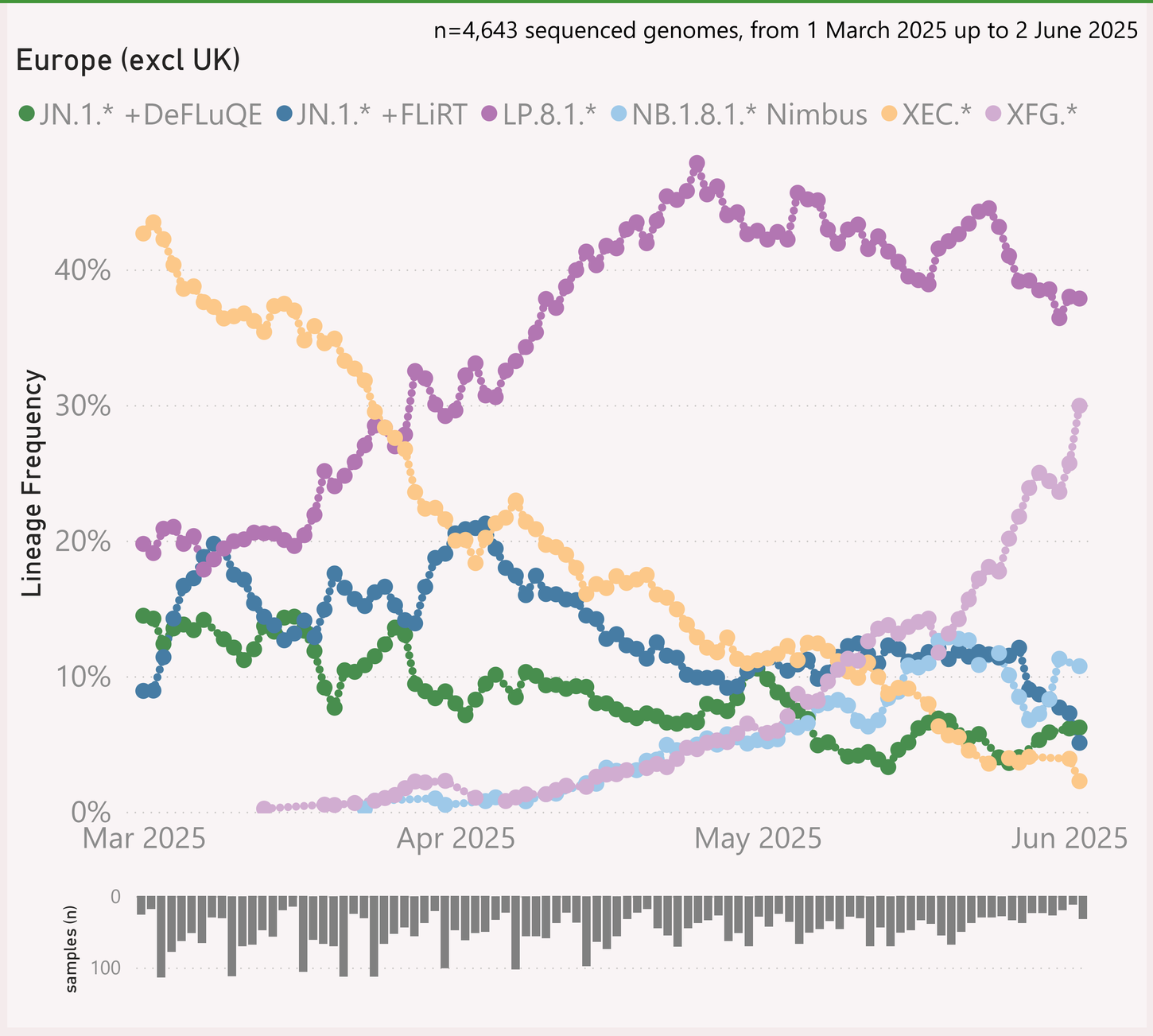


This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.

