Weekly U.S. Influenza Surveillance Report

2017-2018 Influenza Season Week 48 ending December 2, 2017

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

Synopsis:

During week 48 (November 26-December 2, 2017), overall influenza activity increased slightly in the United States.

- **Viral Surveillance:** The most frequently identified influenza virus type reported by public health laboratories during week 48 was influenza A. The percentage of respiratory specimens testing positive for influenza in clinical laboratories declined slightly.
- **Pneumonia and Influenza Mortality:** The proportion of deaths attributed to pneumonia and influenza (P&I) was below the system-specific epidemic threshold in the National Center for Health Statistics (NCHS) Mortality Surveillance System.
- **Influenza-associated Pediatric Deaths:** Two influenza-associated pediatric deaths were reported.
- **Influenza-associated Hospitalizations:** A cumulative rate of 3.0 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 2.3%, which is above the national baseline of 2.2%. Regions 1, 4, 6 and 7 reported ILI at or above region-specific baseline levels. Three states experienced high ILI activity; Puerto Rico and three states experienced moderate ILI activity; the District of Columbia and six states experienced low ILI activity; and New York City and 38 states experienced minimal ILI activity.
- **Geographic Spread of Influenza:** The geographic spread of influenza in seven states was reported as widespread; Puerto Rico and 18 states reported regional activity; 18 states reported local activity; and the District of Columbia, the U.S. Virgin Islands and seven states reported sporadic activity; and Guam did not report.

National and Regional Summary of Select Surveillance Components

	Data for current week			Data cumulative since October 1, 2017 (week 40)							
HHS Surveillance Regions*	**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**
				Influenza test results from public health laboratories only						
Nation	Elevated	26 of 54	6.7%	220	2,125	29 13	229	128	7	
Region 1	Elevated	4 of 6	2.0%	4	55	0 1	4	0	0	
Region 2	Normal	2 of 4	3.0%	3	61	3 0	10	3	0	
Region 3	Normal	1 of 6	3.0%	10	86	0 0	15	2	0	
Region 4	Elevated	6 of 8	8.3%	65	188	2 0	13	38	2	
Region 5	Normal	2 of 6	3.9%	9	331	10 1	41	11	1	
Region 6	Elevated	4 of 5	9.0%	65	224	1 1	15	20	1	
Region 7	Elevated	1 of 4	4.0%	7	134	5 0	35	1	0	
Region 8	Normal	2 of 6	8.3%	9	242	0 1	25	1	0	
Region 9	Normal	2 of 5	7.5%	33	587	8 8	36	44	3	
Region 10	Normal	2 of 4	8.0%	15	217	0 1	35	8	0	

*https://www.hhs.gov/about/agencies/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 U.S. Virgin Islands
‡ National data are for current week; regional data are for the most recent three weeks

U.S. Virologic Surveillance:

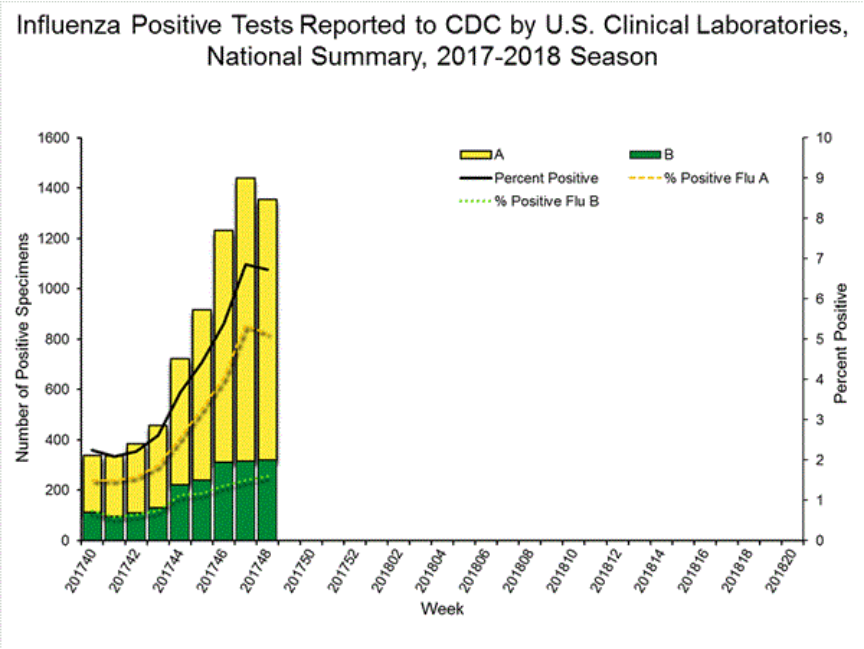
WHO and NREVSS collaborating laboratories, which include both public health and clinical laboratories located in all 50 states, Puerto Rico, and the District of Columbia, report to CDC the total number of respiratory specimens tested for influenza and the number positive for influenza by virus type. 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.

