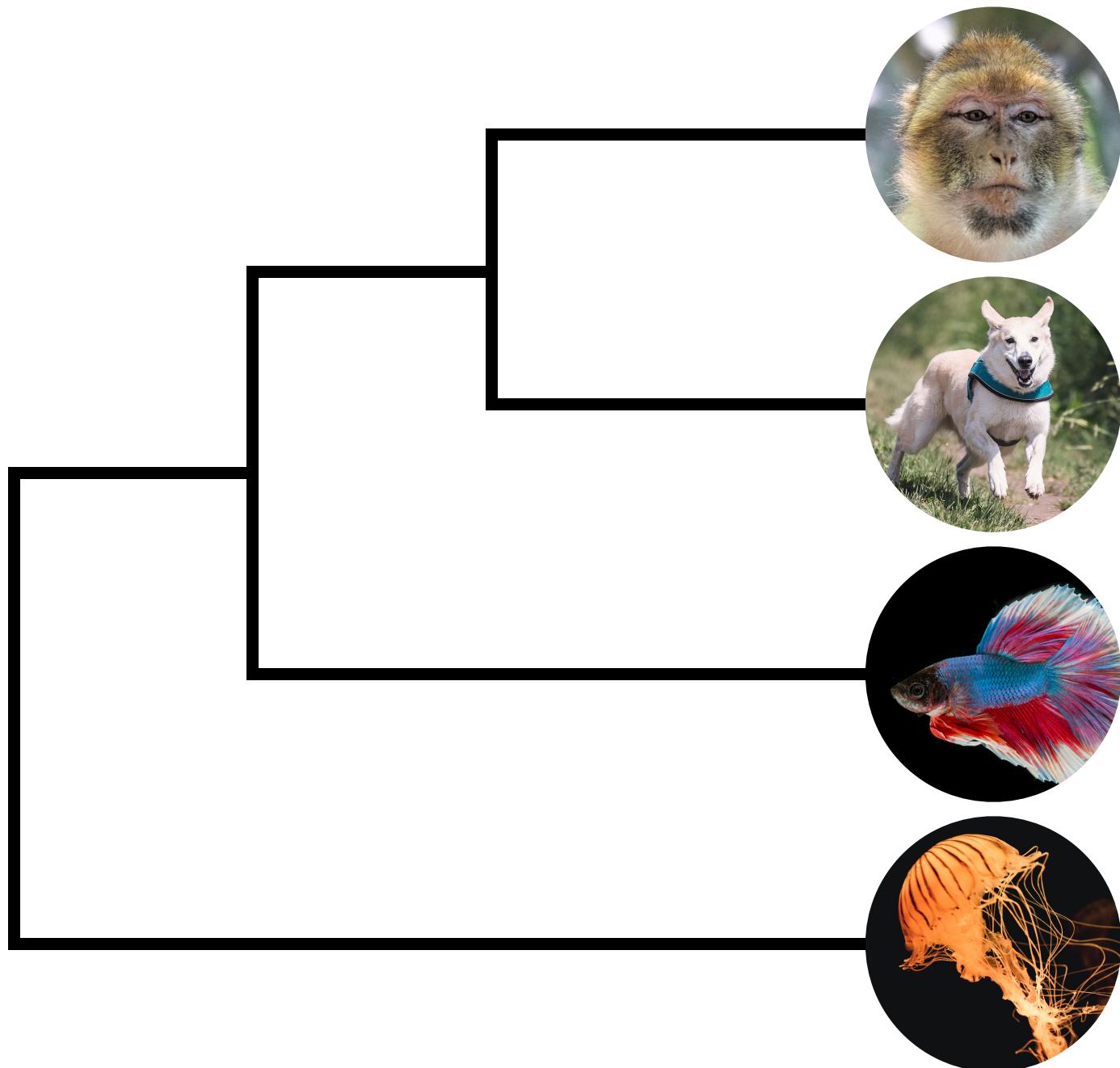
# 集团遺伝学実習



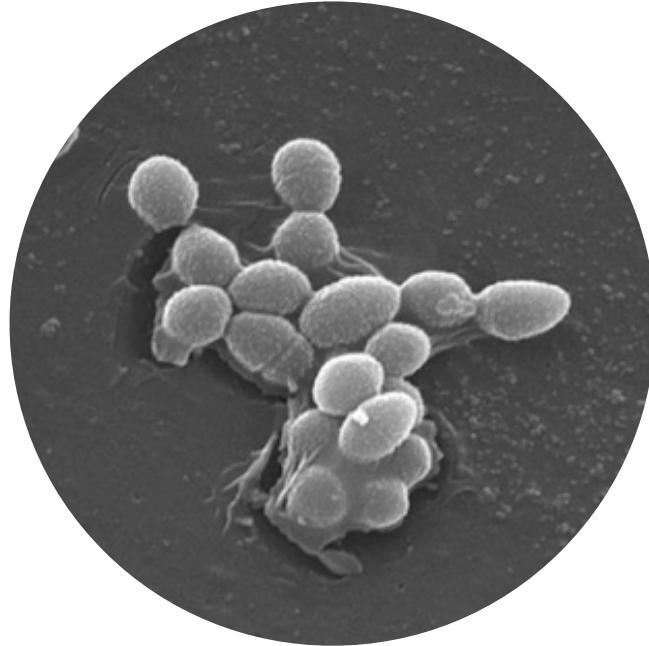


系統関係は？

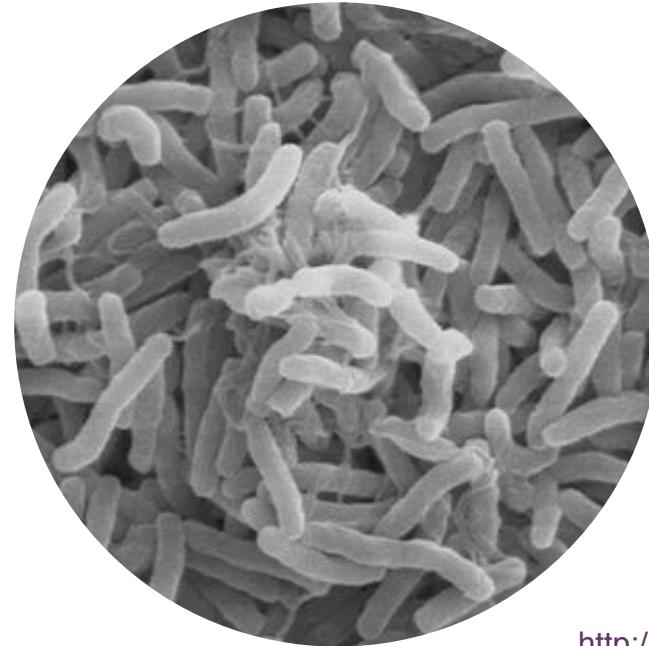
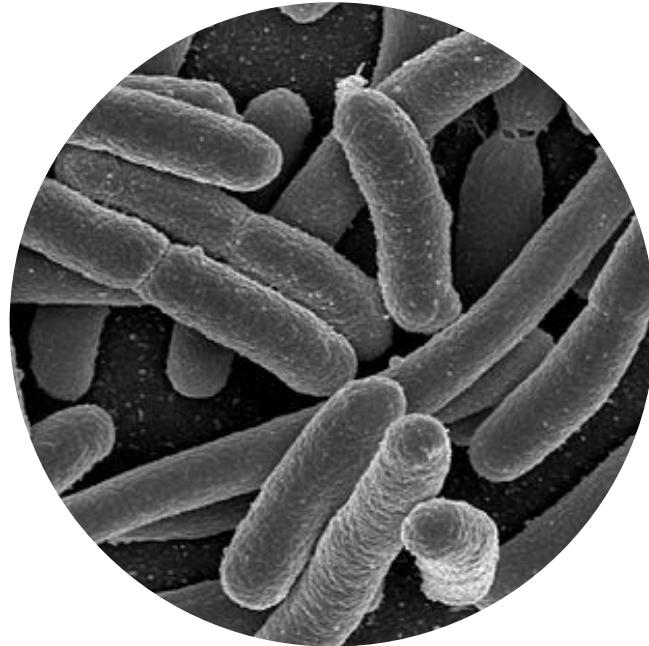