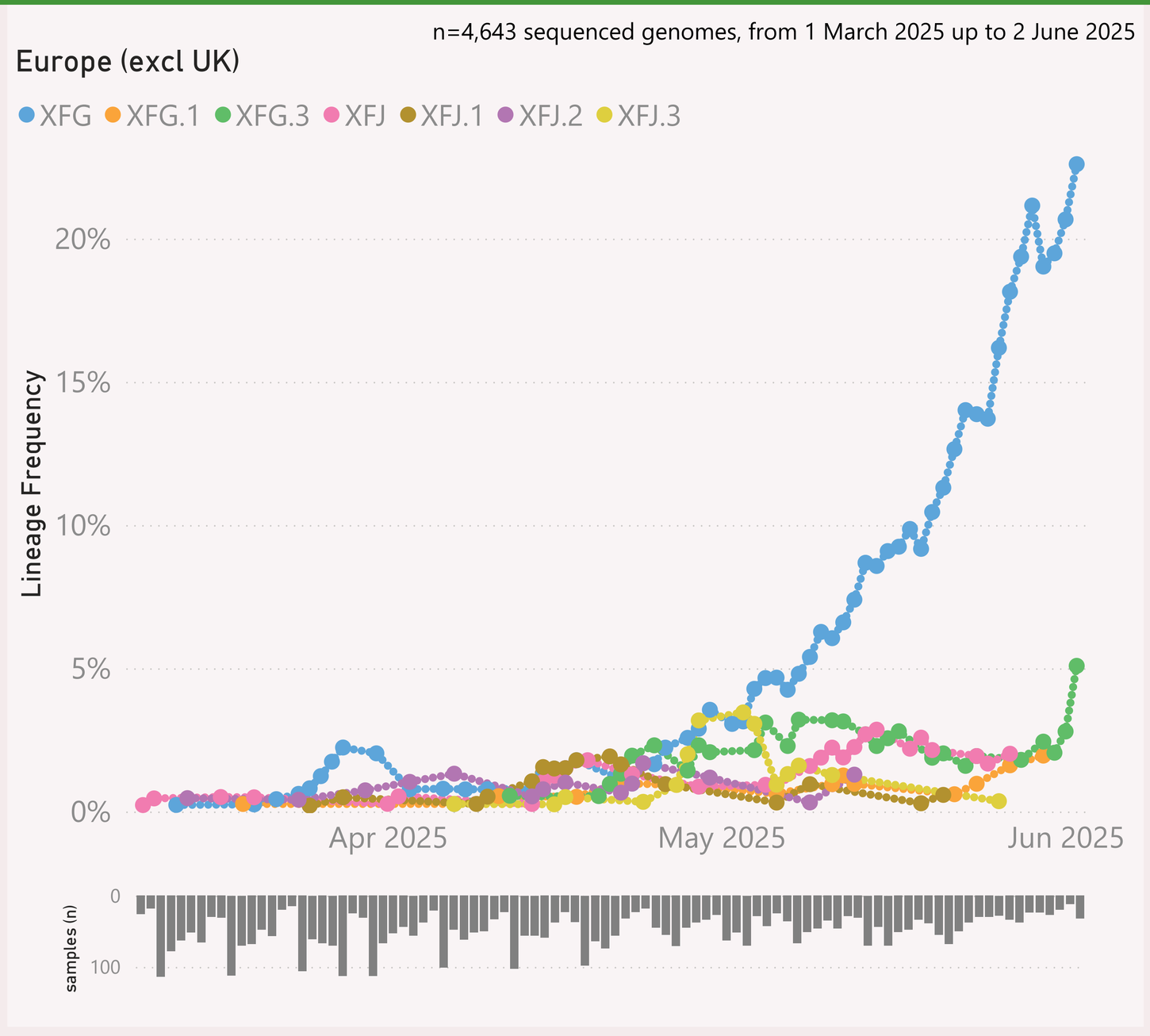
The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

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=4,643 sequenced genomes, from 1 March 2025 up to 2 June 2025



