n=20,273 sequenced genomes, up to 11 April 2025

Europe (excl UK)

- JN.1.* +DeFLuQE
- JN.1.* +FLiRT
- JN.1.* +FLuQE
- LP.8.1.*
- XEC.*
- XEK.*

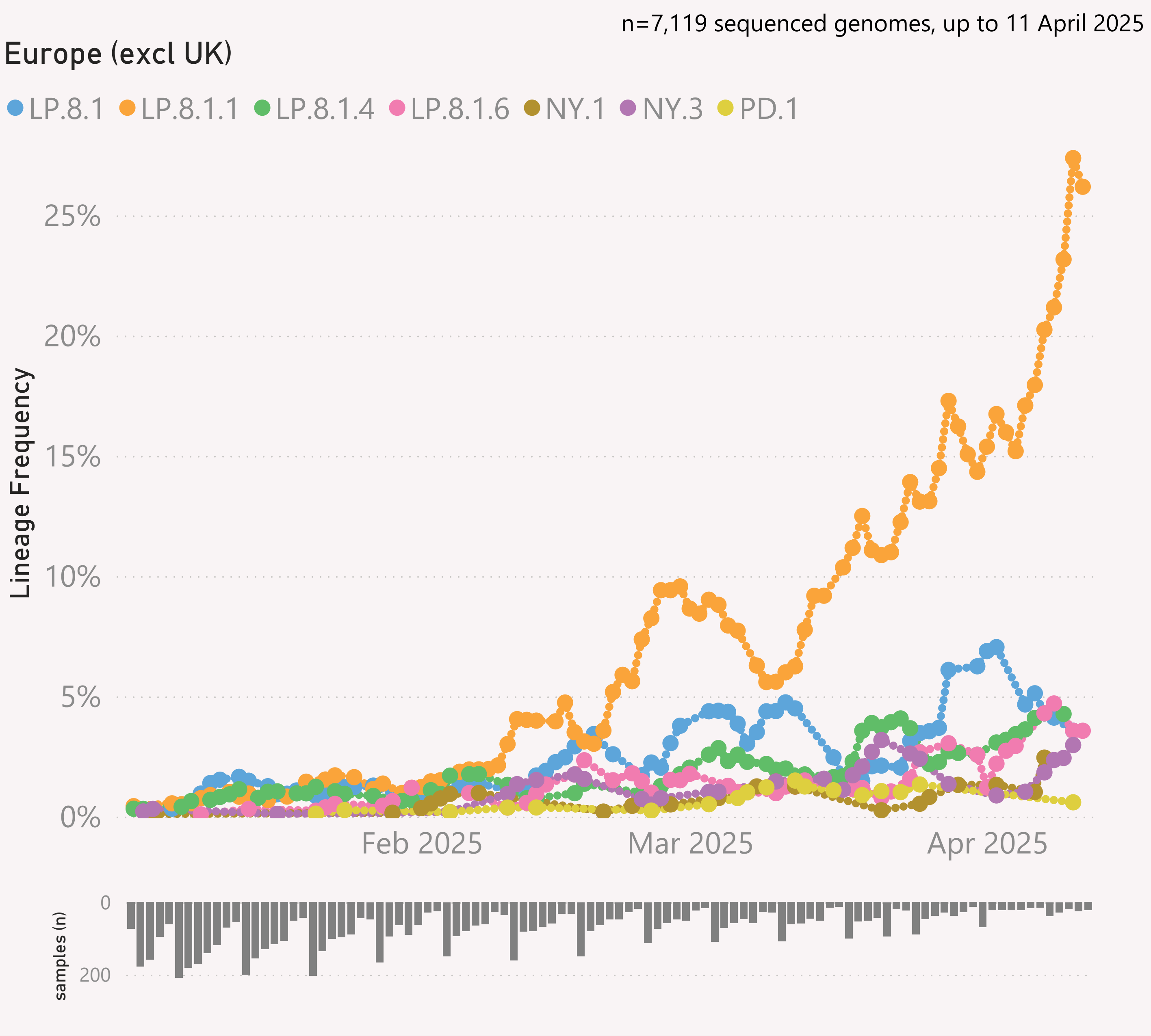This page shows the frequency of the top 6 "L2" lineages, across recent months.

