

2017-2018 Influenza Season Week 2 ending January 13, 2018

All data are preliminary and may change as more reports are received.

Synopsis: During week 2 (January 7-13, 2018), influenza activity increased in the United States.

- **Viral Surveillance:** The most frequently identified influenza virus subtype reported by public health laboratories during week 2 was influenza A(H3). The percentage of respiratory specimens testing positive for influenza in clinical laboratories increased.
- **Pneumonia and Influenza Mortality:** The proportion of deaths attributed to pneumonia and influenza (P&I) was above the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- **Influenza-associated Pediatric Deaths:** Ten influenza-associated pediatric deaths were reported.
- **Influenza-associated Hospitalizations:** A cumulative rate of 31.5 laboratory-confirmed influenza-associated hospitalizations per 100,000 population was reported.
- **Outpatient Illness Surveillance:** The proportion of outpatient visits for influenza-like illness (ILI) was 6.3%, which is above the national baseline of 2.2%. All 10 regions reported ILI at or above region-specific baseline levels. New York City, Puerto Rico, and 32 states experienced high ILI activity; 9 states experienced moderate ILI activity; the District of Columbia and six states experienced low ILI activity; and three states experienced minimal ILI activity.
- **Geographic Spread of Influenza:** The geographic spread of influenza in Puerto Rico and 49 states was reported as widespread; Guam reported regional activity; the District of Columbia and one state reported local activity; and the U.S. Virgin Islands reported sporadic activity.

National and Regional Summary of Select Surveillance Components

HHS Surveillance Regions*	Data for current week			Data cumulative since October 1, 2017 (week 40)						
	Out-patient ILI†	Number of jurisdictions reporting regional or widespread activity	% respiratory specimens positive for flu in clinical laboratories‡	A(H1N1) pdm09	A(H3)	A (Subtyping not performed)	B Victoria lineage	B Yamagata lineage	B lineage not performed	Pediatric Deaths
Nation	Elevated	51 of 54	25.6%	1,219	12,489	219	123	1,366	620	30
Region 1	Elevated	6 of 6	16.9%	32	475	1	3	49	1	0
Region 2	Elevated	3 of 4	19.3%	42	528	4	0	47	43	2
Region 3	Elevated	5 of 6	23.1%	216	959	1	11	175	31	1
Region 4	Elevated	8 of 8	22.4%	213	798	45	3	86	94	6
Region 5	Elevated	6 of 6	26.5%	176	2,805	25	17	204	47	5
Region 6	Elevated	5 of 5	28.7%	181	679	16	2	106	73	6
Region 7	Elevated	4 of 4	25.0%	17	621	26	0	134	2	0
Region 8	Elevated	6 of 6	23.5%	52	1,117	13	7	165	7	0
Region 9	Elevated	4 of 5	30.3%	178	3,787	79	75	240	227	8
Region 10	Elevated	4 of 4	29.7%	112	720	9	5	160	95	2

*<http://www.hhs.gov/about/agencies/staff-divisions/iea/regional-offices/index.html>

† Elevated means the % of visits for ILI is at or above the national or region-specific baseline.

§ Includes all 50 states, the District of Columbia, Guam, Puerto Rico, and the U.S. Virgin Islands

‡ National data are for current week; regional data are for the most recent three weeks.

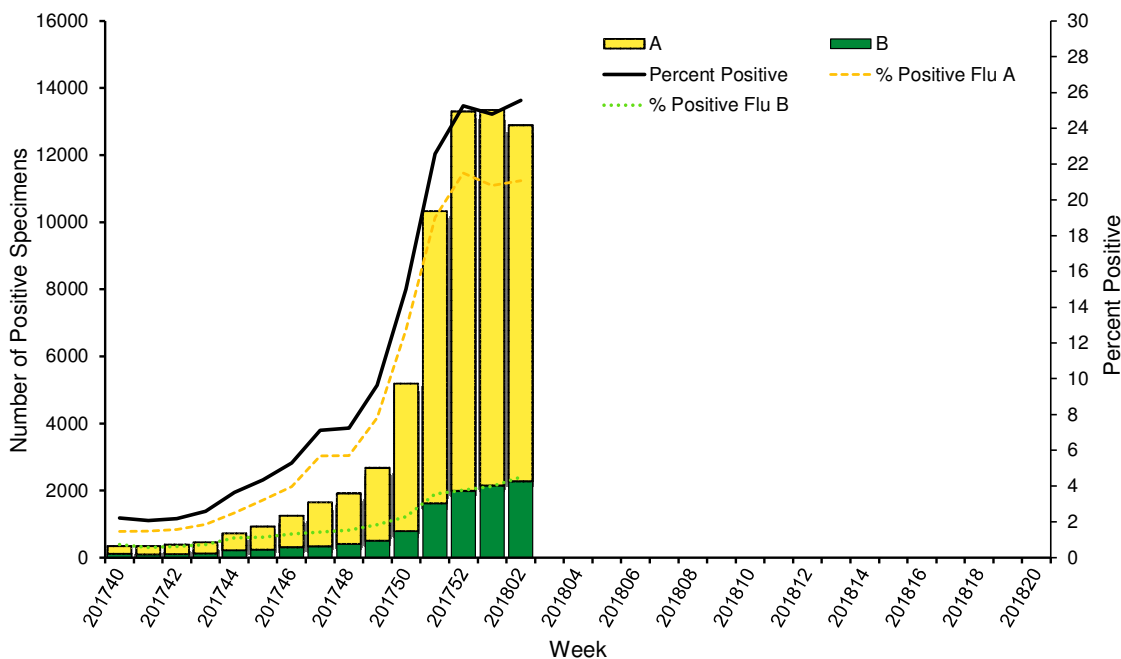
U.S. Virologic Surveillance: WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. In addition, public health laboratories also report the influenza A subtype (H1 or H3) and influenza B lineage information of the viruses they test and the age or age group of the persons from whom the specimens were collected.

Additional virologic data, including national, regional and select state-level data, can be found at: <http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>. Age group proportions and totals by influenza subtype reported by public health laboratories can be found at: http://gis.cdc.gov/grasp/fluview/flu_by_age_virus.html.

The results of tests performed by clinical laboratories are summarized below.

