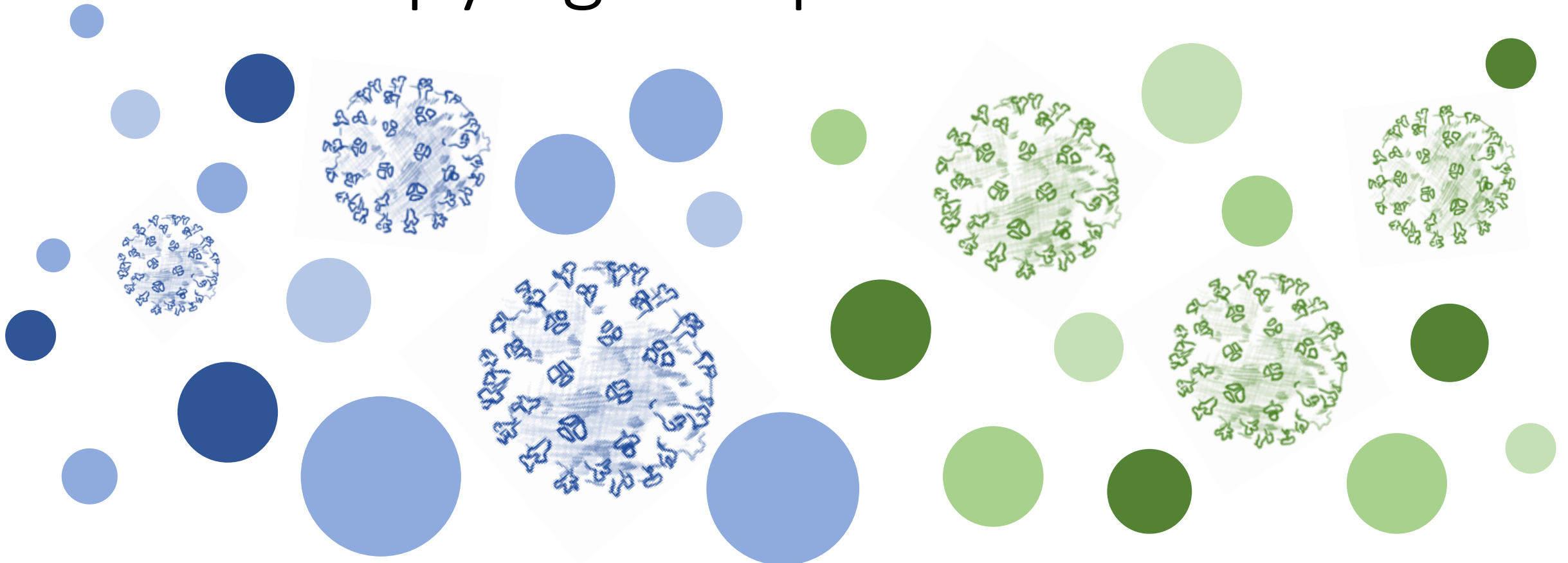


Human pathogenic RNA viruses  
establish noncompeting lineages by  
occupying independent niches