The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=7,119 sequenced genomes, up to 11 April 2025

Europe (excl UK)

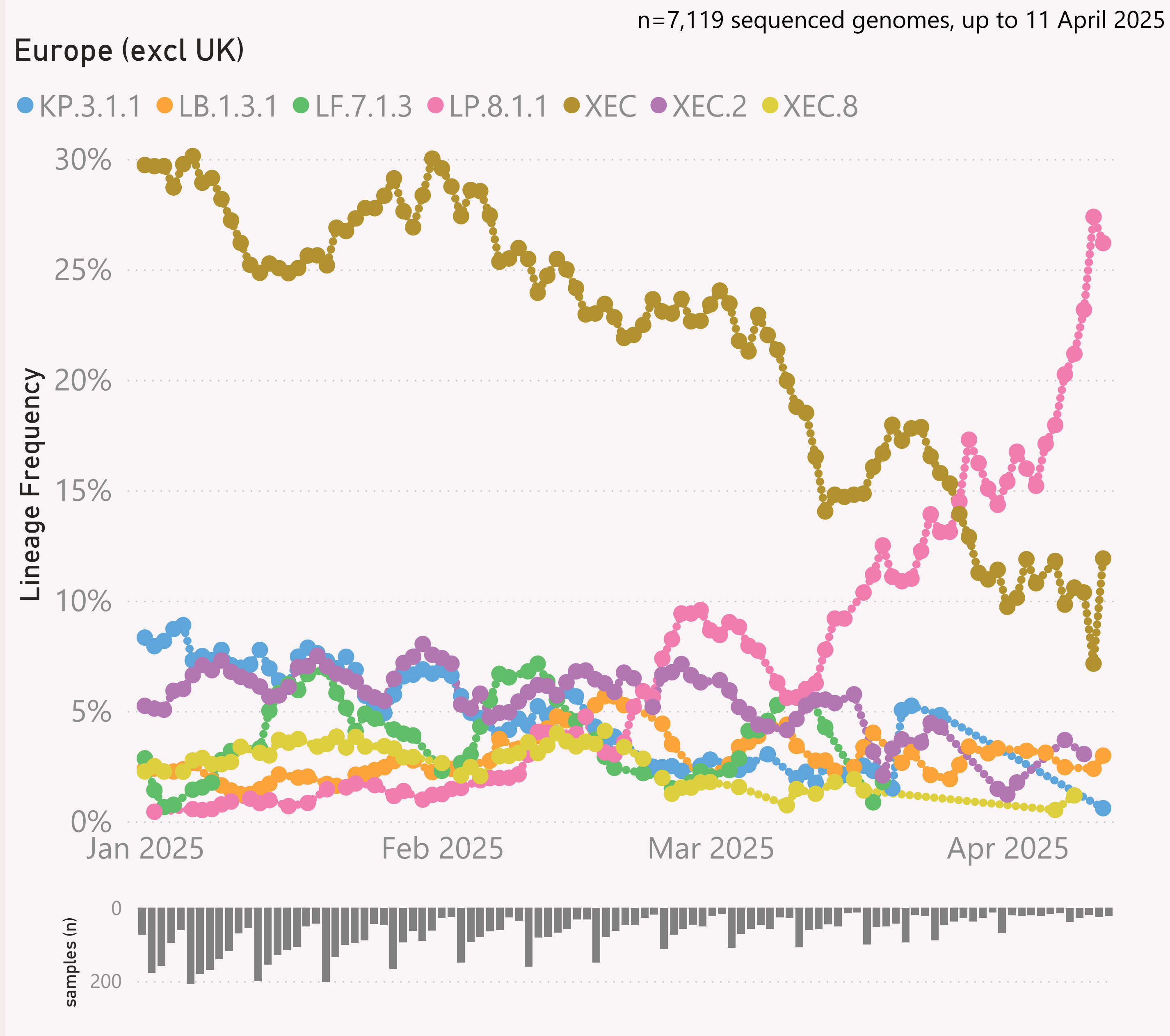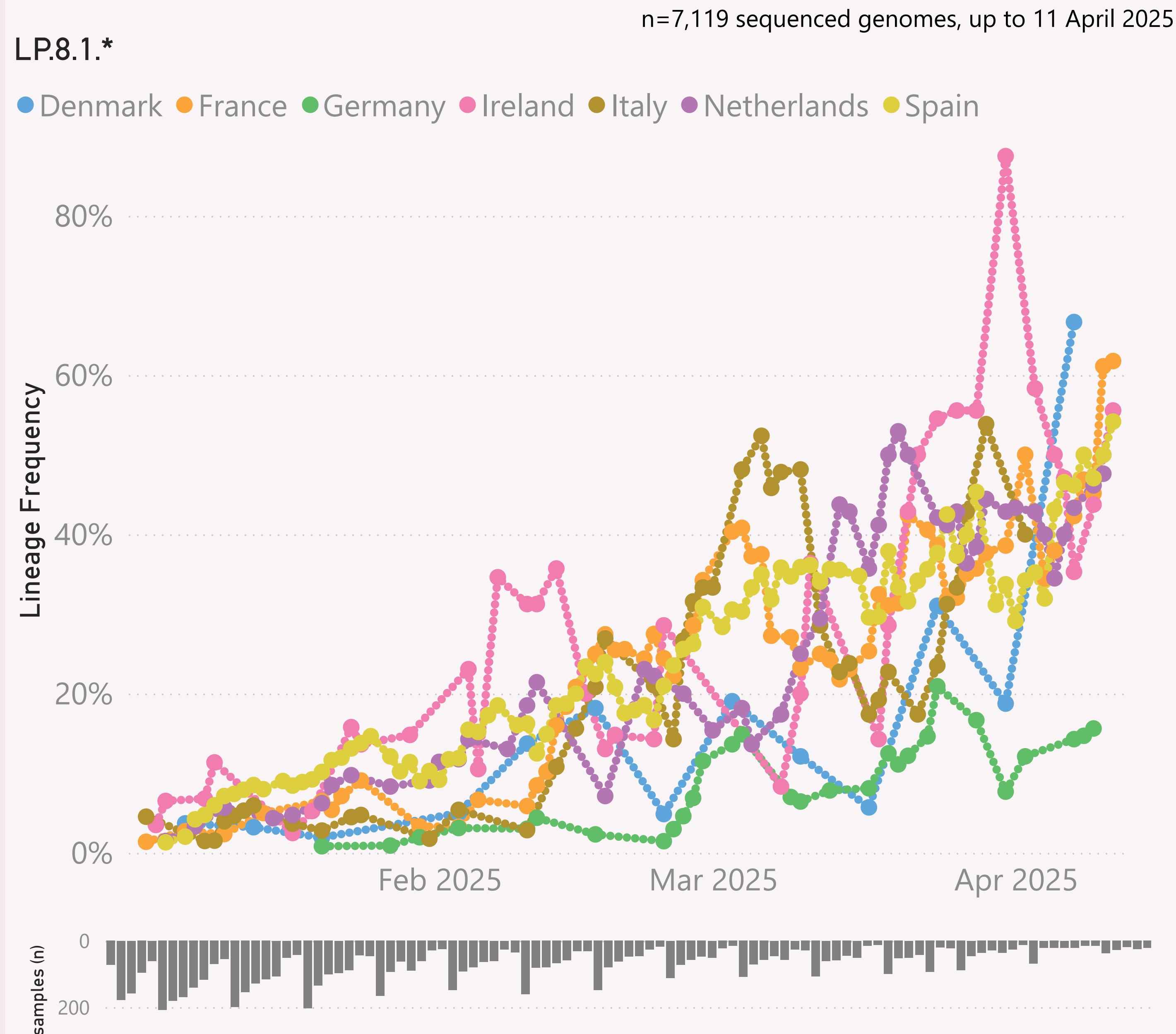● LP.8.1 ● LP.8.1.1 ● LP.8.1.4 ● LP.8.1.6 ● NY.1 ● NY.3 ● PD.1