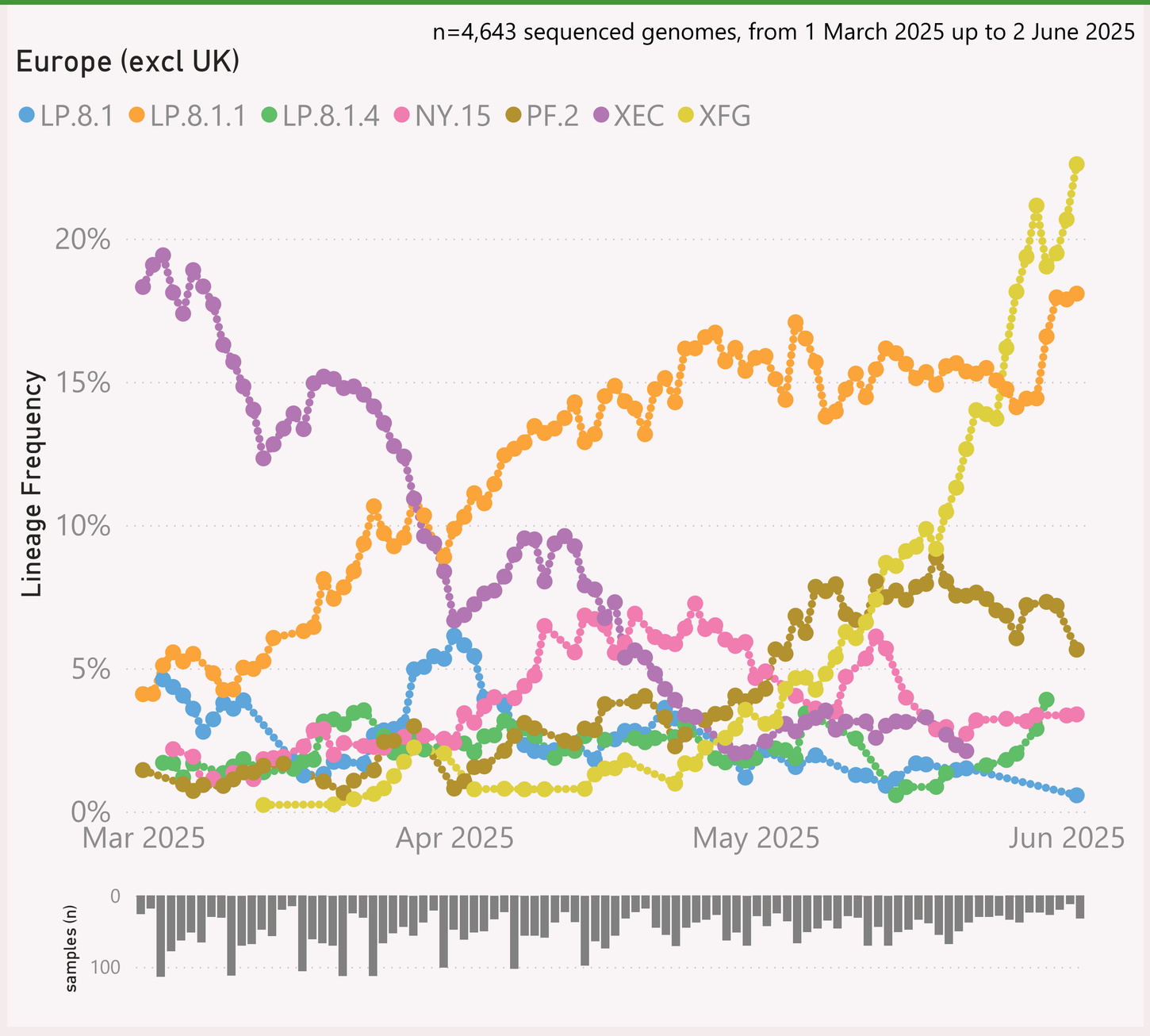
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "XFG.*" and "XFJ.*".

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.



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.