見た目で分かる



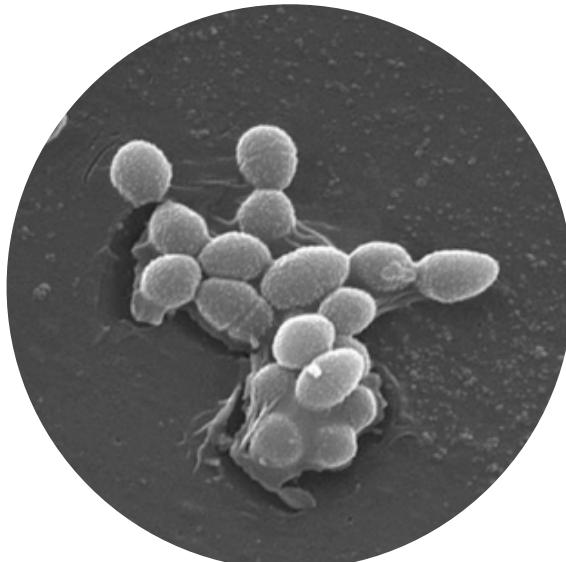
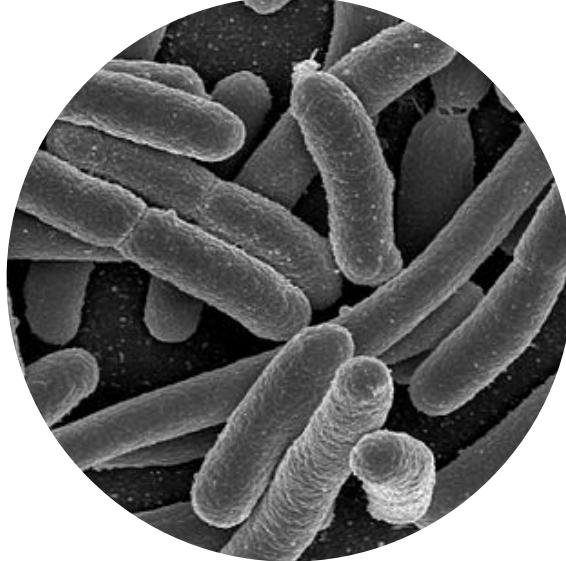
系統関係は？

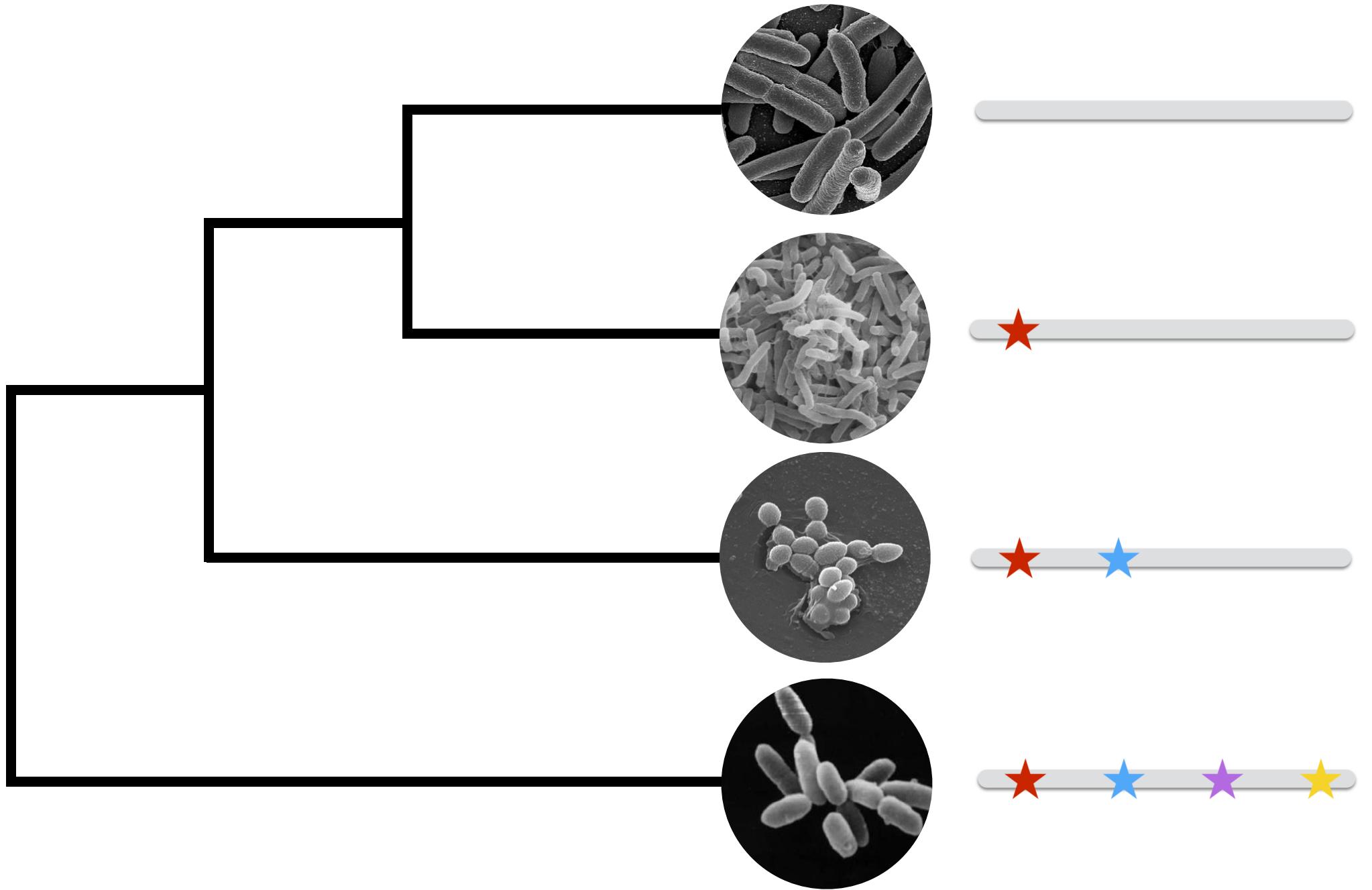




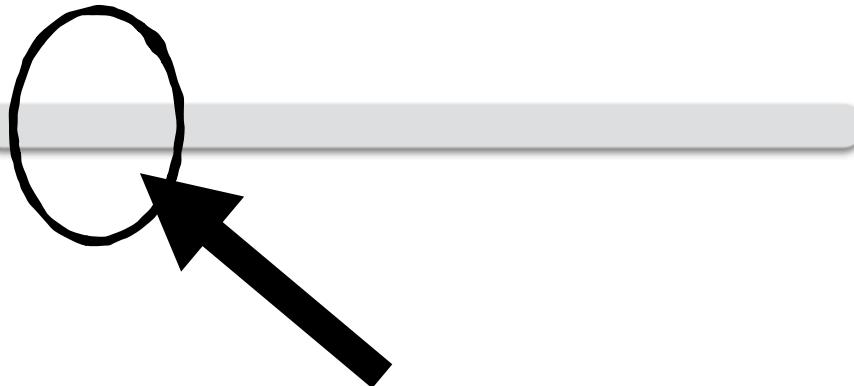
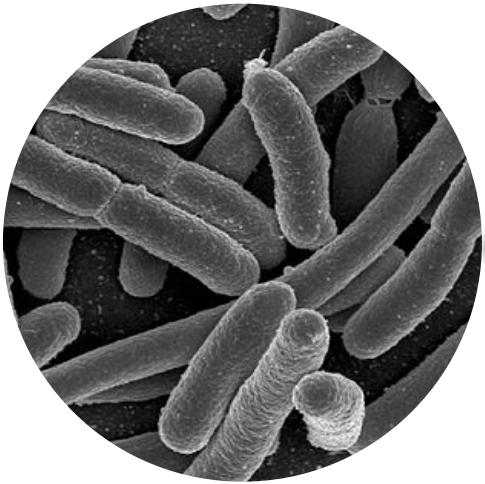
DNA配列