This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "LP.8.1.*".

The Lineage classifications are provided by Nextclade. The colour assignments are random.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=7,119 sequenced genomes, up to 11 April 2025

Europe (excl UK)

● KP.3.1.1　● LB.1.3.1　● LF.7.1.3　● LP.8.1.1　● XEC　● XEC.2　● XEC.8

This page shows the frequency of the top 7 lineages, across recent months.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.
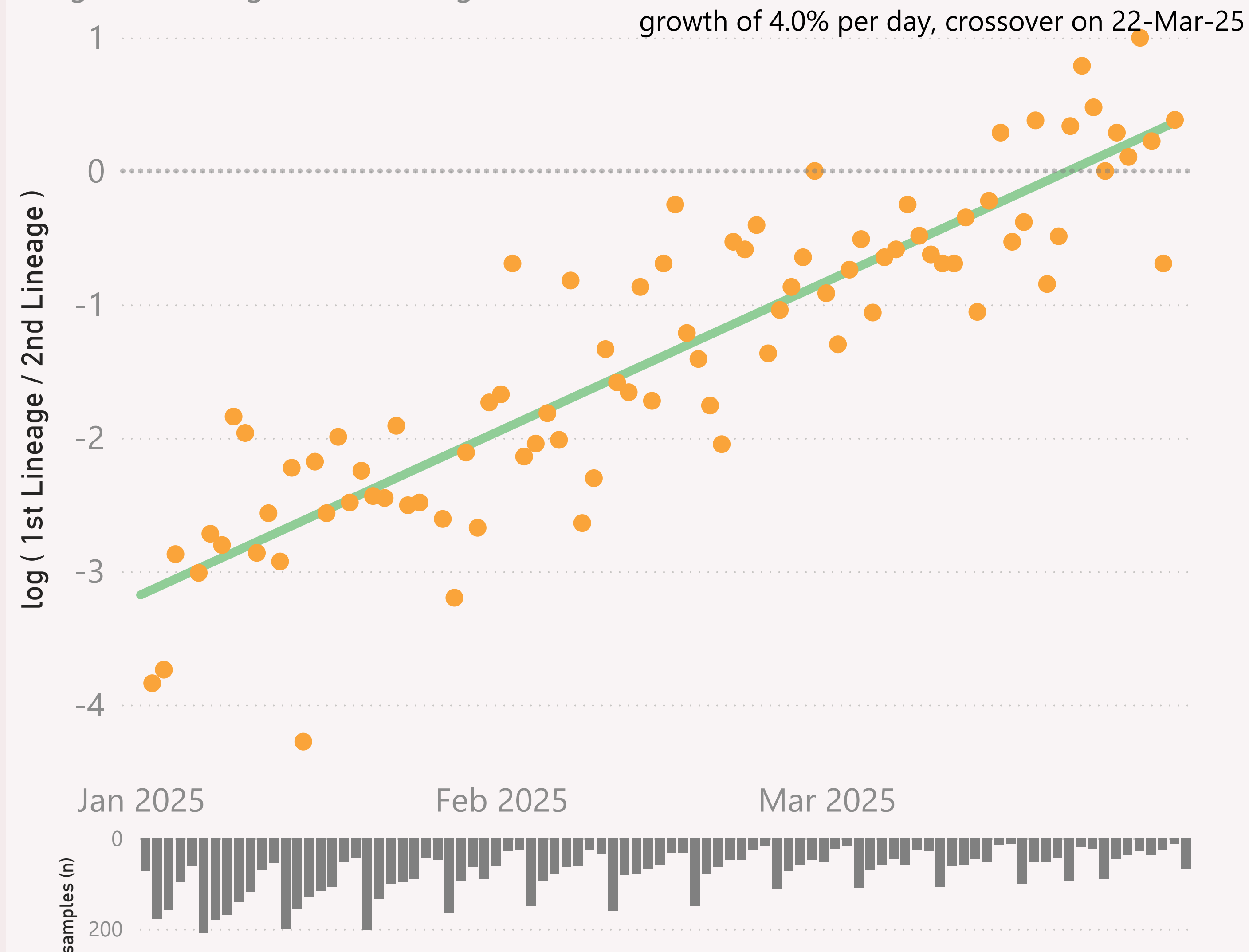
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=7,119 sequenced genomes, up to 11 April 2025