October 1, 2017 (Week 40)

	Week 48	Data Cumulative since
No. of specimens tested	20,143	170,372
No. of positive specimens (%)	1,354 (6.7%)	7,178 (4.2%)
Positive specimens by type		
Influenza A	1,033 (76.3%)	5,322 (74.1%)
Influenza B	321 (23.7%)	1,856 (25.9%)



View National and Regional Level Graphs and Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/data/whoAllregt_cl48.html) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/WhoNPHL48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

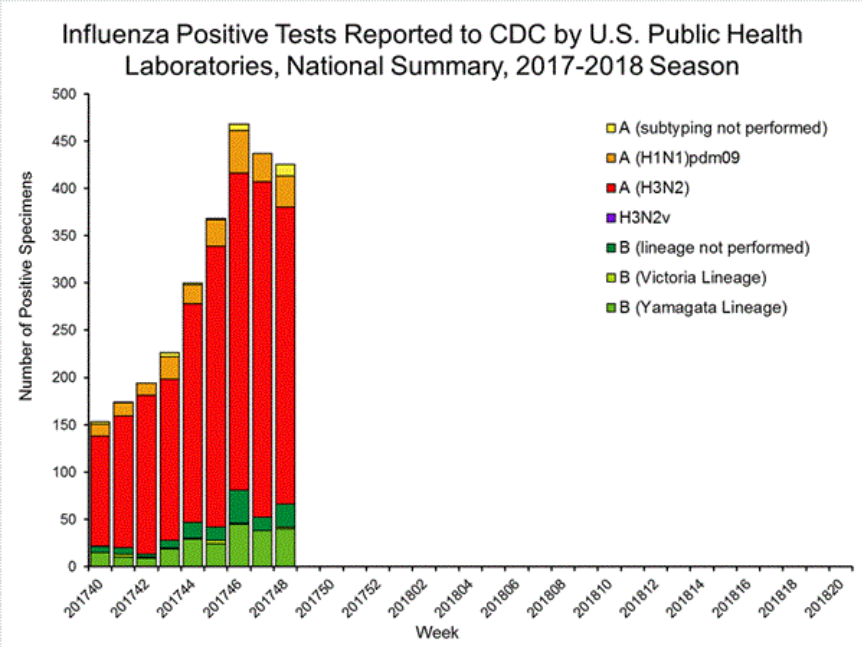
The results of tests performed by public health laboratories, as well as the age group distribution of influenza positive tests, during the current week are summarized below.

October 1, 2017 (Week 40)

	Week 48	Data Cumulative since
No. of specimens tested	1,158	11,017
No. of positive specimens*	425	2,745
Positive specimens by type/subtype		
Influenza A	359 (84.5)	2,374 (86.5%)
A(H1N1)pmd09	33 (9.2%)	220 (9.3%)
H3N2	314 (87.5%)	2,125 (89.5%)

Subtyping not performed	12 (3.3%)	29 (1.2%)
Influenza B	66 (15.5%)	370 (13.5%)
Yamagata lineage	40 (60.6%)	229 (61.9%)
Victoria lineage	2 (3.0%)	13 (3.5%)
Lineage not performed	24 (36.4%)	128 (34.6%)

*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.



View National and Regional Level Graphs and Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/data/whoAllregt_phl48.html) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/WhoPHL48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)
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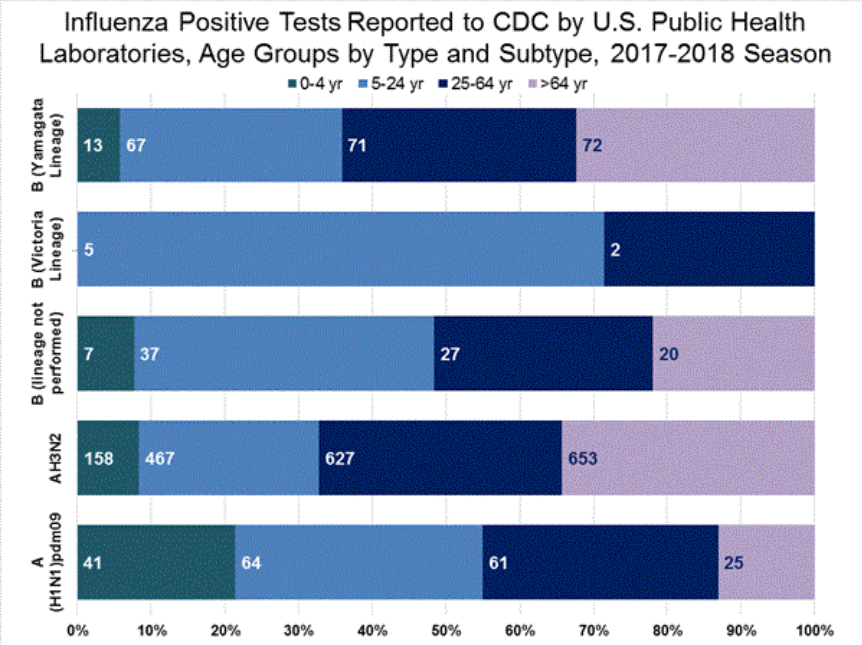