	Week 2	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	50,435	446,698
No. of positive specimens (%)	12,894 (25.6%)	65,735 (14.7%)
Positive specimens by type		
Influenza A	10,622 (82.4%)	54,430 (82.8%)
Influenza B	2,272 (17.6%)	11,305 (17.2%)

Influenza Positive Tests Reported to CDC by U.S. Clinical Laboratories, National Summary, 2017-2018 Season

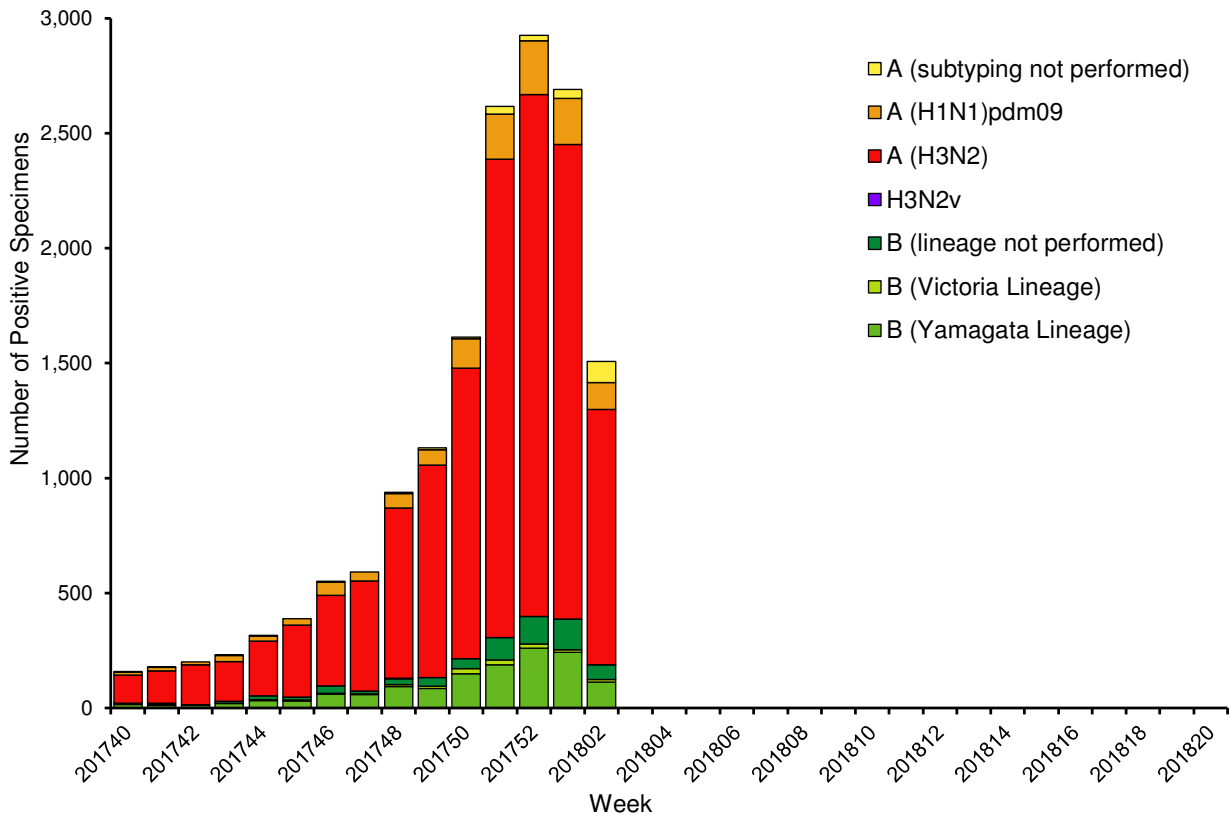


The results of tests performed by public health laboratories, as well as the age group distribution of influenza positive tests, are summarized below.

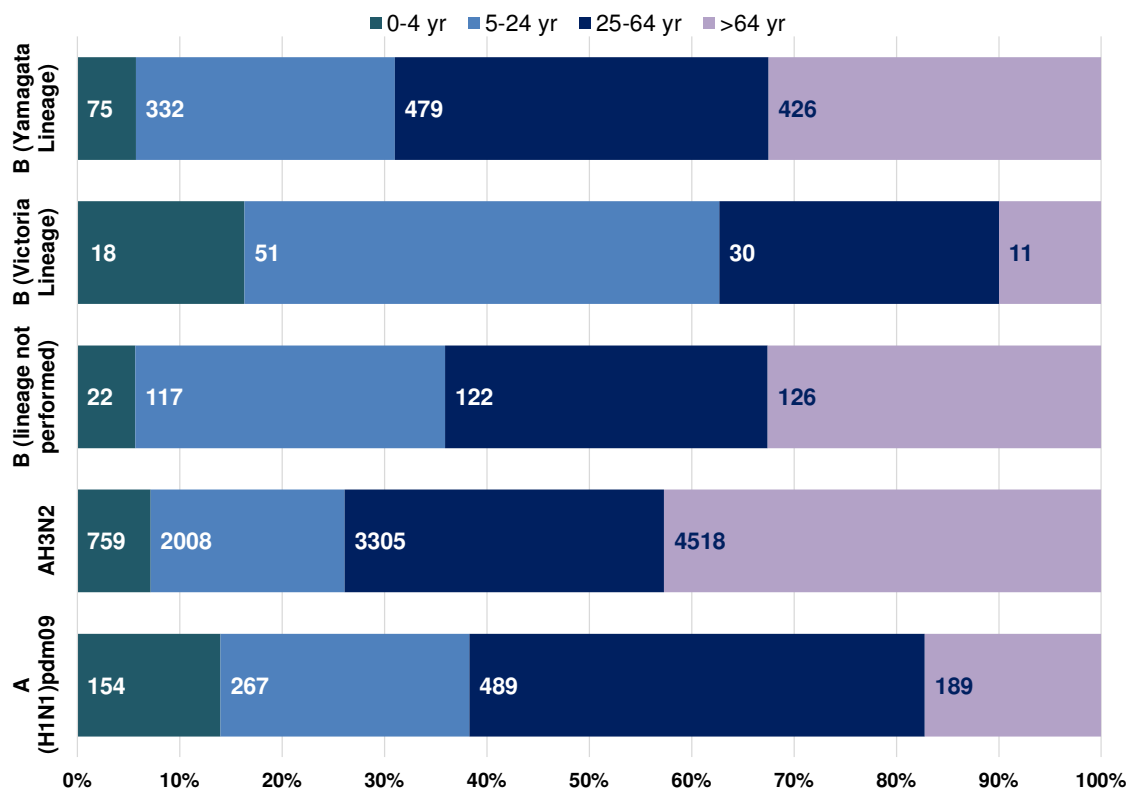
	Week 2	Data Cumulative since October 1, 2017 (Week 40)
No. of specimens tested	2,242	33,651
No. of positive specimens*	1,507	16,036
Positive specimens by type/subtype		
Influenza A	1,319 (87.5%)	13,927 (86.8%)
(H1N1)pdm09	118 (8.9%)	1,219 (8.8%)
H3N2	1,111 (84.2%)	12,489 (89.7%)
Subtyping not performed	90 (6.8%)	219 (1.6%)
Influenza B	188 (12.5%)	2,109 (13.2%)
Yamagata lineage	112 (59.6%)	1,366 (64.8%)
Victoria lineage	11 (5.9%)	123 (5.8%)
Lineage not performed	65 (34.6%)	620 (29.4%)

*The percent of specimens testing positive for influenza is not reported because public health laboratories often receive samples that have already tested positive for influenza at a clinical laboratory and therefore percent positive would not be a valid indicator of influenza activity. Additional information is available at <http://www.cdc.gov/flu/weekly/overview.htm>

Influenza Positive Tests Reported to CDC by U.S. Public Health Laboratories, National Summary, 2017-2018 Season



Age Group Proportions and Totals by Influenza Subtype Reported by Public Health Laboratories, 2017-2018 Season



Influenza Virus Characterization: Close monitoring of influenza viruses is required to better assess the potential impact on public health. CDC characterizes influenza viruses through one or more tests including [genomic sequencing](#) and [antigenic characterization](#) (i.e., hemagglutination inhibition (HI) and/or neutralization assays). These data are used to monitor for changes in circulating influenza viruses and to compare how similar currently circulating influenza viruses are to the reference viruses used for developing influenza vaccines. Antigenic and genetic characterization of circulating influenza viruses can give an indication of the influenza vaccine's ability to produce an immune response against the wide array of influenza viruses co-circulating, but annual [vaccine effectiveness studies](#) are needed to determine how much protection has been provided to the population by vaccination.