LP.8.1.*

Denmark France Germany Ireland Italy Netherlands Spain

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=7,119 sequenced genomes, up to 11 April 2025

LP.8.1

France　Germany　Ireland　Italy　Netherlands　Slovenia　Spain

This page shows the frequency of a selected Lineage of interest, for the 7 countries reporting the most samples over recent months.

The Lineage classifications are provided by Nextclade.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=6,870 sequenced genomes, up to 31 March 2025

Europe (excl UK) – LP.8.1.* vs XEC.*

● log (1st Lineage / 2nd Lineage)　● trend

growth of 4.0% per day, crossover on 22-Mar-25

This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=6,870 sequenced genomes, up to 31 March 2025

Europe (excl UK) - LP.8.1 vs XEC

● log (1st Lineage / 2nd Lineage)   ● trend

growth of 2.9% per day
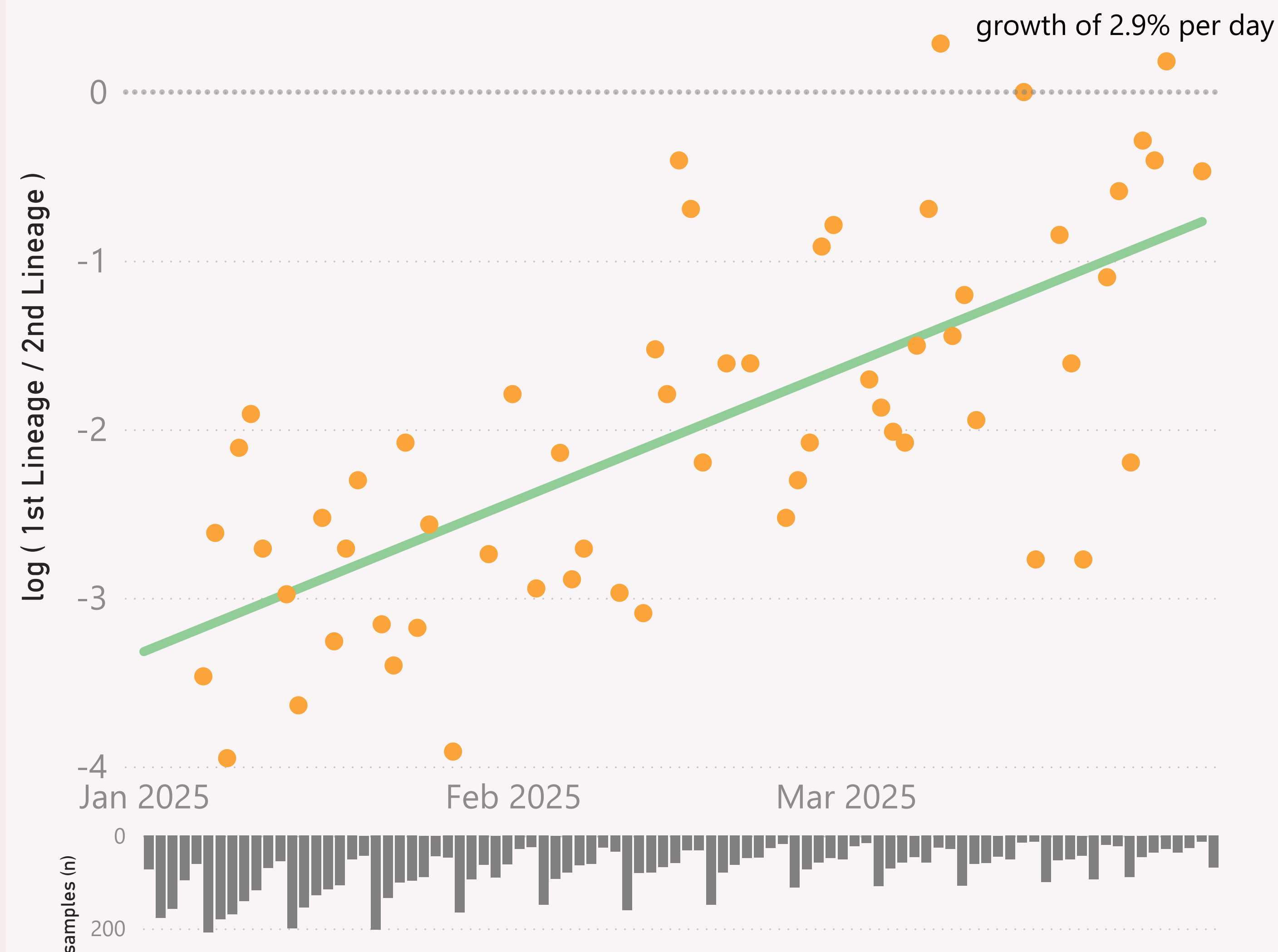
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the incumbent Lineage.