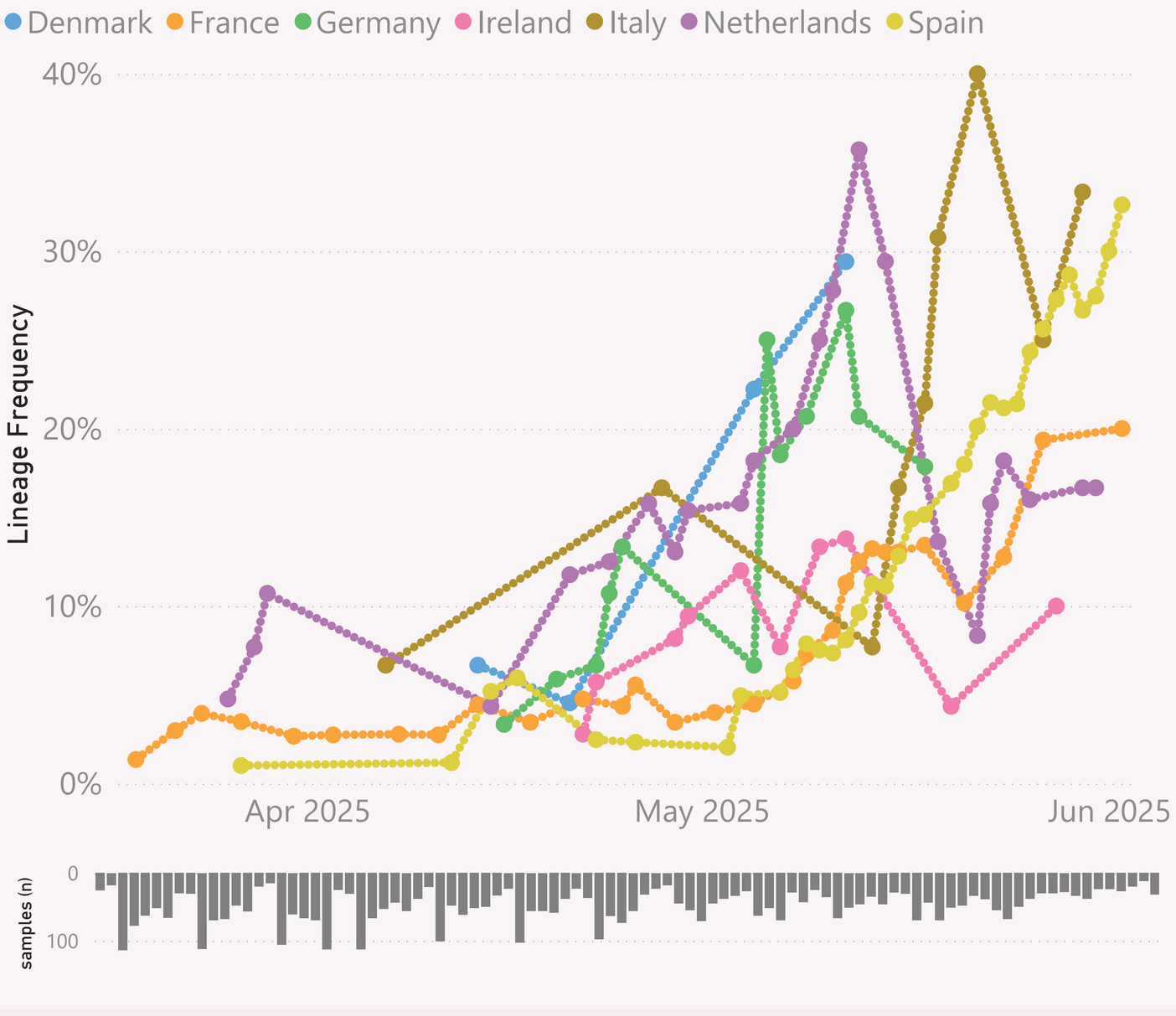
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

COVID-19 Genomic Sequencing analysis - top Countries for a Lineage L2. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-06-14 02:24 (UTC)