For nearly all influenza-positive surveillance samples received at CDC, next-generation sequencing is performed to determine the genetic identity of circulating influenza viruses and to monitor viruses for evidence of genetic changes. Viruses are classified into genetic clades/subclades based on analysis of the genetic sequences of the HA gene segments. However, genetic changes do not always result in antigenic change. Extensive genetic variation may exist in circulating viruses, with no evidence of substantial antigenic drift. Antigenic drift is evaluated by comparing cell-propagated circulating viruses with cell-propagated reference viruses representing currently recommended vaccine components.

CDC has antigenically or genetically characterized 893 influenza viruses collected during October 1, 2017 – January 13, 2018, and submitted by U.S. laboratories, including 146 influenza A(H1N1)pdm09 viruses, 498 influenza A(H3N2) viruses, and 249 influenza B viruses.

Influenza A Viruses

- **A(H1N1)pdm09:** Phylogenetic analysis of the HA genes from 146 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. Eighty-five A(H1N1)pdm09 viruses were antigenically characterized, and all were antigenically similar (analyzed using HI with ferret antisera) to the reference 6B.1 virus A/Michigan/45/2015, representing the recommended influenza A(H1N1)pdm09 reference virus for the 2017–18 Northern Hemisphere influenza vaccines.
- **A(H3N2):** Phylogenetic analysis of the HA genes from 498 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=406), subclade 3C.2a1 (n=87) or clade 3C.3a (n=5). One hundred ninety two influenza A(H3N2) viruses were antigenically characterized, and 189 (98.4%) A(H3N2) viruses tested were well-inhibited (reacting at titers that were within fourfold of the homologous virus titer) by ferret antisera raised against A/Michigan/15/2014 (3C.2a), a cell propagated A/Hong Kong/4801/2014-like reference virus representing the A(H3N2) component of 2017–18 Northern Hemisphere influenza vaccines.

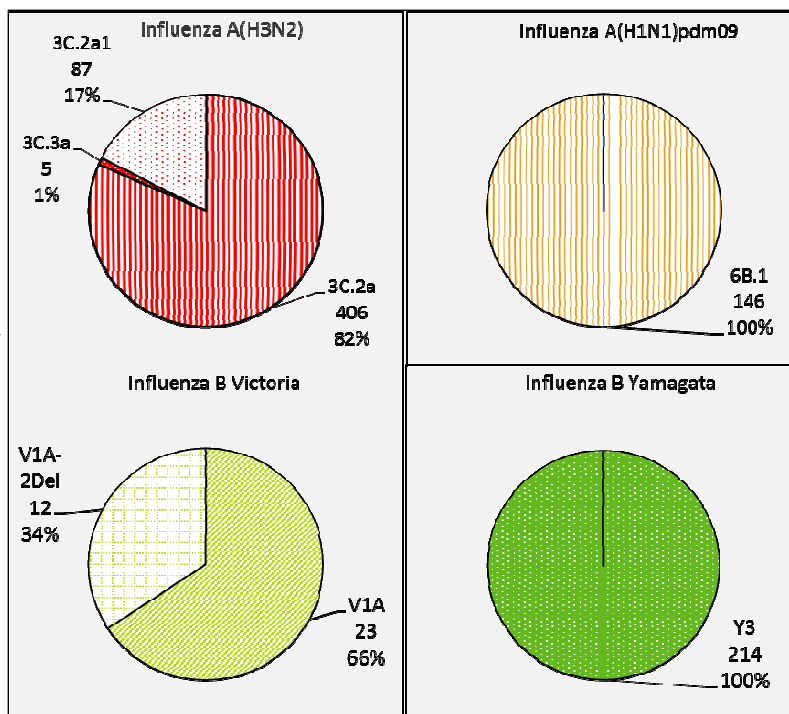
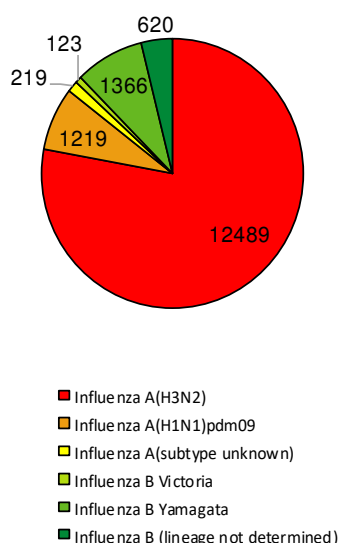
Influenza B Viruses

- **B/Victoria:** Phylogenetic analysis of 35 B/Victoria-lineage viruses indicate that all HA genes belonged to genetic clade V1A, the same genetic clade as the vaccine reference virus, B/Brisbane/60/2008. However, a small number of viruses had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). Fifteen (71.4%) B/Victoria lineage viruses were well-inhibited by ferret antisera raised against cell - propagated B/Brisbane/60/2008 reference virus, representing a recommended B virus component of 2017–18 Northern Hemisphere influenza vaccines. Six (28.6%) B/Victoria lineage viruses reacted poorly (at titers that were 8-fold or greater reduced compared with the homologous virus titer) with ferret antisera raised against cell-propagated B/Brisbane/60/2008, and these viruses had the V1A-2Del HA.
- **B/Yamagata:** Phylogenetic analysis of 214 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 152 influenza B/Yamagata-lineage viruses were antigenically characterized, and all were antigenically similar to cell propagated B/Phuket/3073/2013, the reference vaccine virus representing the influenza B/Yamagata-lineage component of the 2017–18 Northern Hemisphere quadrivalent vaccines.

The majority of U.S. viruses submitted for characterization come from state and local public health laboratories. Due to [Right Size Roadmap](#) considerations, specimen submission guidance to laboratories is that, if available, 2 influenza A(H1N1)pdm09, 2 influenza A(H3N2), and 2 influenza B viruses be submitted every other week. Therefore, the numbers of each virus type/subtype characterized should be more balanced across subtypes/lineages but will not reflect the actual proportion of circulating viruses. In the figure below, the results of tests performed by public health labs are shown on the left and CDC sequence results (by genetic clade/subclade) are shown on the right.

Sequence Results, by Genetic HA Clade/Subclade, of Specimens Submitted to CDC by U.S. Public Health Laboratories, Cumulative, 2017-2018 Season

Influenza Positive Specimens Reported by U.S. Public Health Laboratories, Cumulative, 2017-2018 season



Antiviral Resistance: Testing of influenza A(H1N1)pdm09, influenza A(H3N2), and influenza B virus isolates for resistance to neuraminidase inhibitors (oseltamivir, zanamivir, and peramivir) is performed at CDC using a functional assay. Additional influenza A(H1N1)pdm09 and influenza A(H3N2) viruses from clinical samples are tested for mutations known to confer oseltamivir resistance. The data summarized below combine the results of both testing methods. These samples are routinely obtained for surveillance purposes rather than for diagnostic testing of patients suspected to be infected with antiviral-resistant virus.