基  
準

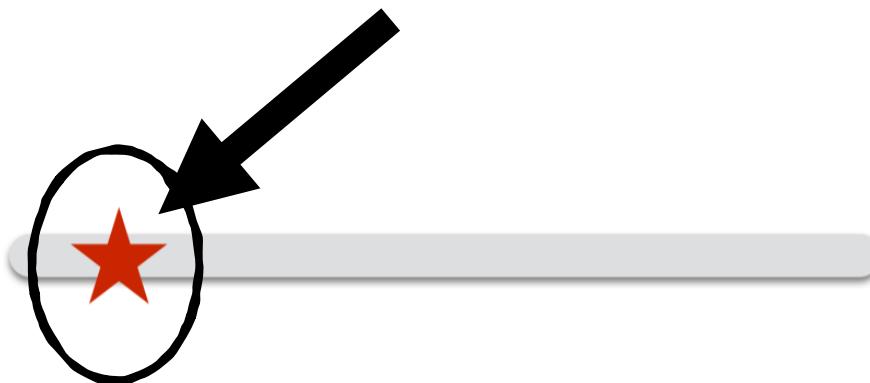




DNA配列で系統関係が分かる

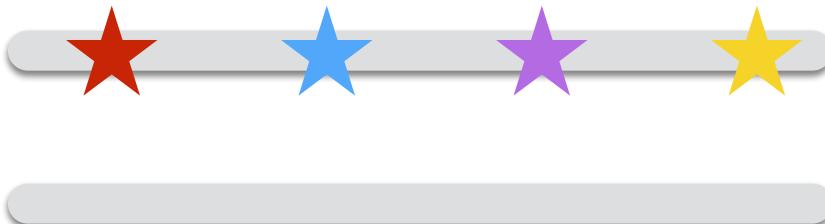


segregating site



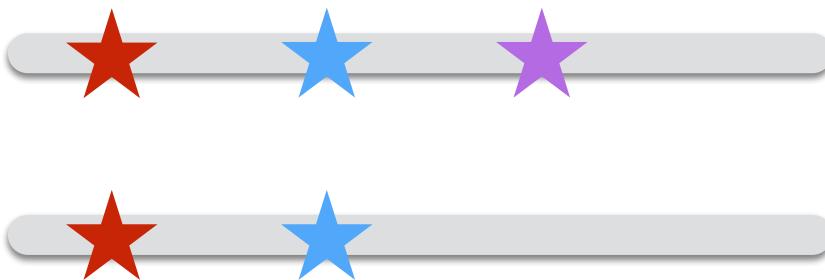
例 1)

segregating site



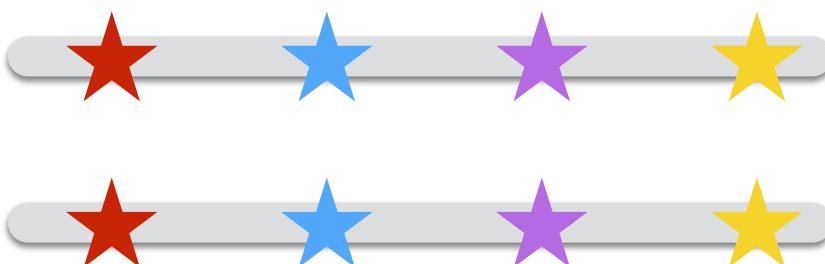
$$S = 4$$

例 2)



$$S = 1$$

例 3)