## Thanks To Coauthors

Guilhem Faure  
Feng Zhang

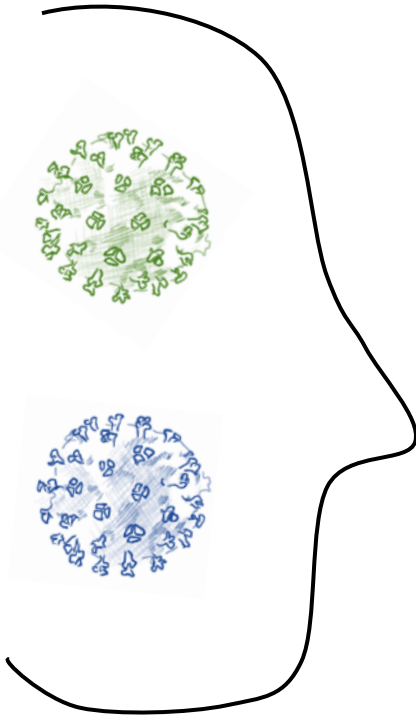


Pascal Mutz  
Yuri Wolf  
Eugene Koonin

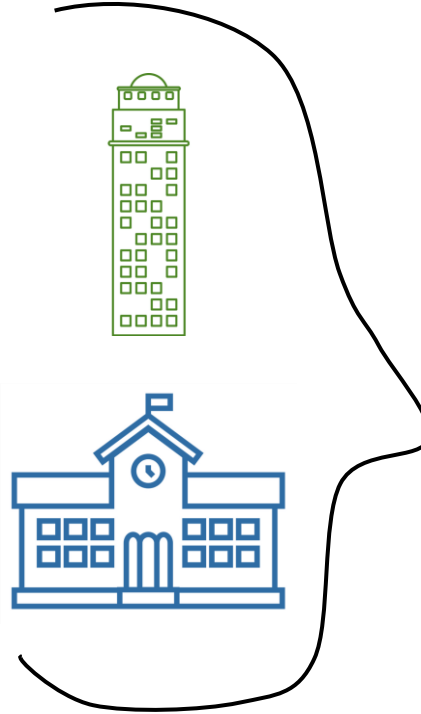


# Human pathogenic RNA viruses establish noncompeting lineages by occupying independent niches

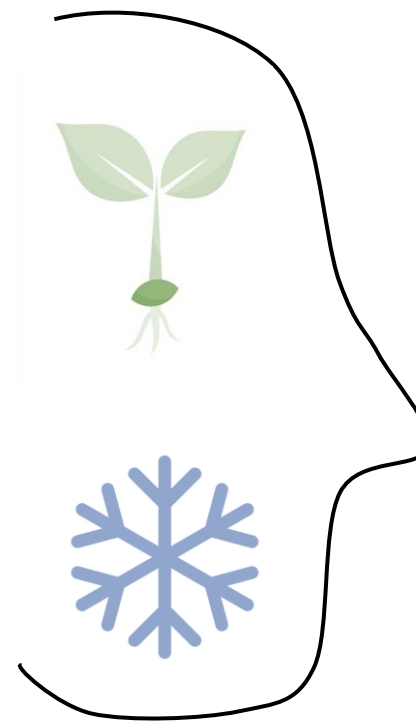