High levels of resistance to the adamantanes (amantadine and rimantadine) persist among influenza A(H1N1)pdm09 and influenza A(H3N2) viruses (the adamantanes are not effective against influenza B viruses). Therefore, data from adamantane resistance testing are not presented below.

Neuraminidase Inhibitor Resistance Testing Results on Samples Collected Since October 1, 2017

	Oseltamivir		Zanamivir		Peramivir	
	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)	Virus Samples tested (n)	Resistant Viruses, Number (%)
Influenza A (H1N1)pdm09	168	2 (1.2)	146	0 (0.0)	168	2 (1.2)
Influenza A (H3N2)	587	0 (0.0)	587	0 (0.0)	456	0 (0.0)
Influenza B	209	0 (0.0)	209	0 (0.0)	209	0 (0.0)

On December 27, 2017, a Health Advisory was released by CDC providing: 1) a notice about increased influenza A(H3N2) activity and its clinical implications; 2) a summary of influenza antiviral drug treatment recommendations; 3) an update about approved treatment drugs and supply this season; and 4) background information for patients about influenza treatment. More information is available at <https://emergency.cdc.gov/han/han00409.asp>.

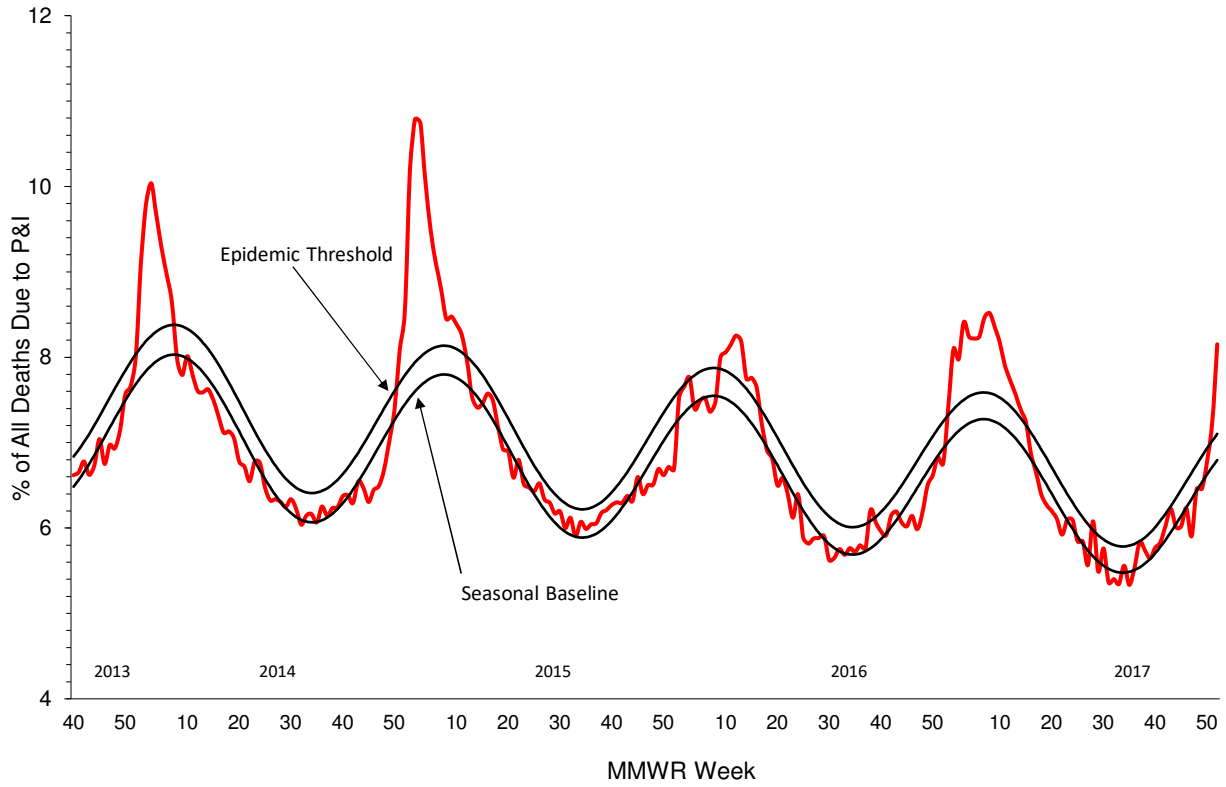
The majority of recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications, oseltamivir, zanamivir, and peramivir; however, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A(H1N1)pdm09 viruses and oseltamivir-resistant influenza A(H3N2) viruses have been detected worldwide. Antiviral treatment as early as possible is recommended for patients with confirmed or suspected influenza who have severe, complicated, or progressive illness; who require hospitalization; or who are at [high risk](#) for serious influenza-related complications. Additional information on recommendations for treatment and chemoprophylaxis of influenza virus infection with antiviral agents is available at <http://www.cdc.gov/flu/antivirals/index.htm>.

[Pneumonia and Influenza \(P&I\) Mortality Surveillance](#): Based on National Center for Health Statistics (NCHS) mortality surveillance data available on January 18, 2018, 8.2% of the deaths occurring during the week ending December 30, 2017 (week 52) were due to P&I. This percentage is above the epidemic threshold of 7.1% for week 52.

Background: Weekly mortality surveillance data include a combination of machine coded and manually coded causes of death collected from death certificates. Percentages of deaths due to P&I are higher among manually coded records than more rapidly available machine coded records. Due to the additional time needed for manual coding, the initially reported P&I percentages may be lower than percentages calculated from final data. Previous longer backlogs in manual coding have been resolved and death records are now coded within 10 days from receipt of a death record by NCHS.

Region and state-specific data are available at <http://gis.cdc.gov/grasp/fluview/mortality.html>.