n=4,643 sequenced genomes, from 1 March 2025 up to 2 June 2025

XFG.*



Date

01/03/2025 31/12/2025

Continent, Country, Location

Multiple selections

Lineage L2

XFG.*

Host

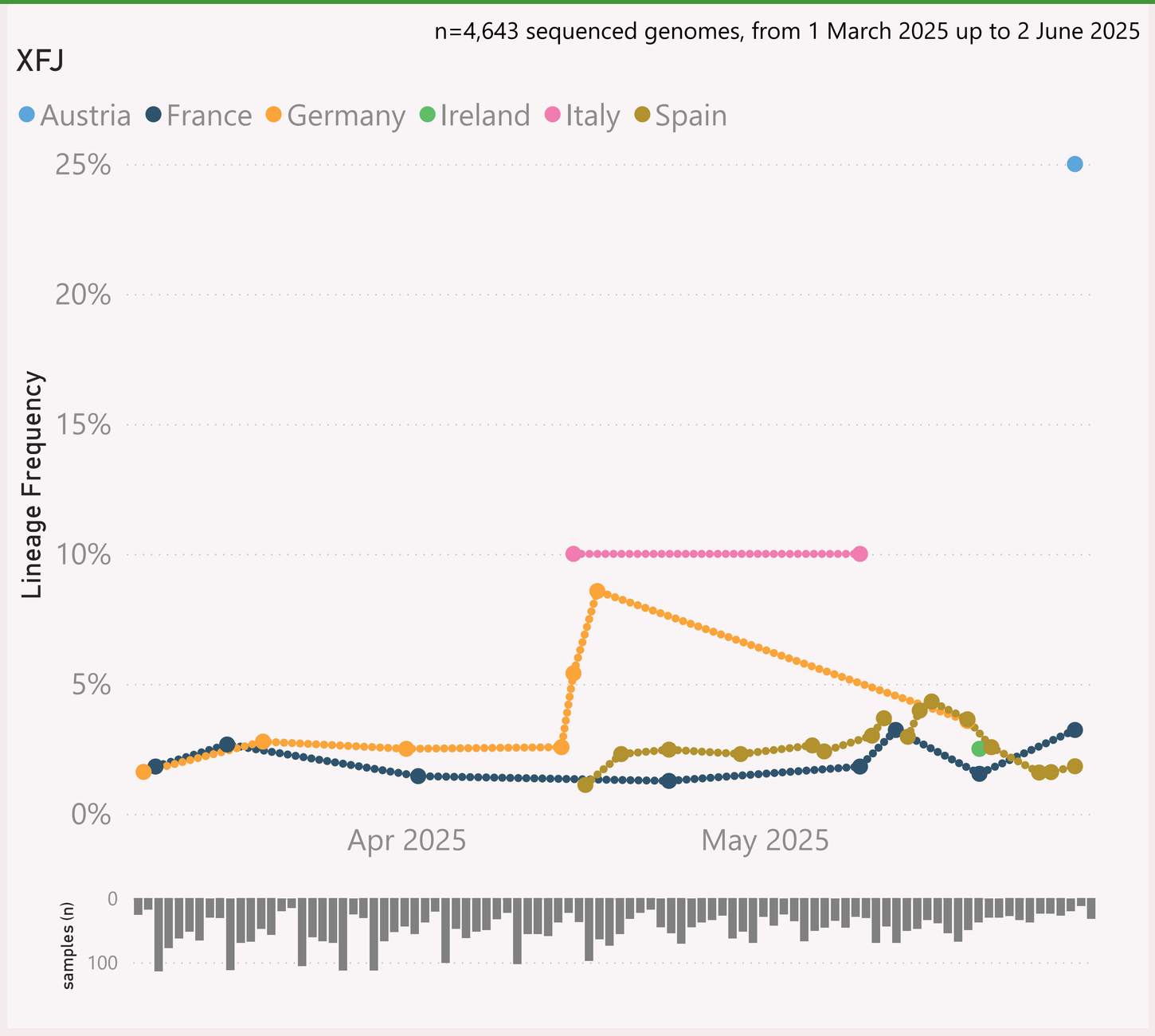
Human

Samples Sequenced (gisaid)

272

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
France	Auvergne-Rho...		02/06/2025	XFG.*	XFG
France	Auvergne-Rho...		02/06/2025	XFG.*	XFG.3
Spain	Basque Country		02/06/2025	XFG.*	XFG
Spain	Basque Country		02/06/2025	XFG.*	XFG.3
Spain	Catalunya		02/06/2025	XFG.*	XFG
Spain	Basque Country		01/06/2025	XFG.*	XFG
Spain	Basque Country		01/06/2025	XFG.*	XFG.3
Spain	Catalunya		01/06/2025	XFG.*	XFG
Spain	Catalunya		31/05/2025	XFG.*	XFG
Spain	Catalunya		31/05/2025	XFG.*	XFG.3
Netherlands	Noord-Brabant		31/05/2025	XFG.*	XFG
Italy			30/05/2025	XFG.*	XFG
Spain	Asturias		30/05/2025	XFG.*	XFG.1
Spain	Asturias		30/05/2025	XFG.*	XFG.3
Spain	Basque Country		30/05/2025	XFG.*	XFG
Netherlands	Overijssel		30/05/2025	XFG.*	XFG.3
Spain	Asturias		29/05/2025	XFG.*	XFG
Spain	Basque Country		29/05/2025	XFG.*	XFG
Spain	Catalunya		29/05/2025	XFG.*	XFG
Spain	Basque Country		28/05/2025	XFG.*	XFG
Spain	Catalunya		28/05/2025	XFG.*	XFG
Ireland	Dublin		28/05/2025	XFG.*	XFG.3