No cross immunity



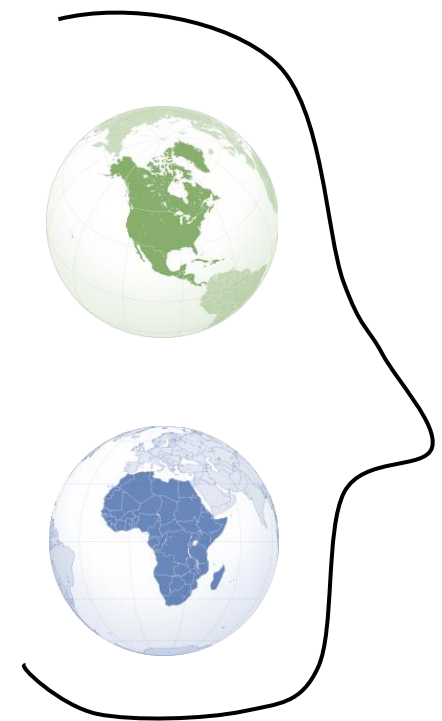
**Local**



Seasonal



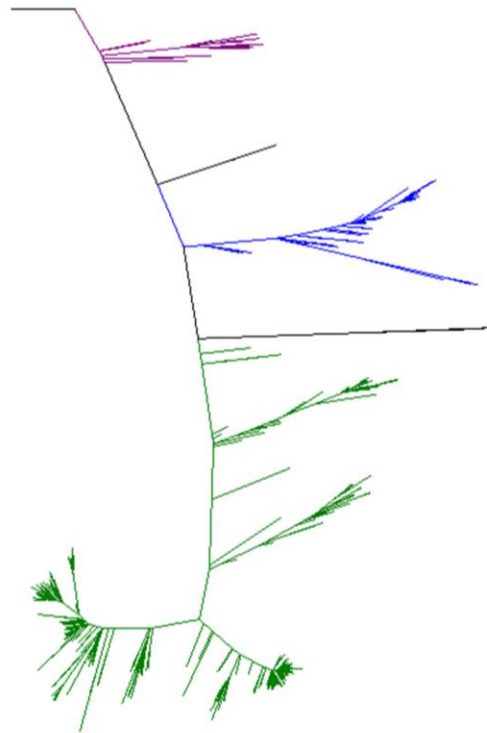
Regional



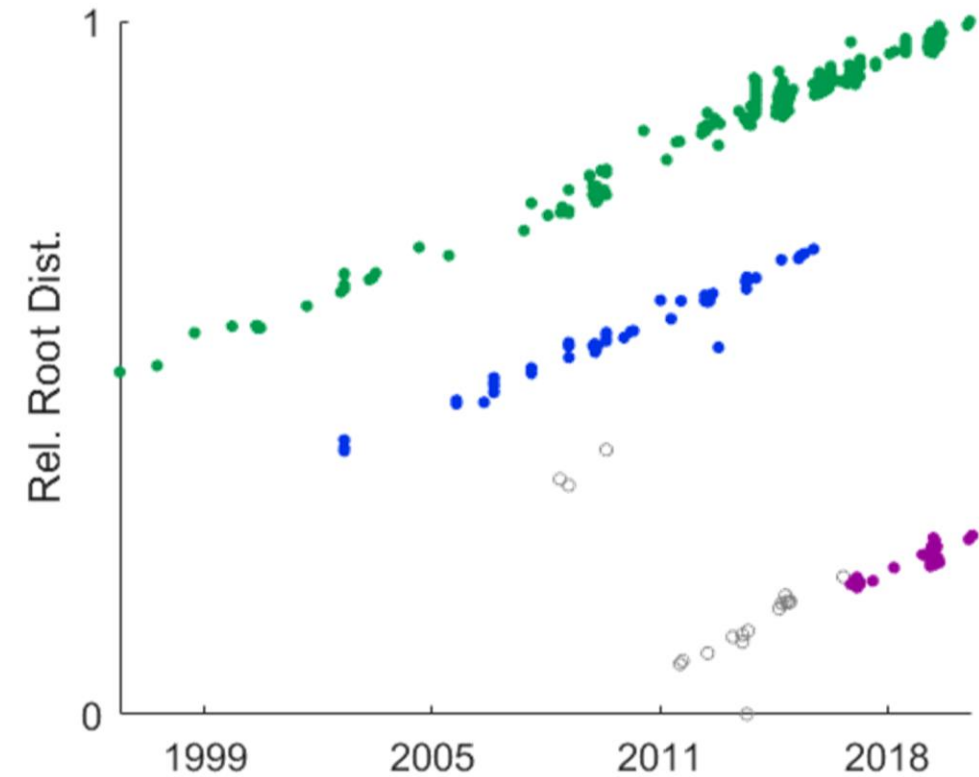
Human pathogenic RNA viruses establish noncompeting **lineages** by occupying independent niches