The Lineage classifications are provided by Nextclade.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

COVID-19 Genomic Sequencing sankey diagram. Data from gisaid.org, with nextclade lineages. Source files and more info on github.

Last Update: 2025-05-03 09:53 (UTC)

n=7,138 sequenced genomes, up to 11 April 2025

Europe (excl UK)

This page shows the hierarchy of the significant Lineages, over recent months.
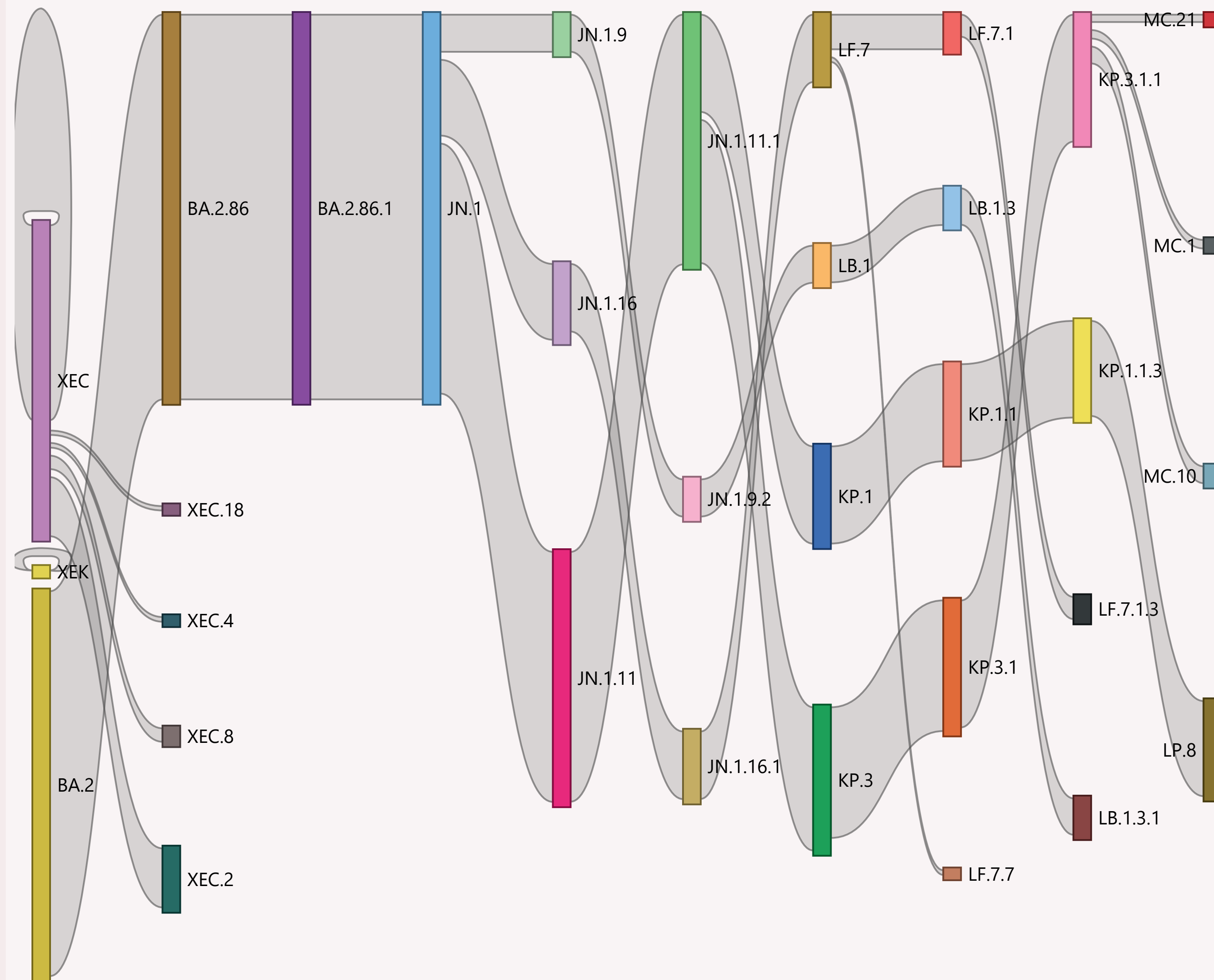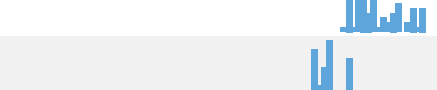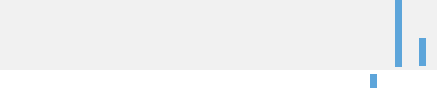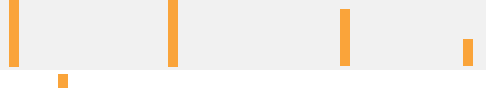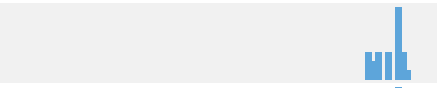