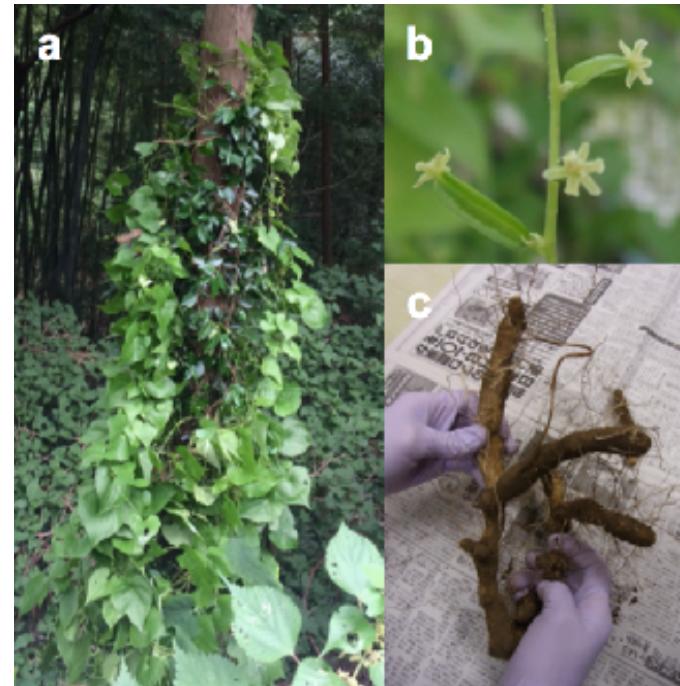
$$S = 0$$

# 実際に計算してみましょう

*Dioscorea tokoro*

$S_2 = ?$

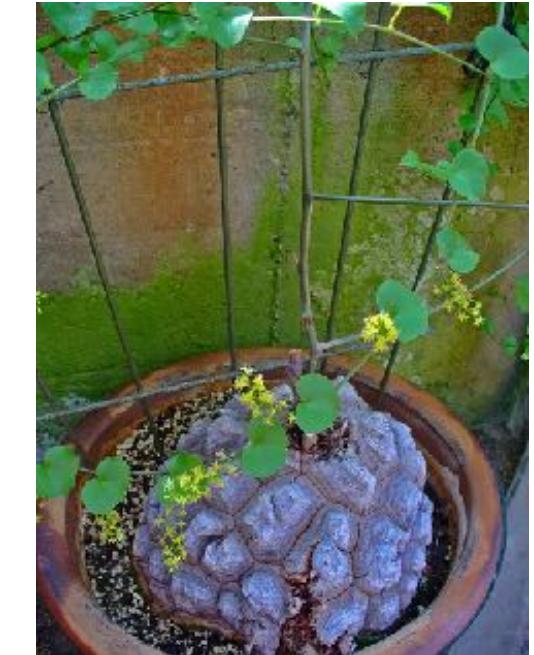
*Dioscorea sylvatica*



$S_1 = ?$

*Dioscorea elephantipes*

$S_3 = ?$

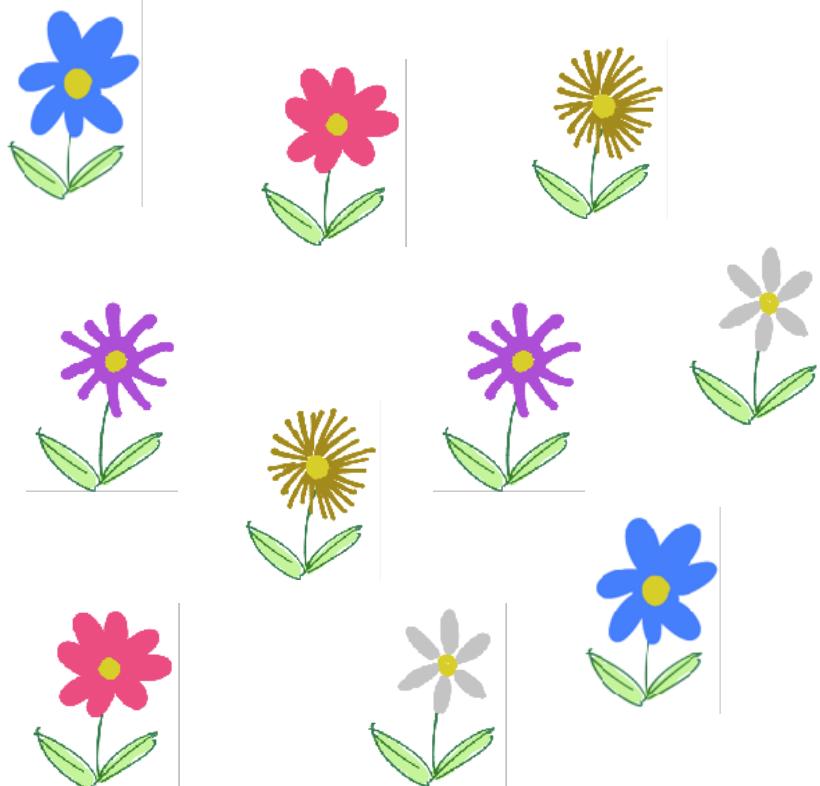




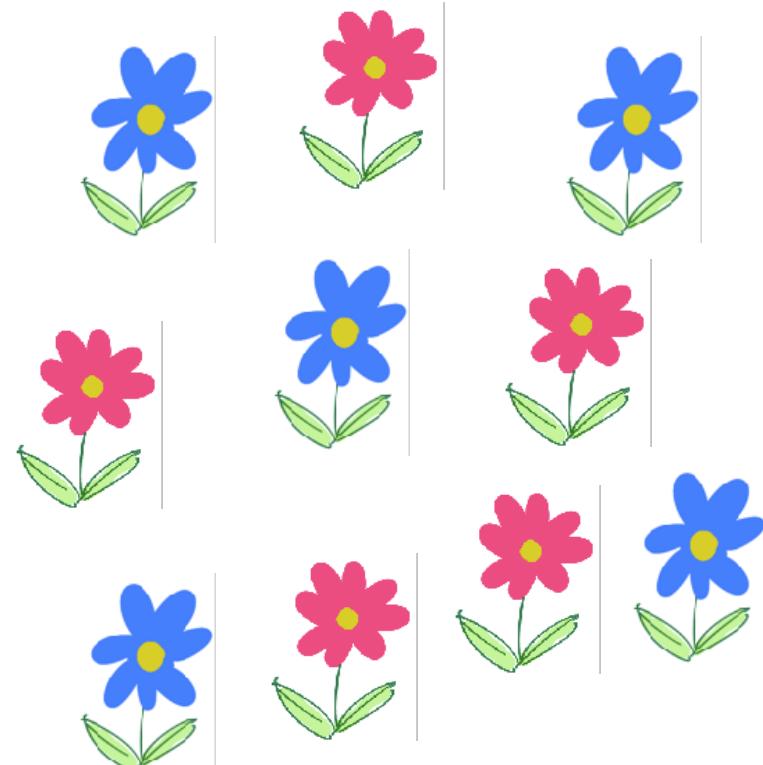
segregating siteで  
多様性が分かる

# どちらが多様だと思いますか？

A

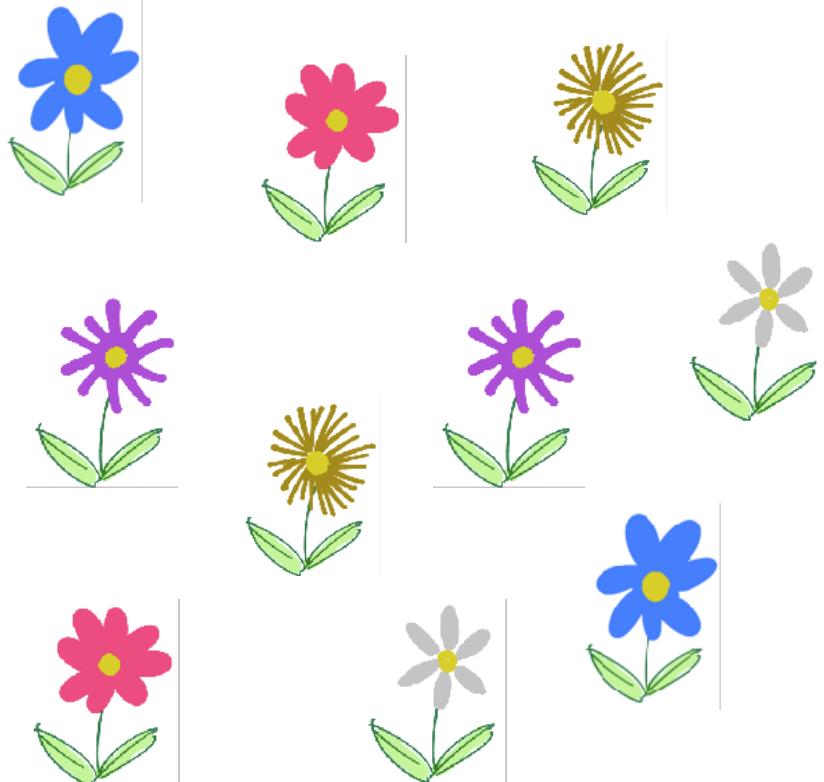


B