Pneumonia and Influenza Mortality from
the National Center for Health Statistics Mortality Surveillance System
Data through the week ending December 30, 2017, as of January 18, 2018

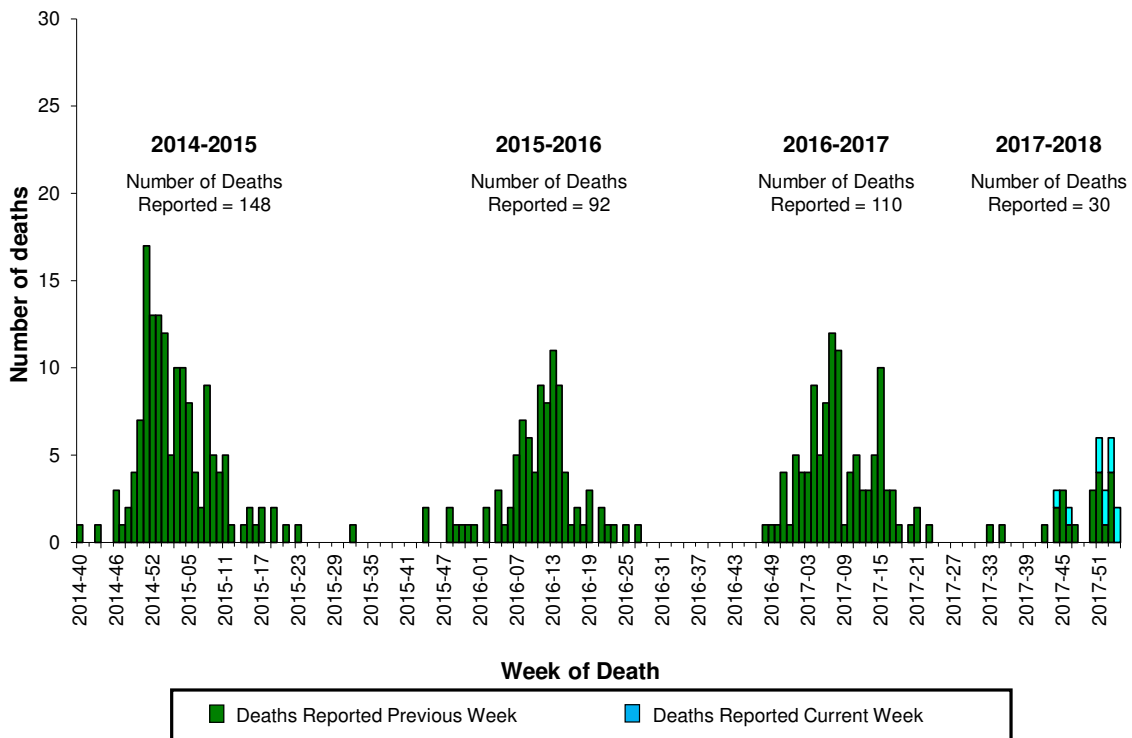


Influenza-Associated Pediatric Mortality: Ten influenza-associated pediatric deaths were reported to CDC during week 2. Four deaths were associated with an influenza A(H1N1)pdm09 virus and occurred during weeks 51, 1 and 2 (the weeks ending December 23, 2017, January 6, 2018, and January 13, 2018, respectively). Three deaths were associated with an influenza A virus for which no subtyping was performed and occurred during weeks 44, 46, and 52 (the weeks ending November 4, 2017, November 18, 2017, and December 30, 2017, respectively). Three deaths were associated with an influenza B virus and occurred during weeks 52, 1, and 2 (the weeks ending December 30, 2017, January 6, 2018, and January 13, 2018, respectively).

A total of 30 influenza-associated pediatric deaths have been reported for the 2017-2018 season.

Additional data can be found at: <http://gis.cdc.gov/GRASP/Fluview/PedFluDeath.html>.

Number of Influenza-Associated Pediatric Deaths by Week of Death:
2014-2015 season to present



Influenza-Associated Hospitalizations: The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza-related hospitalizations in children younger than 18 years of age (since the 2003-2004 influenza season) and adults (since the 2005-2006 influenza season).

The FluSurv-NET covers more than 70 counties in the 10 Emerging Infections Program (EIP) states (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN) and additional Influenza Hospitalization Surveillance Project (IHSP) states. The IHSP began during the 2009-2010 season to enhance surveillance during the 2009 H1N1 pandemic. IHSP sites included IA, ID, MI, OK and SD during the 2009-2010 season; ID, MI, OH, OK, RI, and UT during the 2010-2011 season; MI, OH, RI, and UT during the 2011-2012 season; IA, MI, OH, RI, and UT during the 2012-2013 season; and MI, OH, and UT during the 2013-2014, 2014-15, 2015-16, 2016-17, and 2017-18 seasons.

Data gathered are used to estimate age-specific hospitalization rates on a weekly basis, and describe characteristics of persons hospitalized with influenza illness. The rates provided are likely to be an underestimate as influenza-related hospitalizations can be missed, either because testing is not performed, or because cases may be attributed to other causes of pneumonia or other common influenza-related complications.

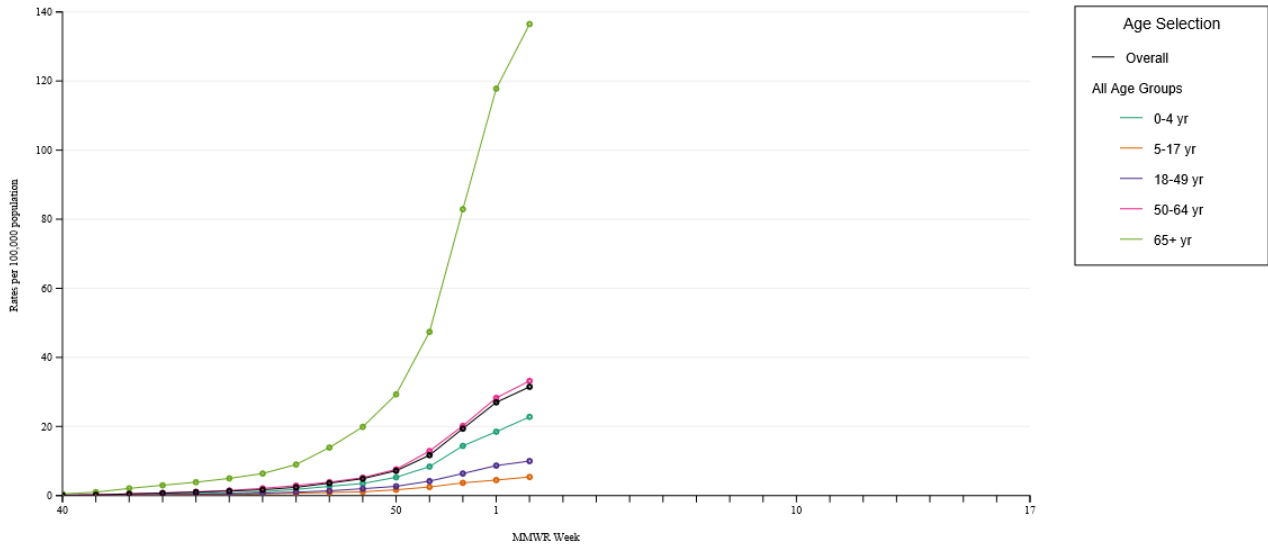
A total of 8,990 laboratory-confirmed influenza-associated hospitalizations were reported between October 1, 2017 and January 13, 2018. The overall hospitalization rate was 31.5 per 100,000 population. The highest rate of hospitalization was among adults aged ≥ 65 years (136.5 per 100,000 population), followed by adults aged 50-64 (33.2 per 100,000 population) and children aged 0-4 years (22.8 per 100,000 population). Among 8,990 hospitalizations, 8,037 (89.4%) were associated with influenza A virus, 908 (10.1%) with influenza B virus, 25 (0.3%) with influenza A virus and influenza B virus co-infection, and 20 (0.2%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 1,866 (85.8%) were A(H3N2) and 310 (14.2%) were A(H1N1)pdm09 virus.