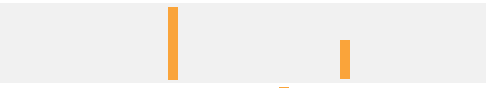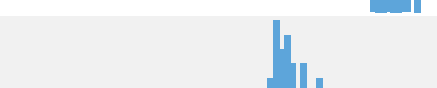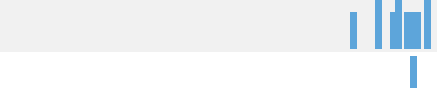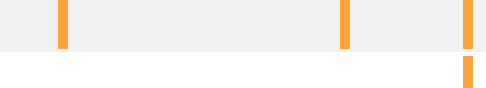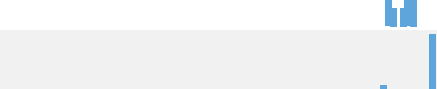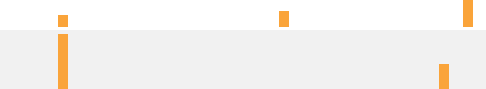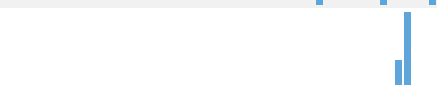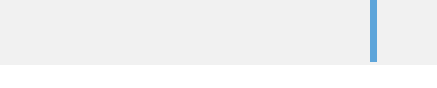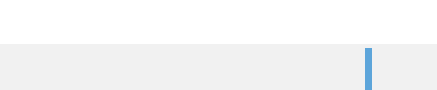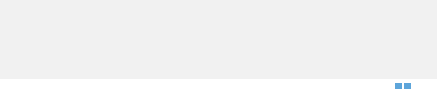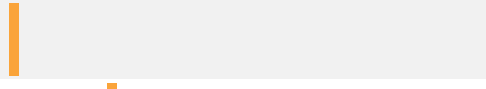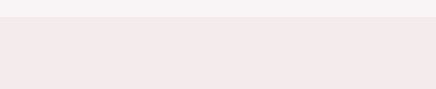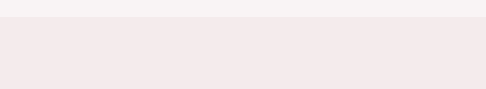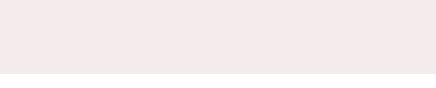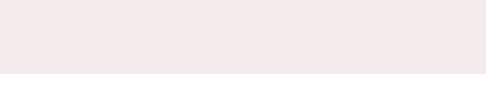
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