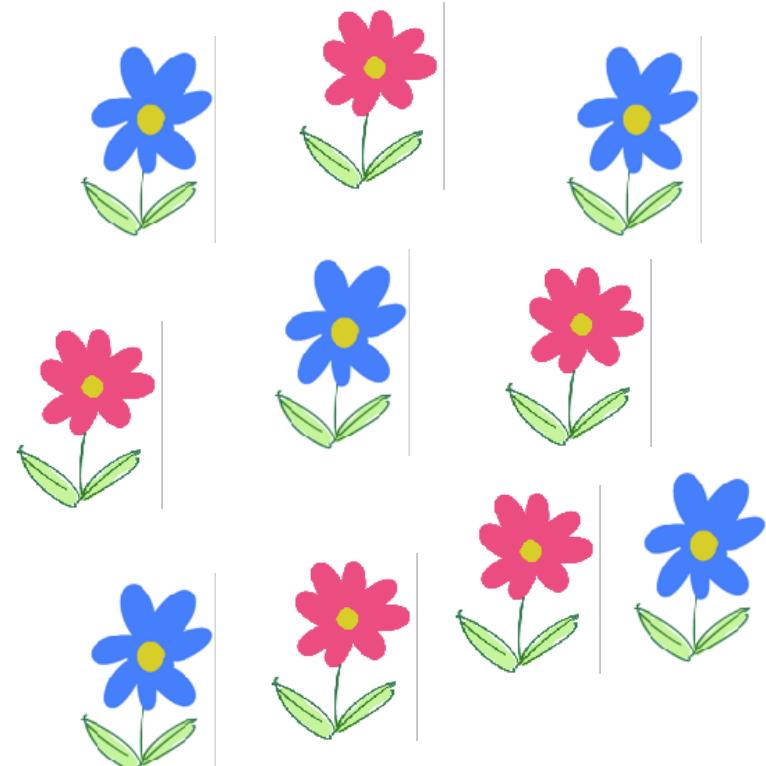


# どちらが多様だと思いますか？

A



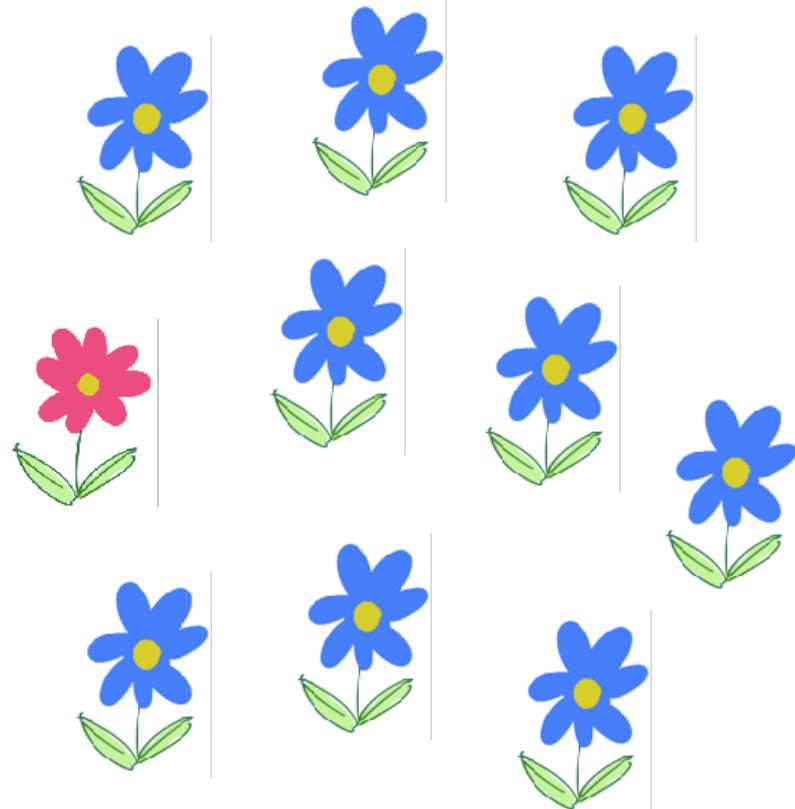
B



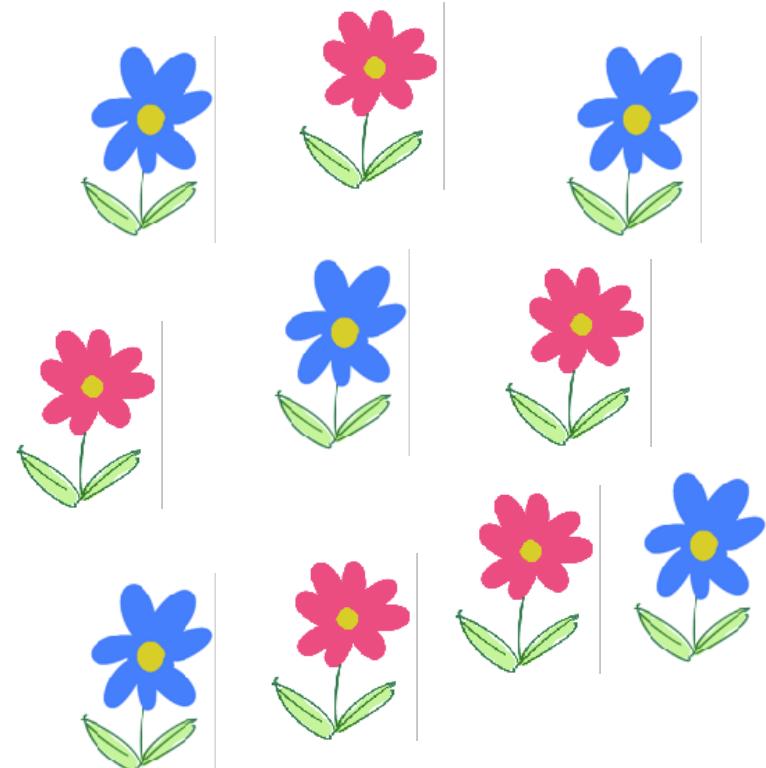
多様性は種類で決まる

# どちらが多様だと思いますか？

A

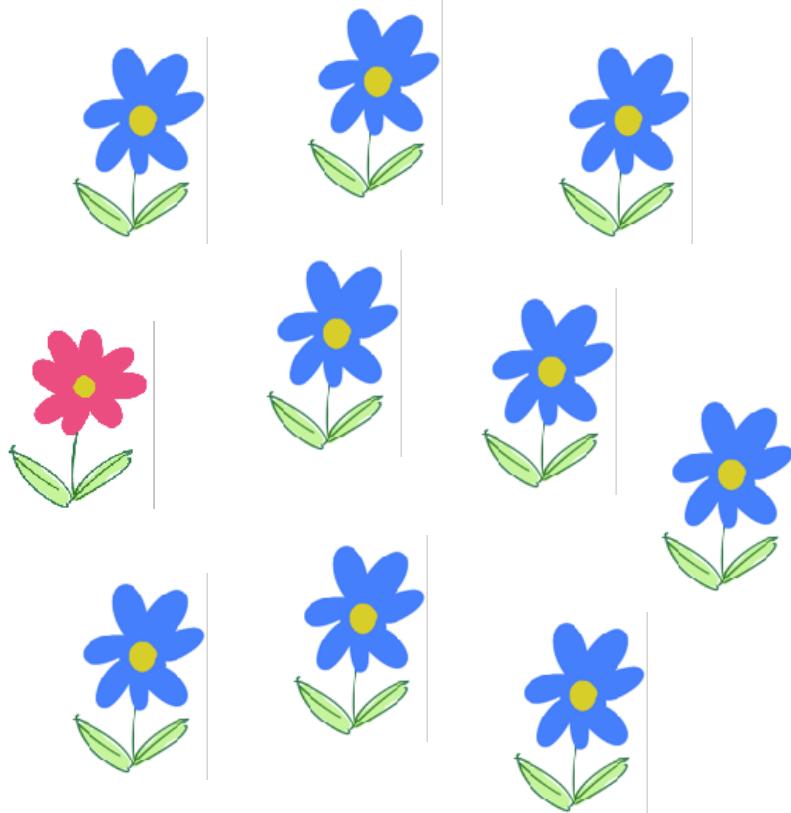


B

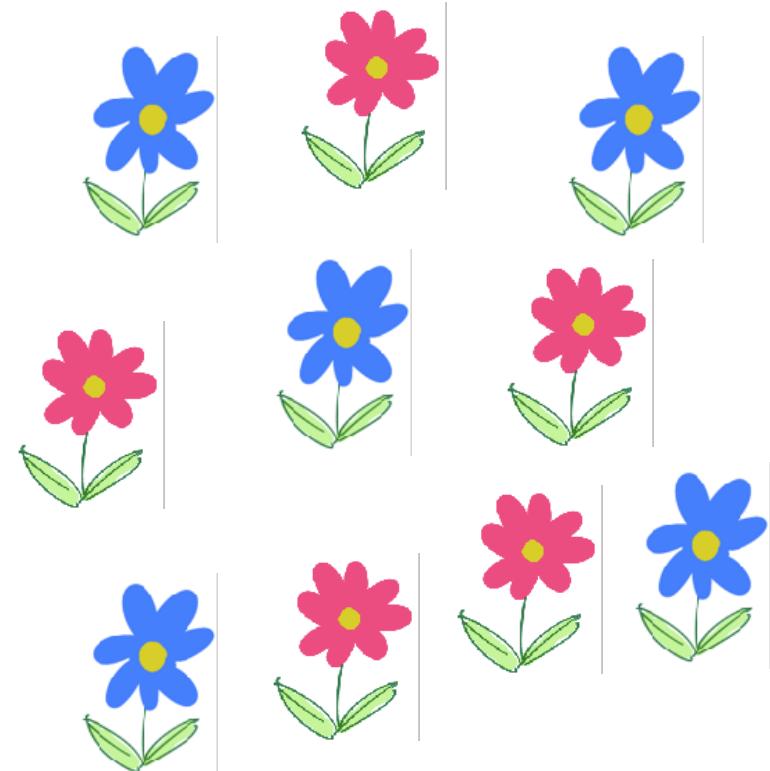


# どちらが多様だと思いますか？

A



B



多様性は頻度でも決まる

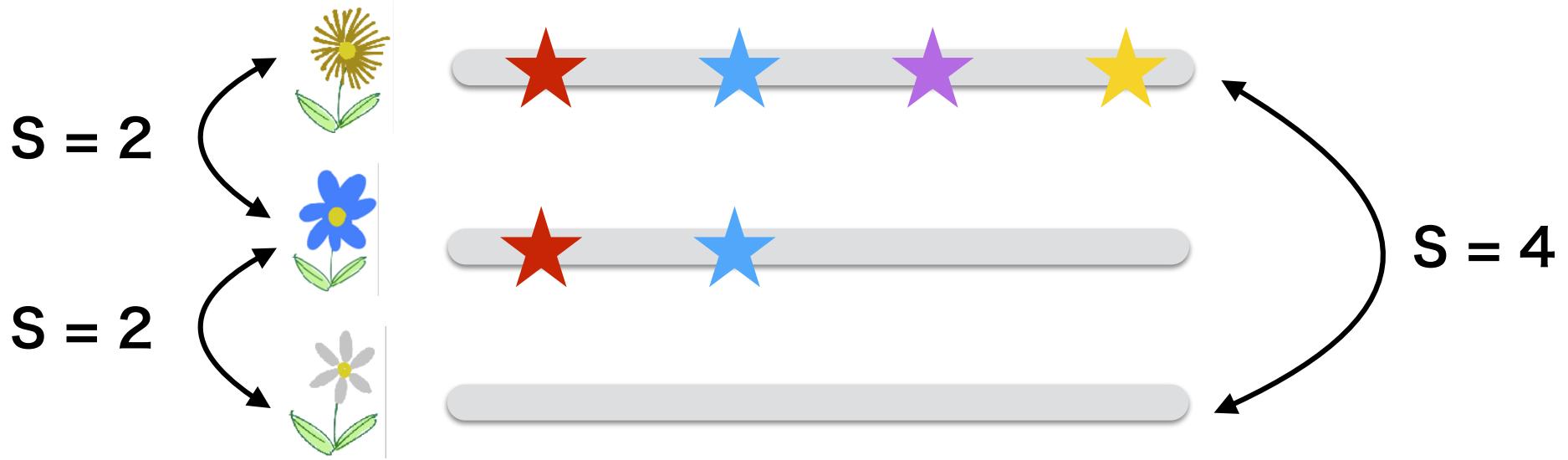


種類

頻度

多樣性

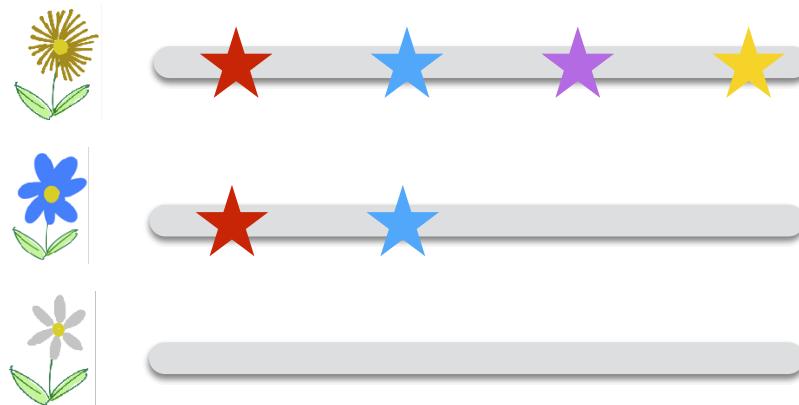