Among 1,154 hospitalized adults with information on underlying medical conditions, 861 (74.6%) had at least one reported underlying medical condition; the most commonly reported were cardiovascular disease, metabolic disorder, obesity, and chronic lung disease. Among 129 hospitalized children with information on underlying medical conditions, 75 (58.1%) had at least one underlying medical condition; the most commonly reported were asthma, neurologic disorder, obesity, and cardiovascular disease. Among 92 hospitalized women of childbearing age (15-44 years) with information on pregnancy status, 25 (27.2%) were pregnant.

Additional FluSurv-NET data can be found at: <http://gis.cdc.gov/GRASP/Fluview/FluHospRates.html> and <http://gis.cdc.gov/grasp/fluview/FluHospChars.html>.

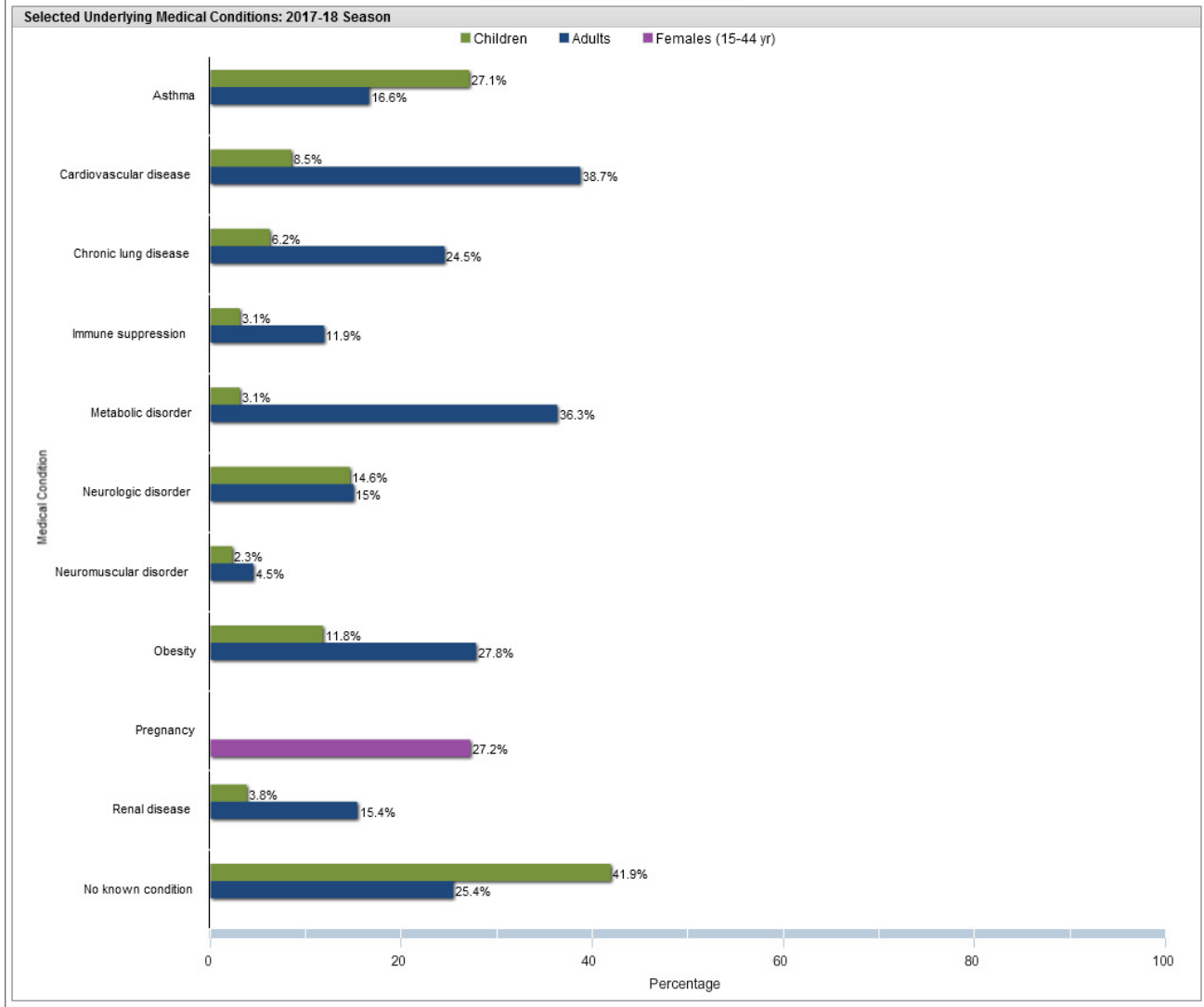
Laboratory-Confirmed Influenza Hospitalizations

Preliminary cumulative rates as of Jan 13, 2018



Data are from the Influenza Hospitalization Surveillance Network (FluSurv-NET), a population-based surveillance for influenza related hospitalizations in children and adults in 13 U.S. states. Incidence rates are calculated using the National Center for Health Statistics' (NCHS) population estimates for the counties included in the surveillance catchment area.

Laboratory-Confirmed Influenza Hospitalizations
Preliminary data as of Jan 13, 2018