Monophyletic group (clade)  
with “good”  
date-constrained tree

Breaks down trees into groups  
separated by periods of  
apparently different  
substitution rates,  
likely environmental conditions

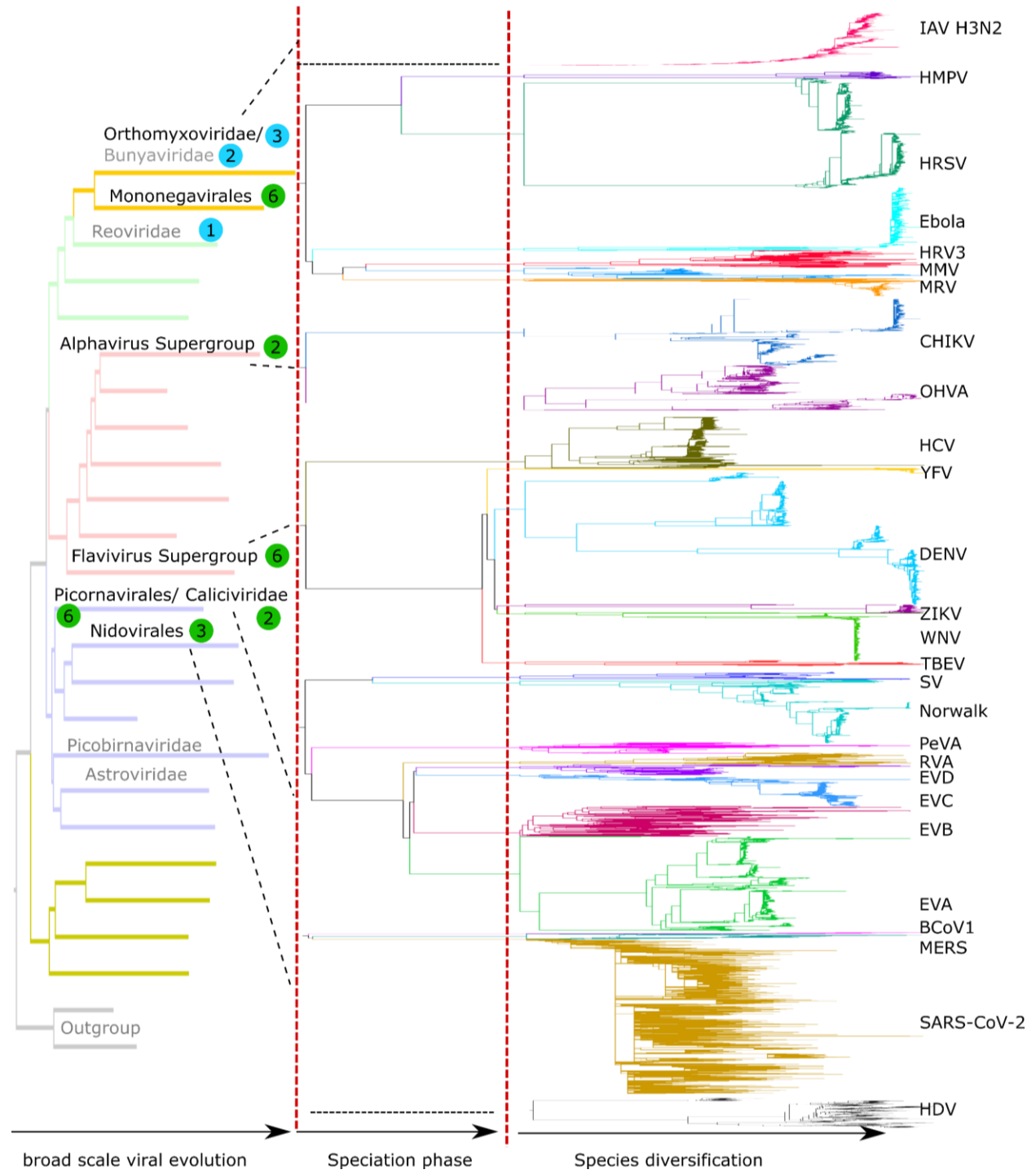


### Enterovirus D



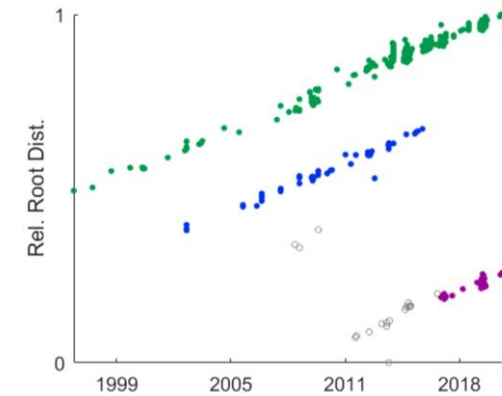
Considered all non-segmented  
RNA viruses with at least ~200  
complete genomes.

Consider events at scale of  
species diversification.

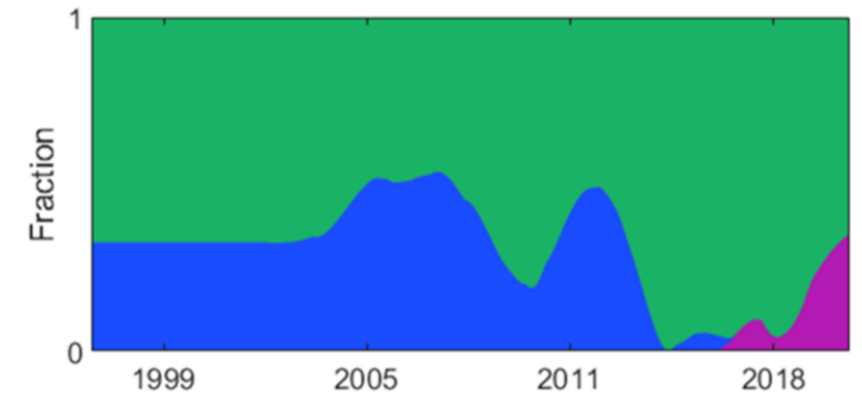


Human pathogenic RNA viruses establish **noncompeting** lineages by occupying independent niches

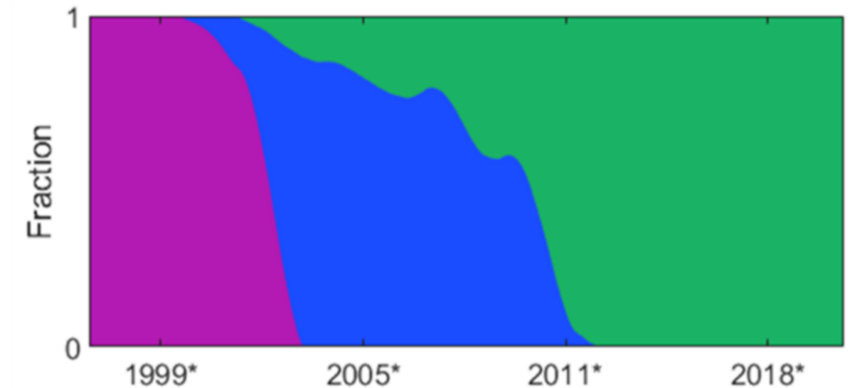
First approach: compare lineage coexistence