The full picture is typically quite busy, so insignificant Lineages (with few samples, or at the extreme top or bottom of the hierarchy) are not shown.

The Lineage classifications are provided by Nextclade.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2025-05-03 09:53 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ France	1,253	11/04/2025		19/04/2025	
⊞ Spain	868	11/04/2025		19/04/2025	
⊞ Luxembourg	390	01/04/2025		16/04/2025	
⊞ Greece	321	04/04/2025		15/04/2025	
⊞ Germany	312	11/04/2025		19/04/2025	
⊞ Denmark	278	07/04/2025		19/04/2025	
⊞ Italy	232	10/04/2025		19/04/2025	
⊞ Netherlands	169	11/04/2025		19/04/2025	
⊞ Russia	148	19/03/2025		29/03/2025	
⊞ Finland	131	24/03/2025		09/04/2025	
⊞ Norway	123	21/03/2025		04/04/2025	
⊞ Ireland	113	11/04/2025		19/04/2025	
⊞ Sweden	98	25/03/2025		15/04/2025	
⊞ Czechia	74	09/12/2024		24/03/2025	
⊞ Croatia	69	21/03/2025		10/04/2025	
⊞ Belgium	48	05/04/2025		19/04/2025	
⊞ Slovenia	44	26/03/2025		19/04/2025	
⊞ Poland	38	11/04/2025		17/04/2025	
⊞ Portugal	15	17/03/2025		01/04/2025	
⊞ Switzerland	7	28/02/2025		31/03/2025	
⊞ Serbia	6	09/01/2025		04/04/2025	
⊞ Slovakia	5	11/03/2025		19/04/2025	
⊞ Hungary	4	28/01/2025		25/03/2025	
⊞ Lithuania	2	14/02/2025		13/03/2025	
⊞ Romania	2	14/03/2025		21/03/2025	
Total	**4,750**	**11/04/2025**		**19/04/2025**	

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks, for the countries sharing the most samples.

Each sample shared comes with a Collection date - when the PCR test for that sample was collected. The GISAID system also records a Submission date for each sample, which is typically the date that sample was uploaded.

The latest date of each type is shown, along with "sparkline"-style mini charts to give a flavour for the spread of recent data by Collection date and by Submission date.