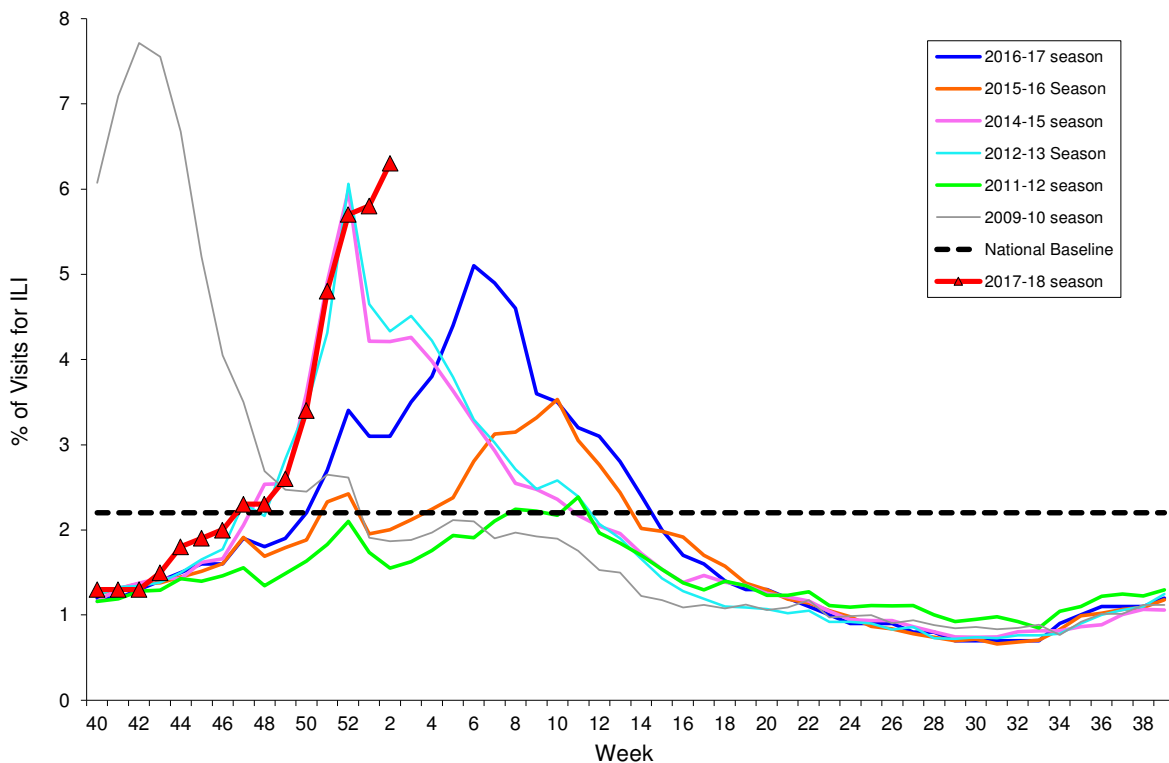


FluSurv-NET data are preliminary and displayed as they become available. Therefore, figures are based on varying denominators as some variables represent information that may require more time to be collected. Data are refreshed and updated weekly. Asthma includes a medical diagnosis of asthma or reactive airway disease; Cardiovascular diseases include conditions such as coronary heart disease, cardiac valve disorders, congestive heart failure, and pulmonary hypertension; does not include isolated hypertension; Chronic lung diseases include conditions such as chronic obstructive pulmonary disease, bronchiolitis obliterans, chronic aspiration pneumonia, and interstitial lung disease; Immune suppression includes conditions such as immunoglobulin deficiency, leukemia, lymphoma, HIV/AIDS, and individuals taking immunosuppressive medications; Metabolic disorders include conditions such as diabetes mellitus; Neurologic diseases include conditions such as seizure disorders, cerebral palsy, and cognitive dysfunction; Neuromuscular diseases include conditions such as multiple sclerosis and muscular dystrophy; Obesity was assigned if indicated in patient's medical chart or if body mass index (BMI) >30 kg/m²; Pregnancy percentage calculated using number of influenza-positive females aged between 15 and 44 years of age as the denominator; Renal diseases include conditions such as acute or chronic renal failure, nephrotic syndrome, glomerulonephritis, and impaired creatinine clearance; No known condition indicates that the person did not have any known high risk medical condition indicated in medical chart at the time of hospitalization.

Outpatient Illness Surveillance: Nationwide during week 2, 6.3% of patient visits reported through the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet) were due to influenza-like illness (ILI). This percentage is above the national baseline of 2.2%. (ILI is defined as fever (temperature of 100 °F [37.8 °C] or greater) and cough and/or sore throat.)

Additional ILINet data, including national, regional and select state-level data, are available at <http://gis.cdc.gov/grasp/fluview/fluportaldashboard.html>.

Percentage of Visits for Influenza-like Illness (ILI) Reported by the U.S. Outpatient Influenza-like Illness Surveillance Network (ILINet), Weekly National Summary, 2017-2018 and Selected Previous Seasons



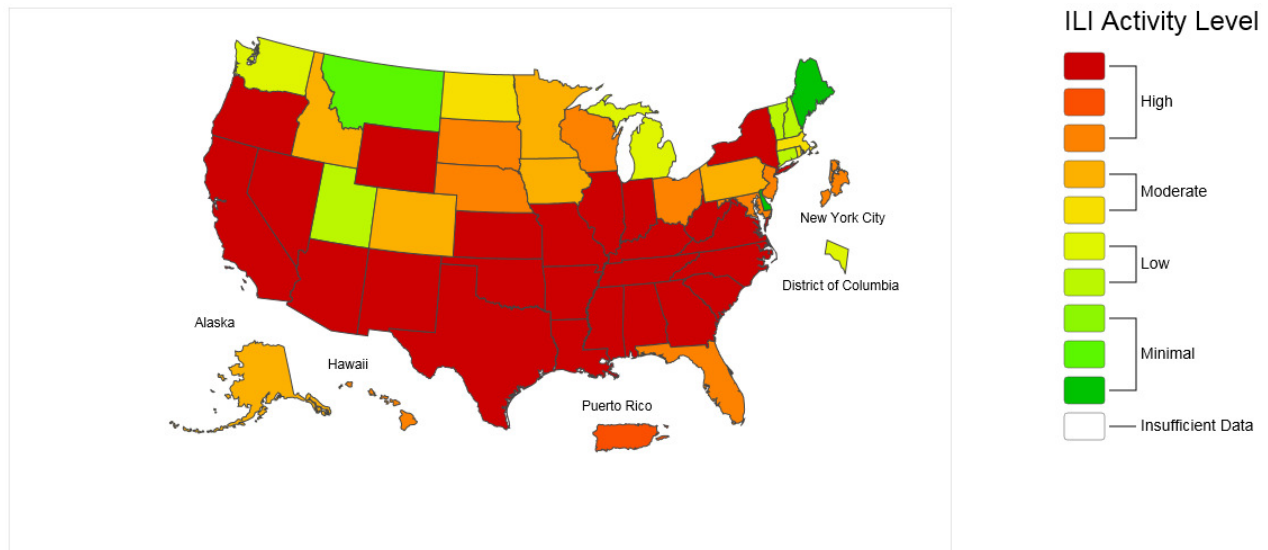
On a regional level, the percentage of outpatient visits for ILI ranged from 2.7% to 12.6% during week 2. All 10 regions reported percentages of outpatient visits for ILI at or above their region specific baselines.

ILINet State Activity Indicator Map: Data collected in ILINet are used to produce a measure of ILI activity* by state. Activity levels are based on the percent of outpatient visits in a state due to ILI and are compared to the average percent of ILI visits that occur during weeks with little or no influenza virus circulation. Activity levels range from minimal, which would correspond to ILI activity from outpatient clinics being below, or only slightly above, the average, to high, which would correspond to ILI activity from outpatient clinics being much higher than average.

During week 2, the following ILI activity levels were experienced:

- New York City, Puerto Rico, and 32 states experienced high activity (Alabama, Arizona, Arkansas, California, Florida, Georgia, Hawaii, Illinois, Indiana, Kansas, Kentucky, Louisiana, Maryland, Mississippi, Missouri, Nebraska, Nevada, New Jersey, New Mexico, New York, North Carolina, Ohio, Oklahoma, Oregon, South Carolina, South Dakota, Tennessee, Texas, Virginia, West Virginia, Wisconsin, and Wyoming).
- Nine states experienced moderate ILI activity (Alaska, Colorado, Idaho, Iowa, Massachusetts, Minnesota, North Dakota, Pennsylvania, and Rhode Island).
- The District of Columbia and six states experienced low ILI activity (Connecticut, Michigan, New Hampshire, Utah, Vermont, and Washington).
- Three states experienced minimal ILI activity (Delaware, Maine, and Montana).

**Influenza-Like Illness (ILI) Activity Level Indicator Determined by Data Reported to ILINet
2017-18 Influenza Season Week 2 ending Jan 13, 2018**



*This map uses the proportion of outpatient visits to health care providers for influenza-like illness to measure the ILI activity level within a state. It does not, however, measure the extent of geographic spread of flu within a state. Therefore, outbreaks occurring in a single city could cause the state to display high activity levels.