Real distribution  
of isolates



Expected distribution  
of isolates based  
on root distances

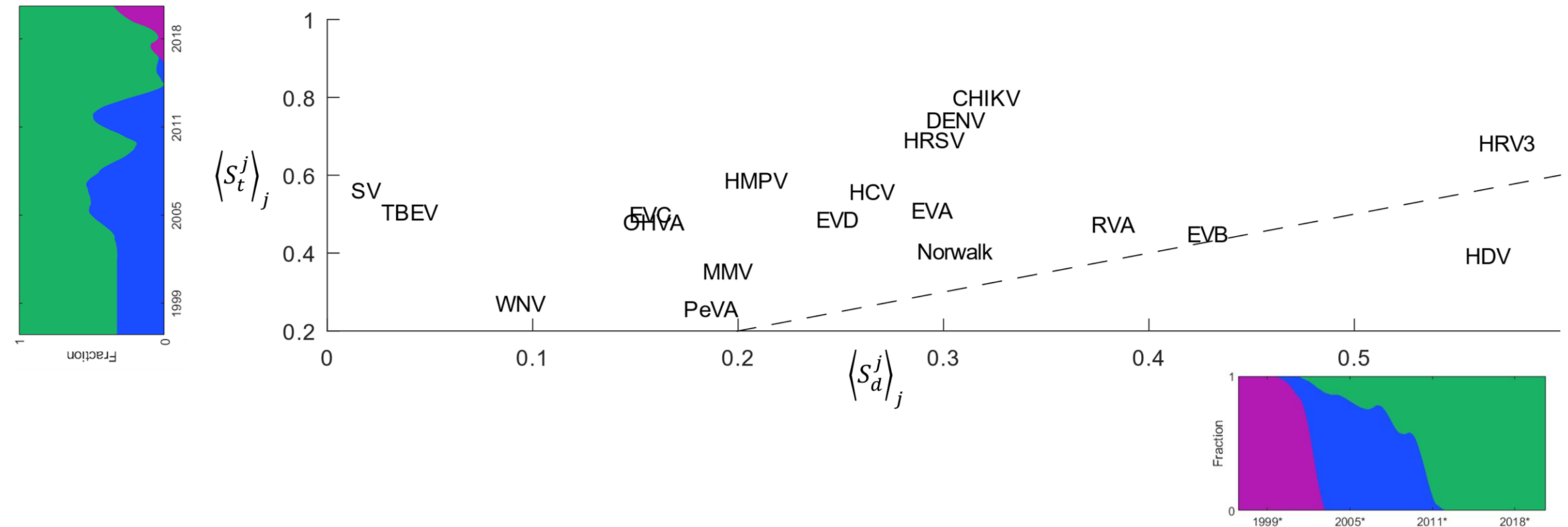


**Enterovirus D**

Human pathogenic RNA viruses establish **noncompeting** lineages by occupying independent niches

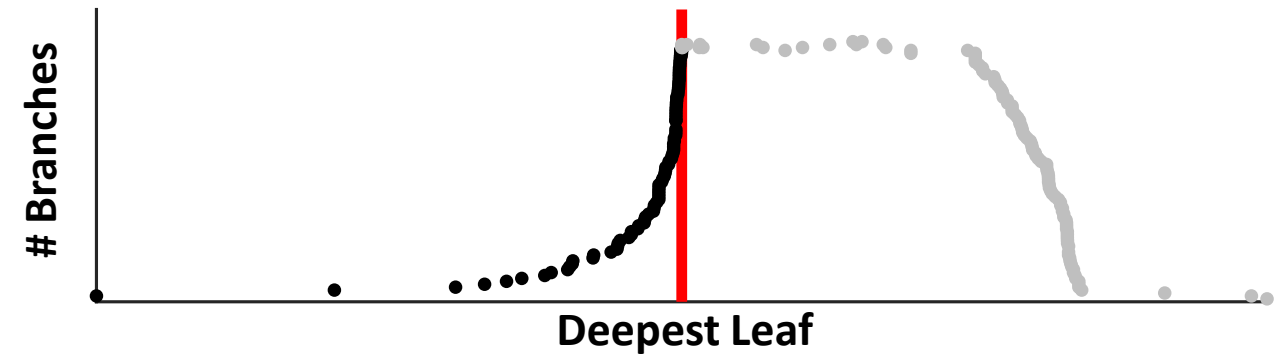
First approach: compare lineage coexistence

Lineages coexist longer than estimated from substitutions alone (no dates)

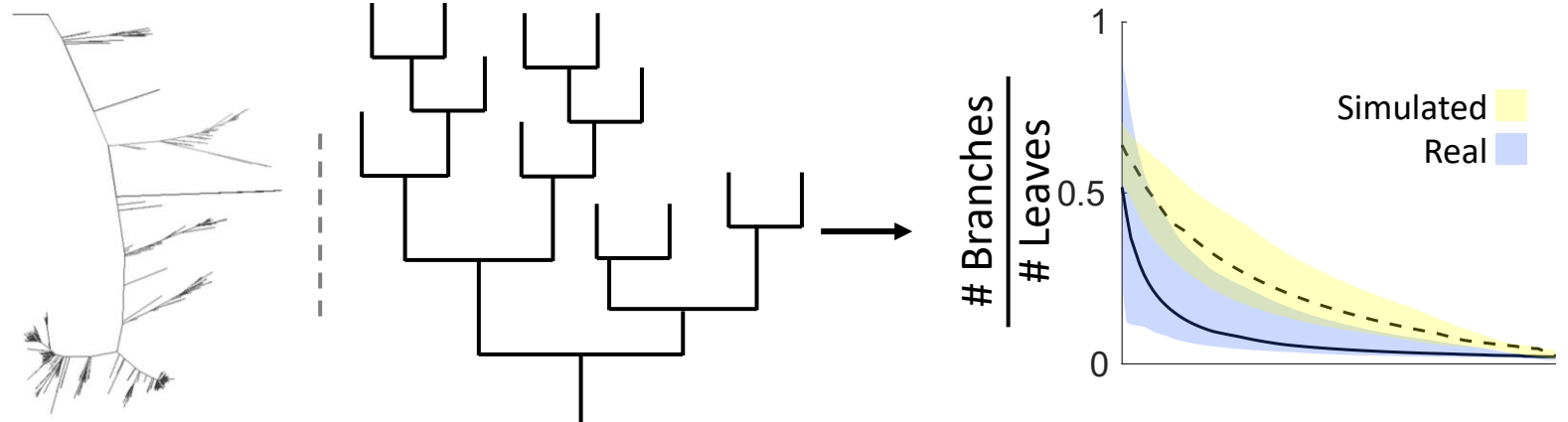


Human pathogenic RNA viruses establish **noncompeting** lineages by occupying independent niches