Total



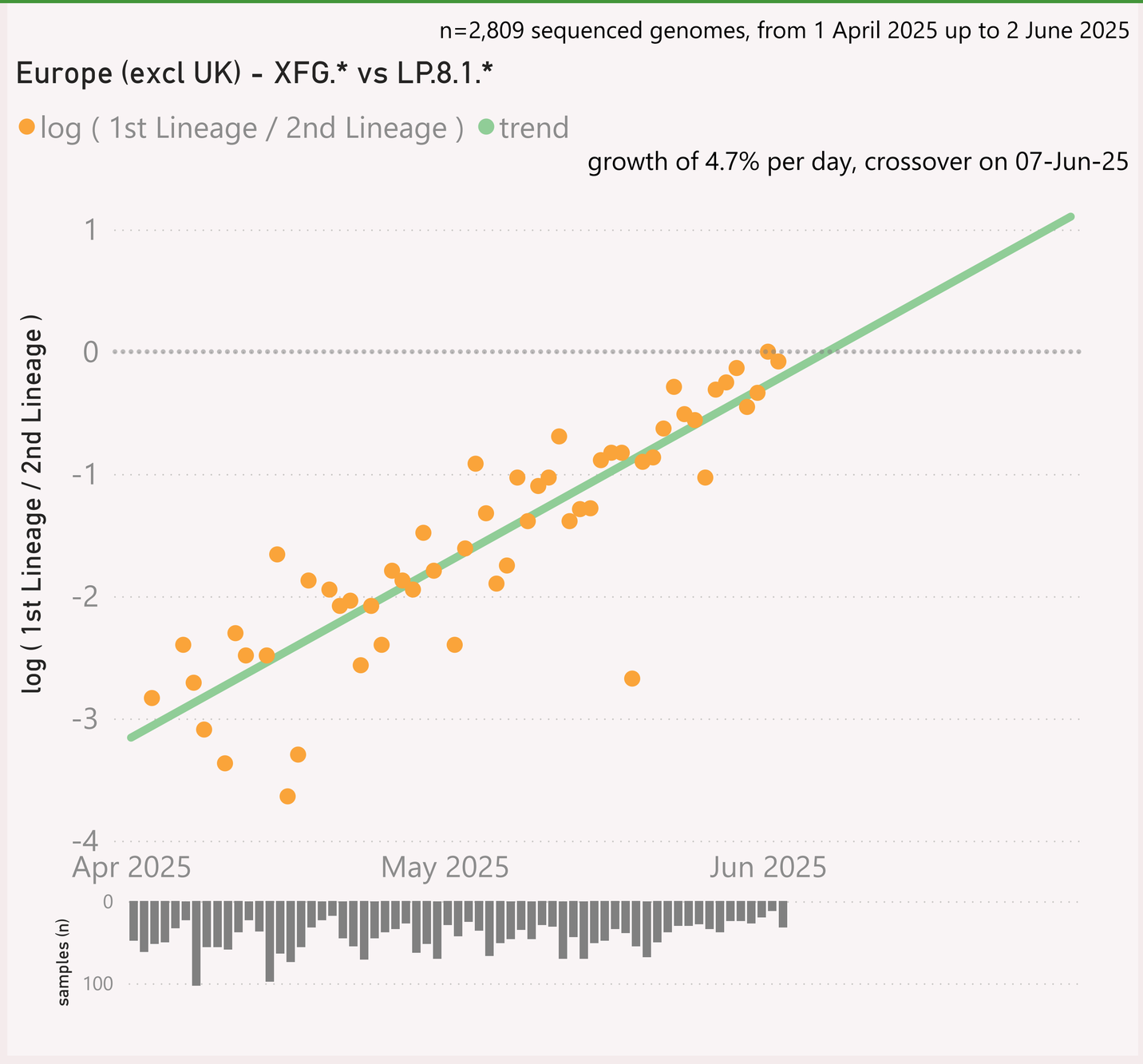
This page shows the frequency of a selected Lineage of interest, for the 7 countries reporting the most samples over recent months.

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.