# 多様性の評価（方法1）



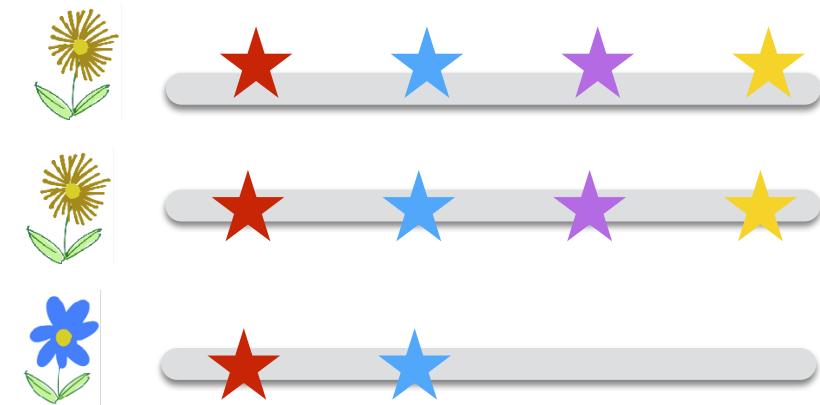
$$\pi = \frac{\text{(全ての組み合わせのSの総和)}}{\text{(配列の組み合わせ)}} = \frac{2 + 2 + 4}{3} = \frac{8}{3}$$

# どちらが多様でしょうか？

A



B



$$\frac{2 + 2 + 4}{3} = \frac{8}{3}$$

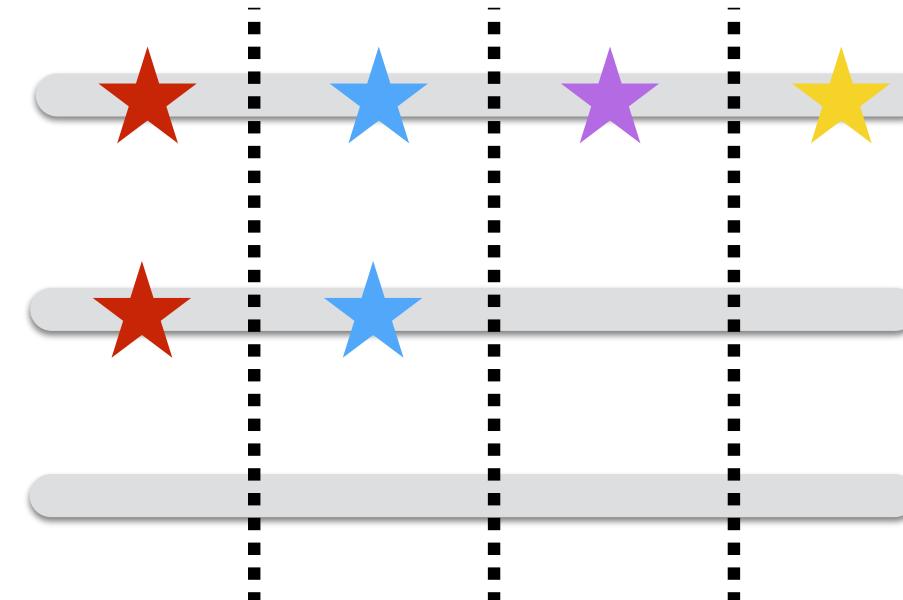
>

$$\frac{0 + 2 + 2}{3} = \frac{4}{3}$$

# 多様性の評価（方法2）

\* 方法1と方法2は同じ結果を示します。

基準配列



(1) 基準配列も含めて

基準と同じ

基準と違う

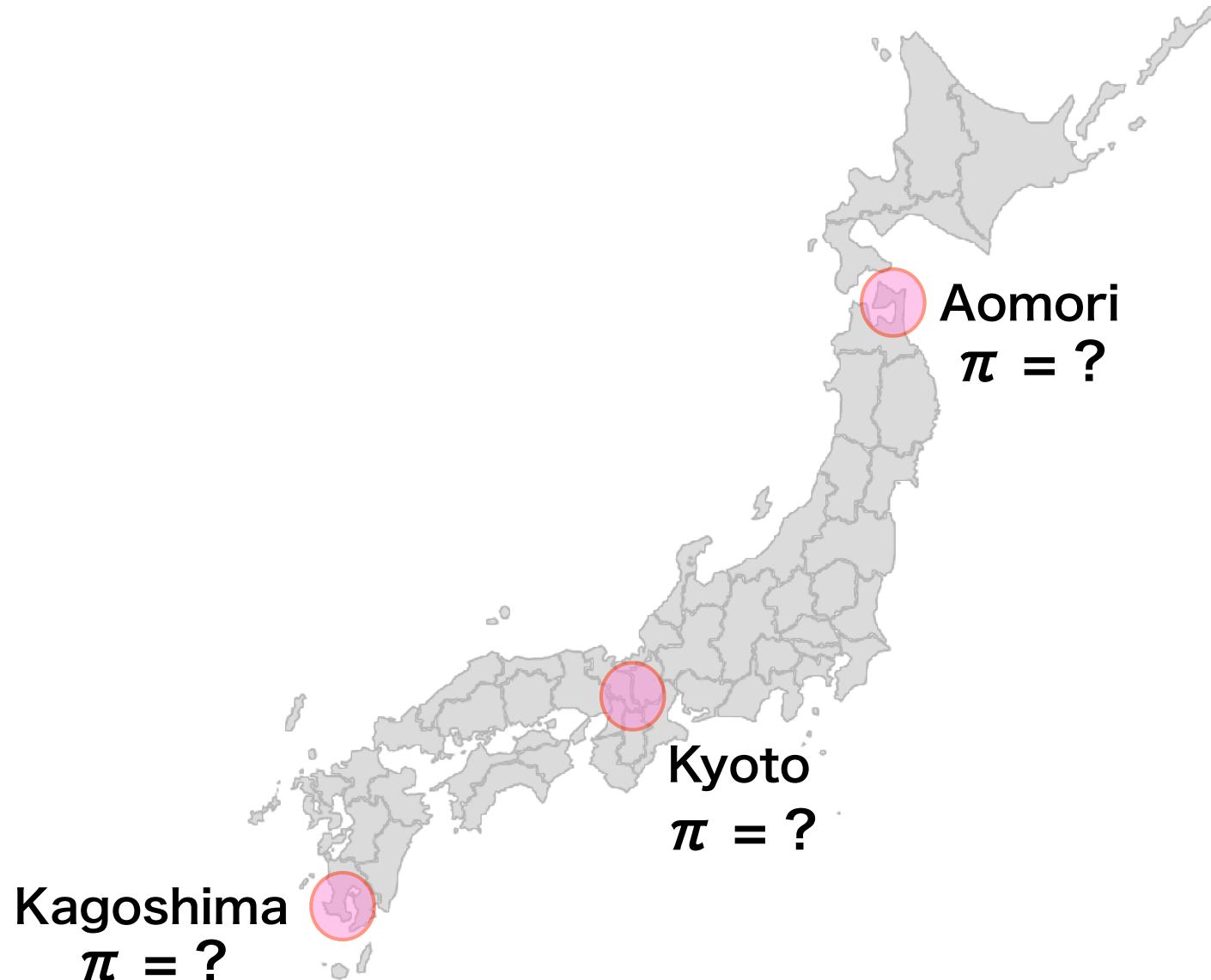
(2) (基準と同じ) × (基準と違う)