Second approach: measure coalescence rate



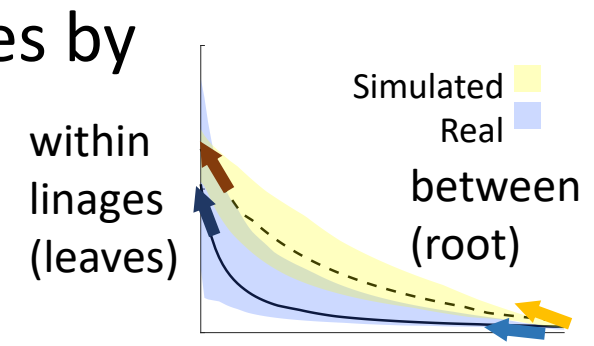
Build simulated trees according to neutral expectation (Yule-Harding)





Human pathogenic RNA viruses establish **noncompeting** lineages by occupying independent niches

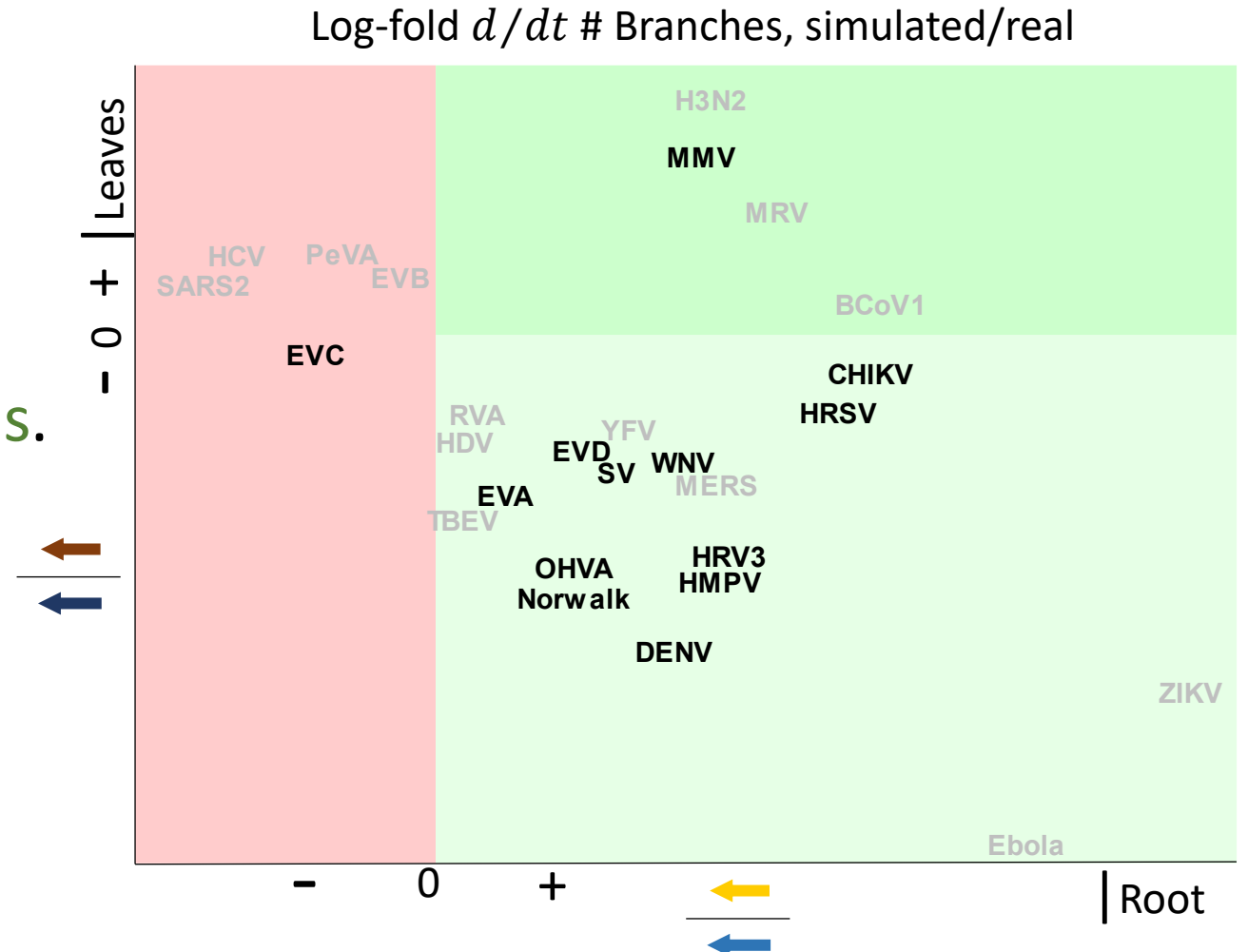
Second approach: measure coalescence rate



**2+ lineages, other**

All but EVC demonstrates **reduced coalescence** (competition) relative to neutral expectation **between lineages**.