Data collected in ILINet may disproportionately represent certain populations within a state, and therefore, may not accurately depict the full picture of influenza activity for the whole state.

Data displayed in this map are based on data collected in ILINet, whereas the State and Territorial flu activity map is based on reports from state and territorial epidemiologists. The data presented in this map is preliminary and may change as more data are received.

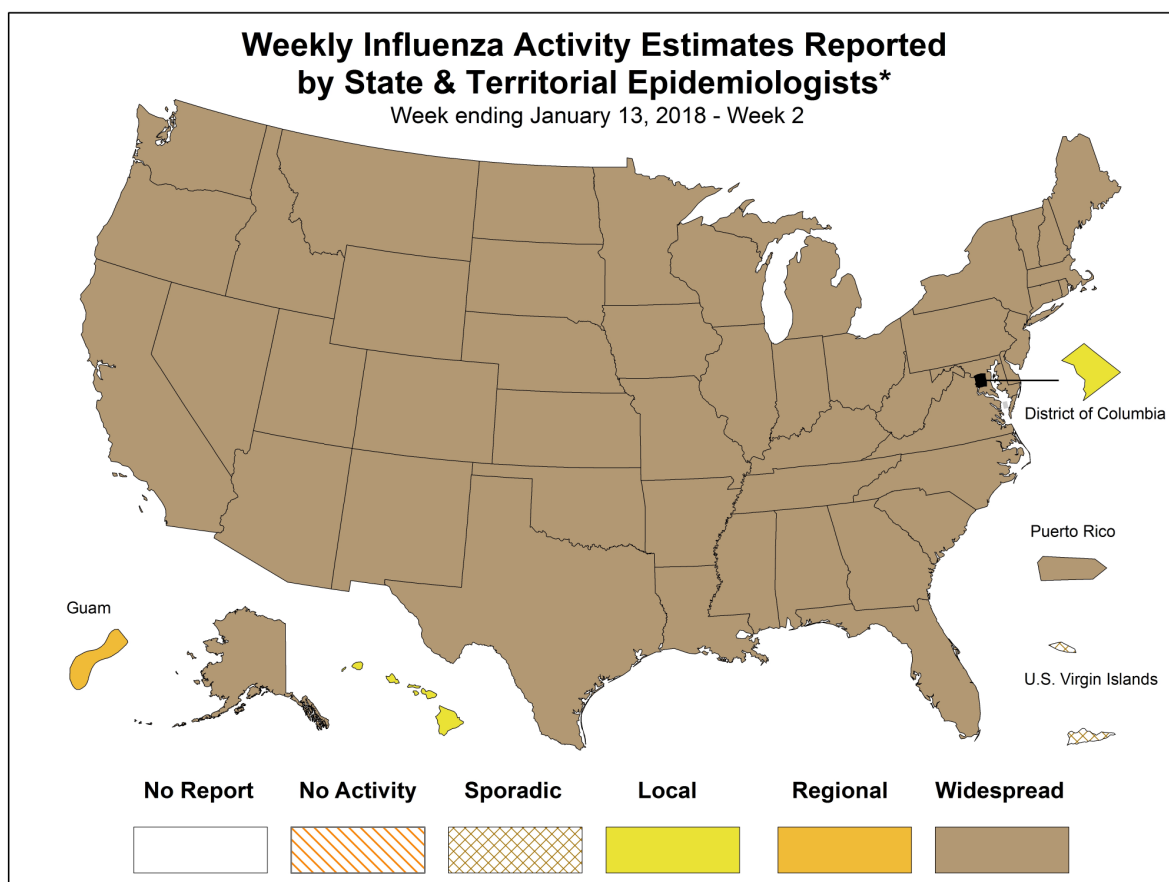
Differences in the data presented here by CDC and independently by some state health departments likely represent differing levels of data completeness with data presented by the state likely being the more complete.

Geographic Spread of Influenza as Assessed by State and Territorial Epidemiologists: The influenza activity reported by state and territorial epidemiologists indicates geographic spread of influenza viruses, but does not measure the severity of influenza activity.

Additional data can be found at: <https://gis.cdc.gov/grasp/fluview/FluView8.html>.

During week 2, the following influenza activity was reported:

- Widespread influenza activity was reported by Puerto Rico and 49 states (Alabama, Alaska, Arizona, Arkansas, California, Colorado, Connecticut, Delaware, Florida, Georgia, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Louisiana, Maine, Maryland, Massachusetts, Michigan, Minnesota, Mississippi, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, North Dakota, Ohio, Oklahoma, Oregon, Pennsylvania, Rhode Island, South Carolina, South Dakota, Tennessee, Texas, Utah, Vermont, Virginia, Washington, West Virginia, Wisconsin, and Wyoming).
- Regional influenza activity was reported by Guam.
- Local influenza activity was reported by the District of Columbia and one state (Hawaii).
- Sporadic activity was reported by the U.S. Virgin Islands.



* This map indicates geographic spread & does not measure the severity of influenza activity

Additional National and International Influenza Surveillance Information

FluView Interactive: FluView includes enhanced web-based interactive applications that can provide dynamic visuals of the influenza data collected and analyzed by CDC. These FluView Interactive applications allow people to create customized, visual interpretations of influenza data, as well as make comparisons across flu seasons, regions, age groups and a variety of other demographics. To access these tools, visit <http://www.cdc.gov/flu/weekly/fluviewinteractive.htm>.

U.S. State, territorial, and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

Alabama	Alaska	Arizona	Arkansas	California
Colorado	Connecticut	Delaware	District of Columbia	Florida
Georgia	Hawaii	Idaho	Illinois	Indiana
Iowa	Kansas	Kentucky	Louisiana	Maine
Maryland	Massachusetts	Michigan	Minnesota	Mississippi
Missouri	Montana	Nebraska	Nevada	New Hampshire
New Jersey	New Mexico	New York	North Carolina	North Dakota
Ohio	Oklahoma	Oregon	Pennsylvania	Rhode Island
South Carolina	South Dakota	Tennessee	Texas	Utah
Vermont	Virginia	Washington	West Virginia	Wisconsin
Wyoming	New York City	Puerto Rico	U.S. Virgin Islands	

World Health Organization: Additional influenza surveillance information from participating WHO member nations is available through [FluNet](#) and the [Global Epidemiology Reports](#).

WHO Collaborating Centers for Influenza are located in [Australia](#), [China](#), [Japan](#), the [United Kingdom](#), and the [United States](#) (CDC in Atlanta, Georgia).

Europe: For the most recent influenza surveillance information from Europe, please see WHO/Europe and the European Centre for Disease Prevention and Control at <http://www.flunewseurope.org/>

Public Health Agency of Canada: The most up-to-date influenza information from Canada is available at <http://www.phac-aspc.gc.ca/fluwatch/>.

Public Health England: The most up-to-date influenza information from the United Kingdom is available at <https://www.gov.uk/government/statistics/weekly-national-flu-reports>.

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An overview of the CDC influenza surveillance system, including methodology and detailed descriptions of each data component, is available at: <http://www.cdc.gov/flu/weekly/overview.htm>.

Report prepared: January 19, 2018