$$2 + 2 + 1 + 1 = 8$$

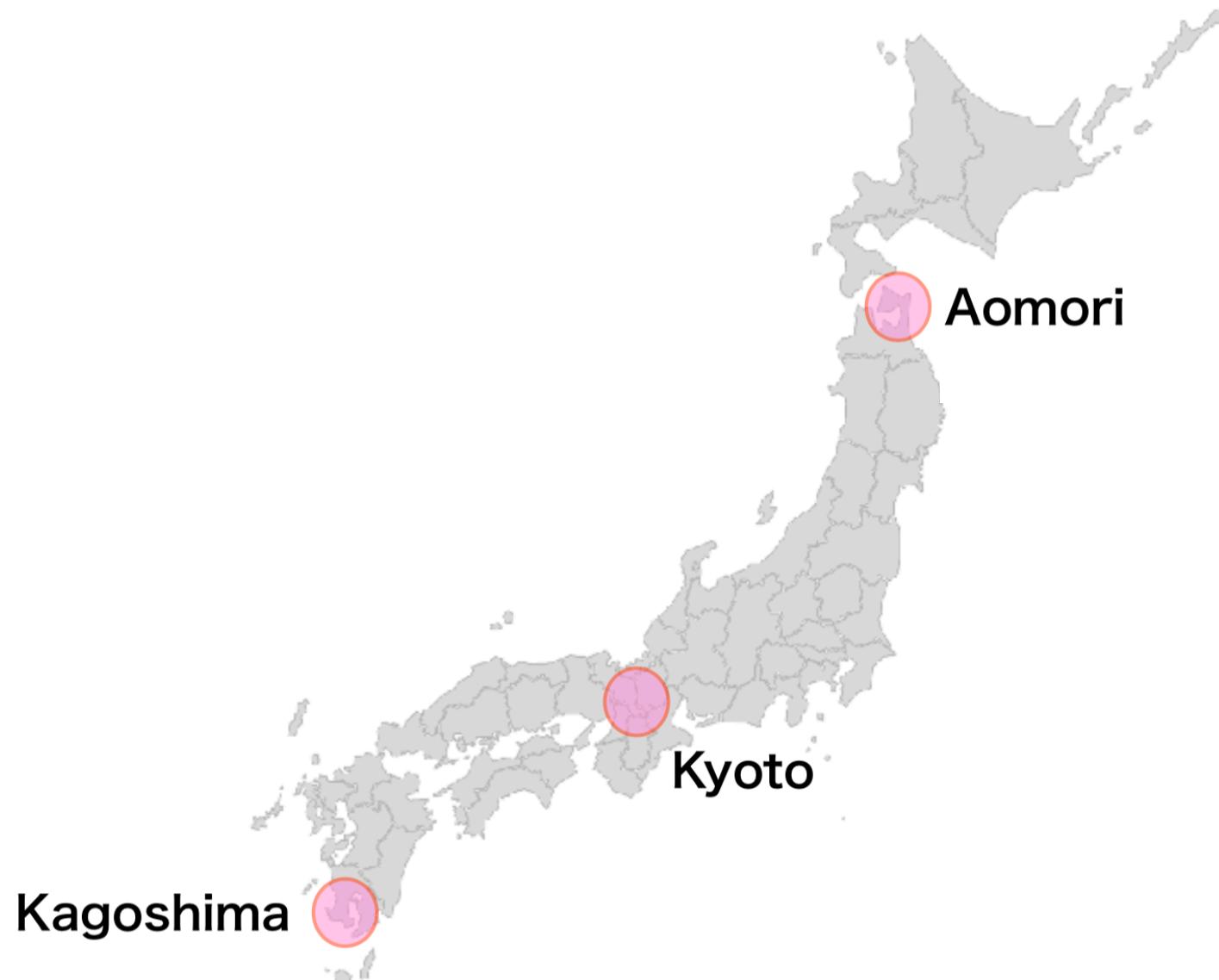
(3) 配列の総組み合わせで割る

$$8 / {}_3C_2 = 8/3$$

# 実際に計算してみましょう

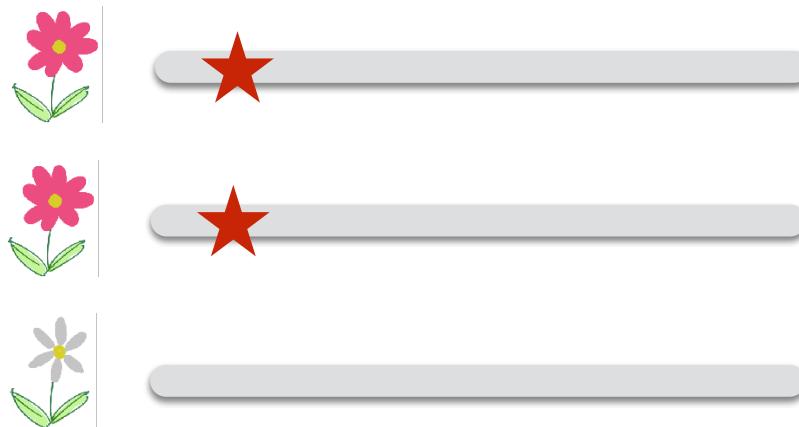


# 3地点の関係は？

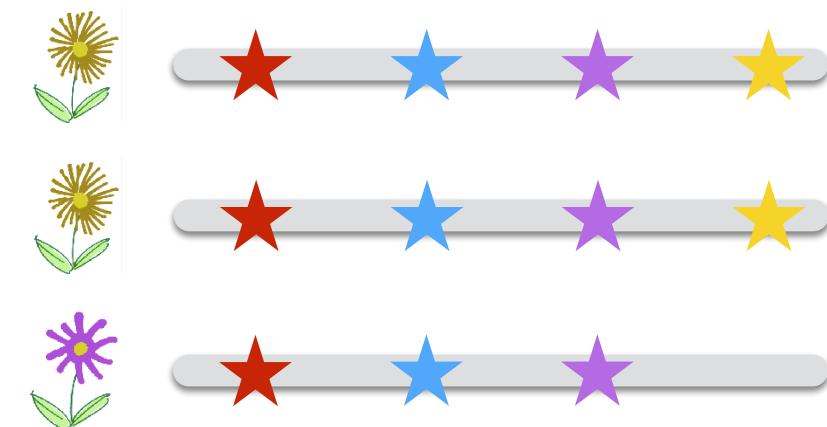


# 集団間の遺伝的距离の評価方法

集団 1



集団 2

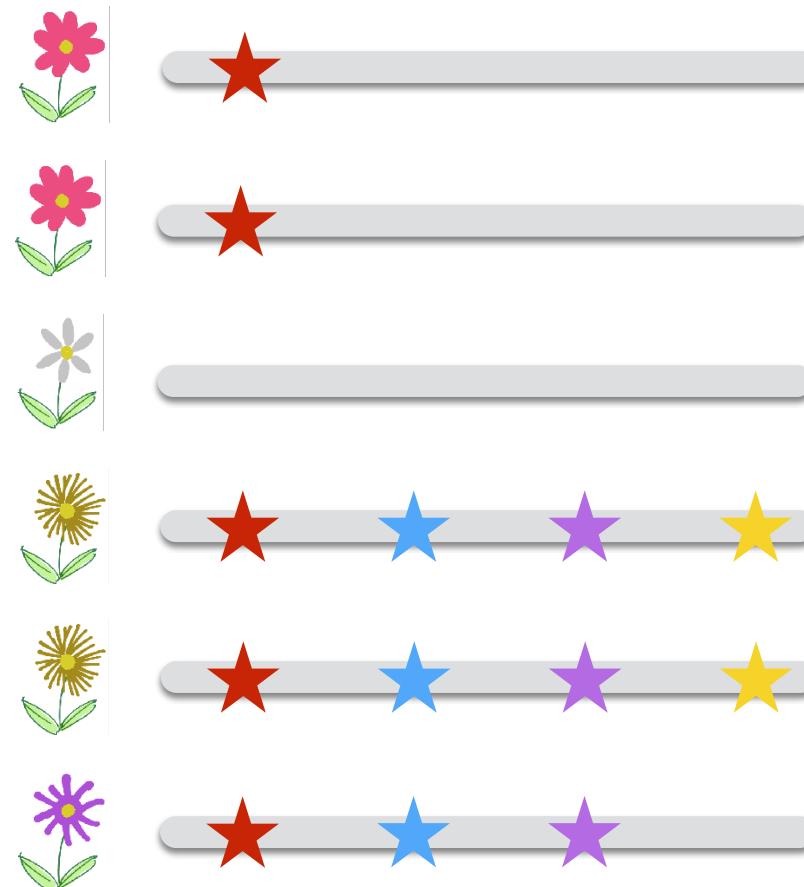


$$\pi_1 = \frac{2 \times 1}{3} = \frac{2}{3}$$

$$\pi_2 = \frac{2 \times 1}{3} = \frac{2}{3}$$

# 集団間の遺伝的距離の評価方法

集団1と集団2が同じ集団だと仮定する



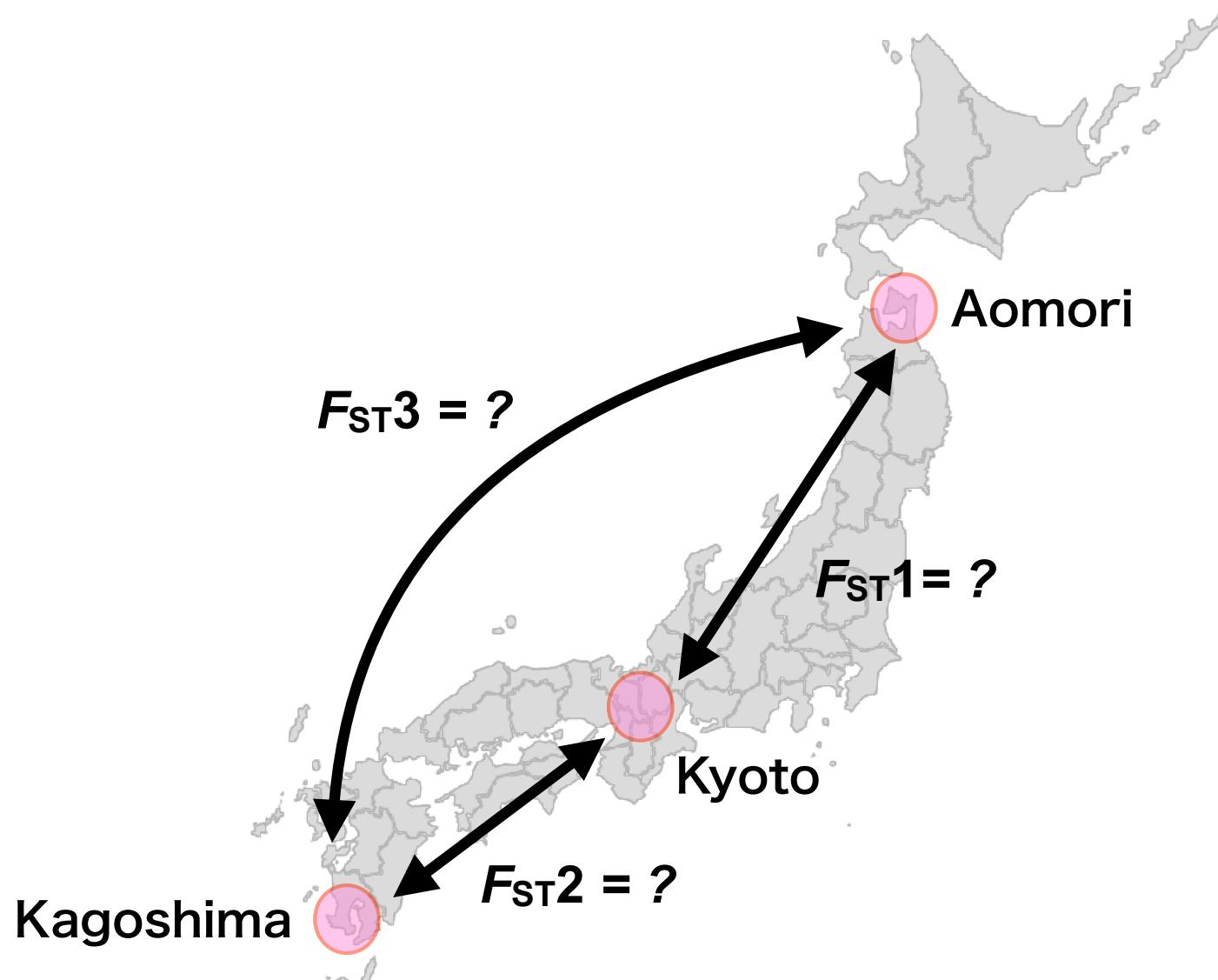