All but MMV demonstrates increased coalescence within lineages.



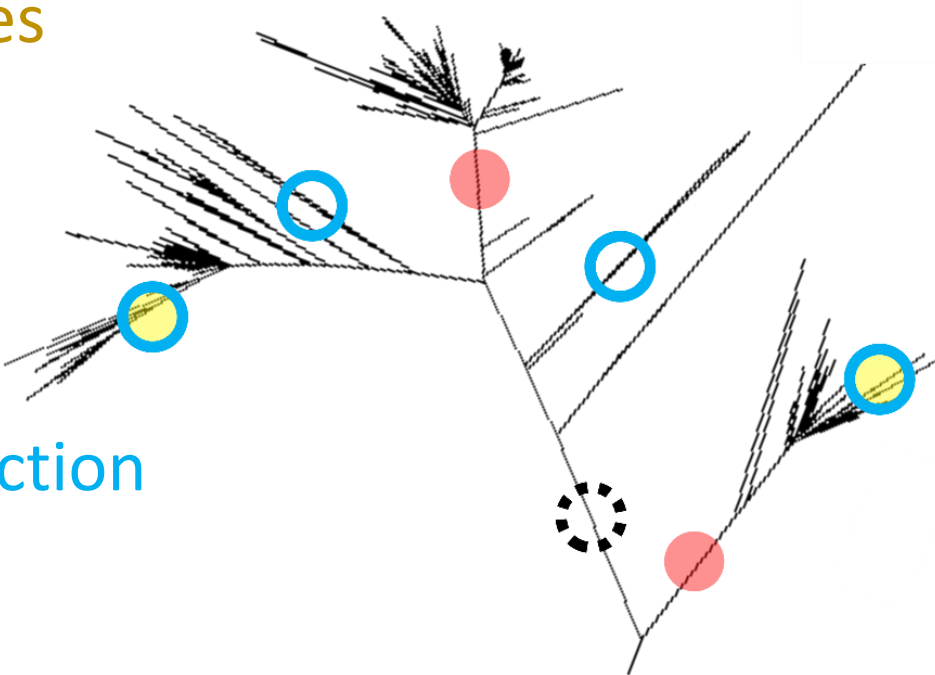
Only tempo, not the mode, of molecular evolution appears to vary substantially intra- vs. inter-lineage.

Comparison of site density of **Multiple Shallow** representing best estimate of **adaptive sites**