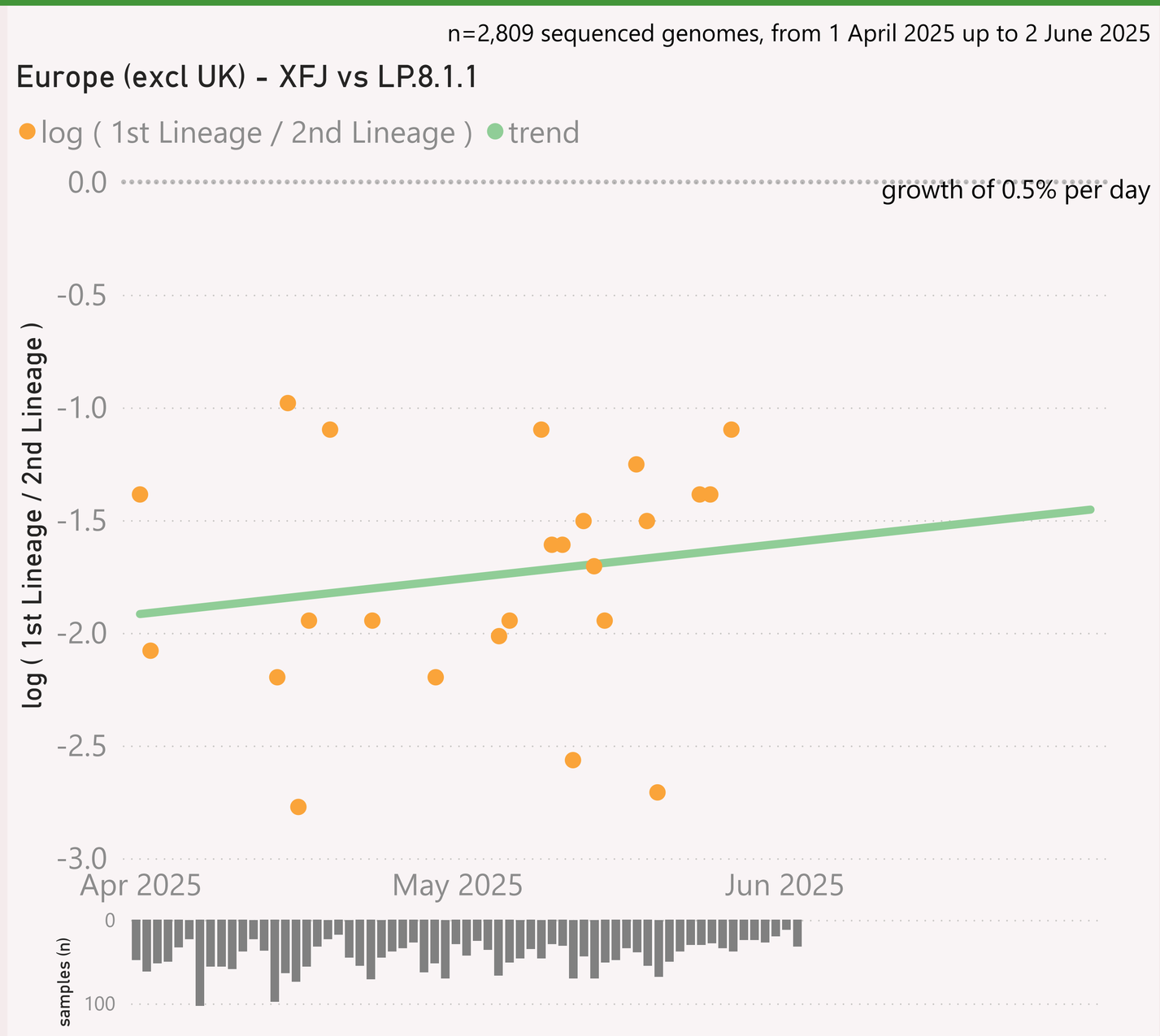
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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=2,809 sequenced genomes, from 1 April 2025 up to 2 June 2025