$$\pi_{12} = \frac{5 \times 1 + 3 \times 3 + 3 \times 3 + 4 \times 2}{6C_2} = \frac{31}{15}$$

# 集団間の遺伝的距離の評価方法

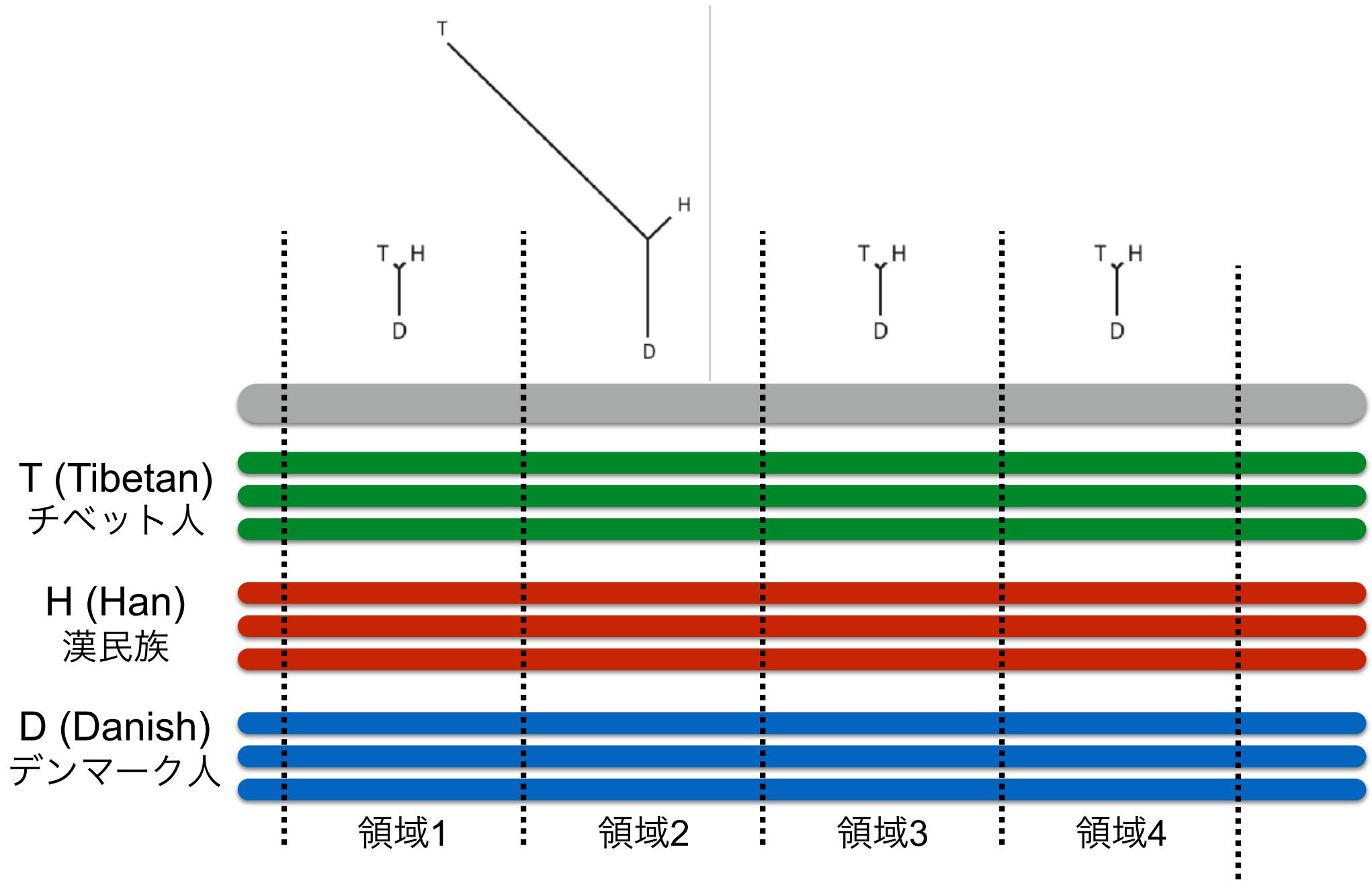
$$F_{ST} = \frac{\pi_{12} - (\pi_1 + \pi_2) / 2}{\pi_{12}}$$
$$= \frac{\frac{31}{15} - (\frac{2}{3} + \frac{2}{3}) / 2}{\frac{31}{15}}$$
$$= \frac{21}{31}$$

$F_{ST}$ は 0 ~ 1 の間の値をとる指標で、およそ 0.4 より大きいと高いと言われています。

# 実際に計算してみましょう



# $F_{ST}$ を用いてのゲノムスキャン



# $F_{ST}$ を用いてのゲノムスキャン