**Multiple Deep**, best estimate of **linage-defining sites**

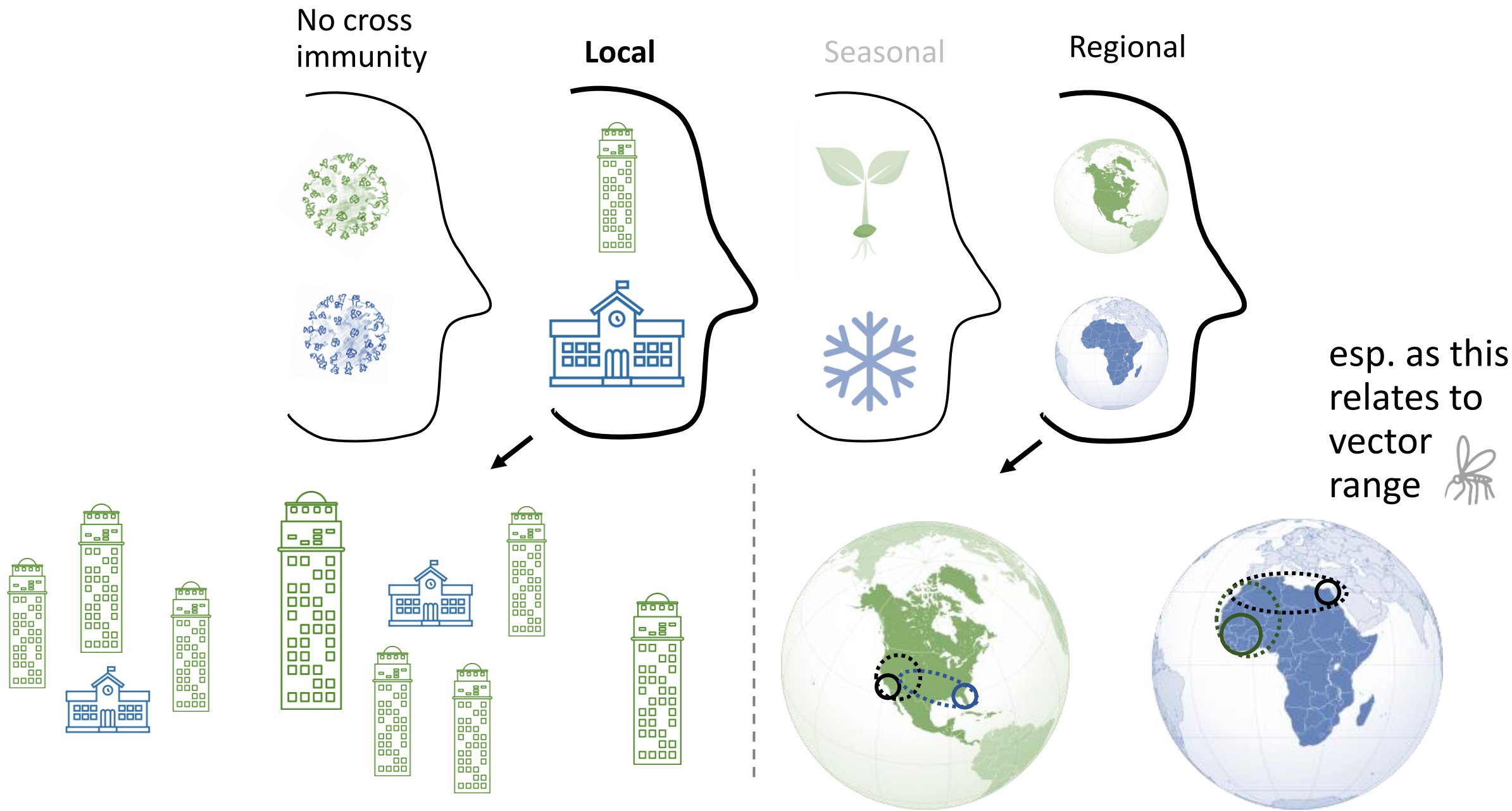
**All Shallow**, unrelated to selection

Site densities are correlated (Pearson). Exception, picornaviruses (RVA/HDV low confidence)

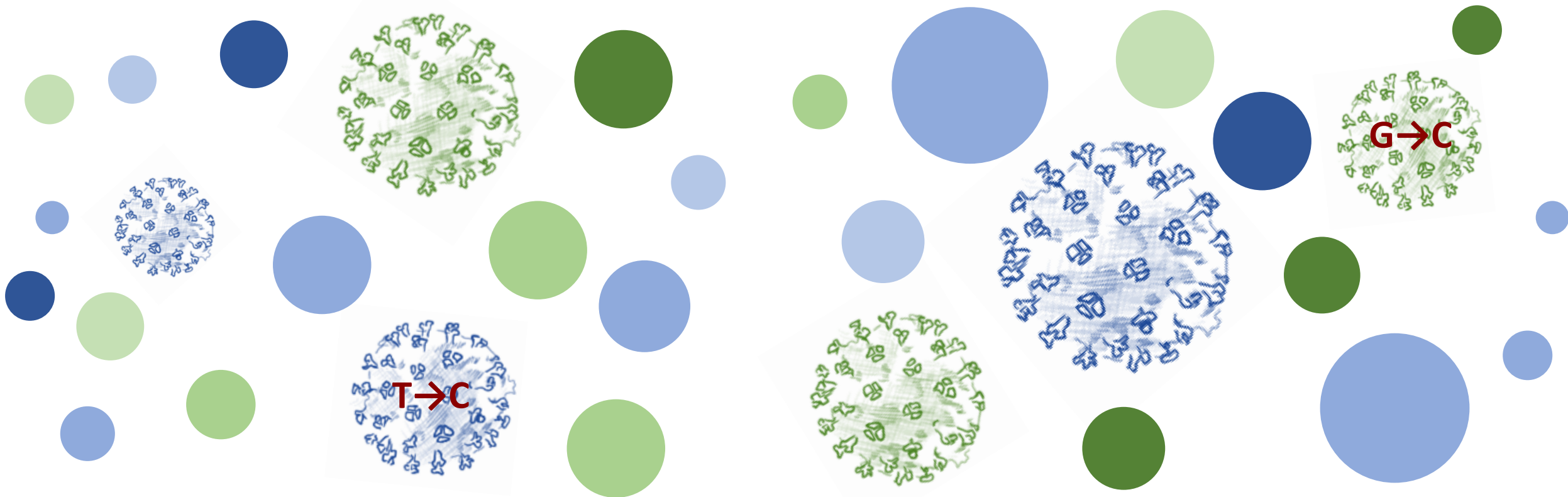


	AS MS	AS MD	MS MD
RVA	94	-28	-27
HDV	93	-9	-25
PeVA	80	-20	9
EVA	69	-3	2
EVC	62	61	3
EVB	81	56	30
WNV	90	46	46
EVD	67	52	29
HMPV	94	78	59
SV	73	50	47
HCV	87	71	67
OHVA	83	84	65
TBEV	44	42	31
MMV	50	80	41
CHIKV	80	65	73
Norwalk	89	80	86
HRV3	93	90	90
HRSV	83	87	91
DENV	53	48	78

# Environmental change: urbanization and climate change may disrupt niches



Human pathogenic RNA viruses  
establish ~~non~~competing lineages by  
~~occupying independent niches~~



# Thanks For Listening

Guilhem Faure  
Feng Zhang



Pascal Mutz  
Yuri Wolf  
Eugene Koonin



**World Health  
Organization**