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

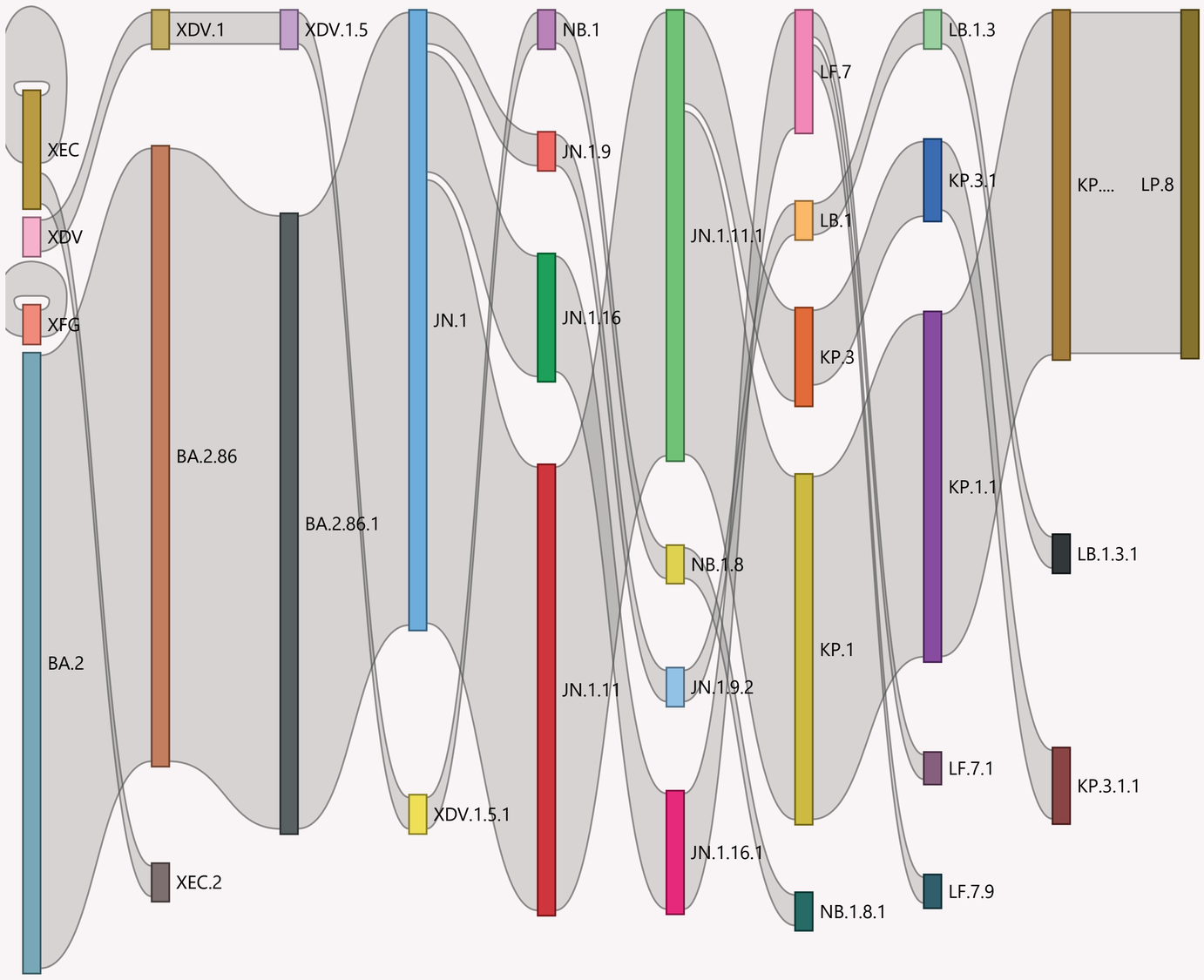
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

n=4,643 sequenced genomes, from 1 March 2025 up to 2 June 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: 2025-06-14 02:24 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
France	1,413	02/06/2025		28/05/2025	
Spain	1,333	02/06/2025		28/05/2025	
Ireland	300	28/05/2025		28/05/2025	
Italy	179	30/05/2025		28/05/2025	
Germany	170	27/05/2025		28/05/2025	
Netherlands	166	02/06/2025		28/05/2025	
Denmark	151	12/05/2025		28/05/2025	
Norway	139	15/05/2025		28/05/2025	
Sweden	104	31/05/2025		28/05/2025	
Russia	71	15/04/2025		17/05/2025	
Belgium	48	15/05/2025		28/05/2025	
Switzerland	47	20/05/2025		28/05/2025	
Finland	42	05/05/2025		19/05/2025	
Portugal	40	14/04/2025		26/05/2025	
Slovenia	37	11/05/2025		21/05/2025	
Poland	24	22/04/2025		28/05/2025	
Lithuania	9	04/04/2025		08/05/2025	
Austria	7	27/05/2025		28/05/2025	
Croatia	7	11/04/2025		14/05/2025	
Slovakia	1	11/03/2025		22/04/2025	
Total	**4,288**	**02/06/2025**		**28/05/2025**	

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.