(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/Whoageshorizontal48.html)
View Interactive Application | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/Whoageshorizontal48.html)

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 hemagglutination inhibition (HI) (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 estimates 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 277 influenza viruses collected during October 1 – November 25, 2017, and submitted by U.S. laboratories, including 38 influenza A(H1N1)pdm09 viruses, 187 influenza A(H3N2) viruses, and 52 influenza B viruses.

Influenza A Viruses

- **A (H1N1)pdm09:** Phylogenetic analysis of the HA genes from 38 A(H1N1)pdm09 viruses showed that all belonged to clade 6B.1. 38 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.

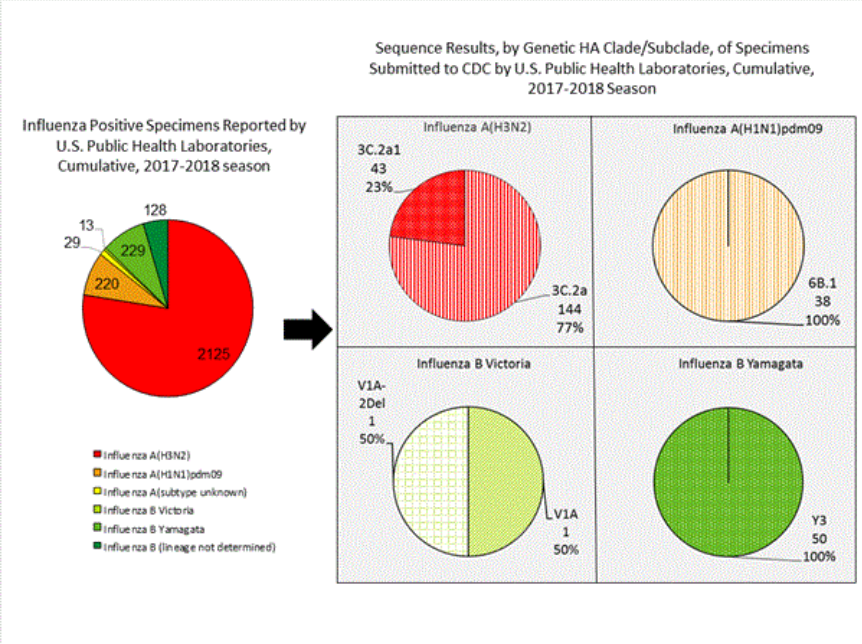
- **A (H3N2):** Phylogenetic analysis of the HA genes from 187 A(H3N2) viruses revealed extensive genetic diversity with multiple clades/subclades co-circulating. The HA genes of circulating viruses belonged to clade 3C.2a (n=144) or subclade 3C.2a1 (n=43). 64 influenza A(H3N2) viruses were antigenically characterized, and 63 (98%) 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 two 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 identified in 2017 had a 6-nucleotide deletion (encoding amino acids 162 and 163) in the HA (abbreviated as V1A-2Del). One (50%) of two 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. One B/Victoria lineage virus 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 this virus had the two amino acid deletion in the HA of the V1A-2Del viruses.

- **B/Yamagata:** Phylogenetic analysis of 50 influenza B/Yamagata-lineage viruses indicate that the HA genes belonged to clade Y3. A total of 14 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.



View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/data/Genetic48.csv) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/Genetic48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

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	
Influenza A (H1N1)pdm09	48	0 (0.0)	43	0 (0.0)	48	0 (0.0)
Influenza A (H3N2)	243	0 (0.0)	243	0 (0.0)	190	0 (0.0)
Influenza B	59	0 (0.0)	59	0 (0.0)	59	0 (0.0)

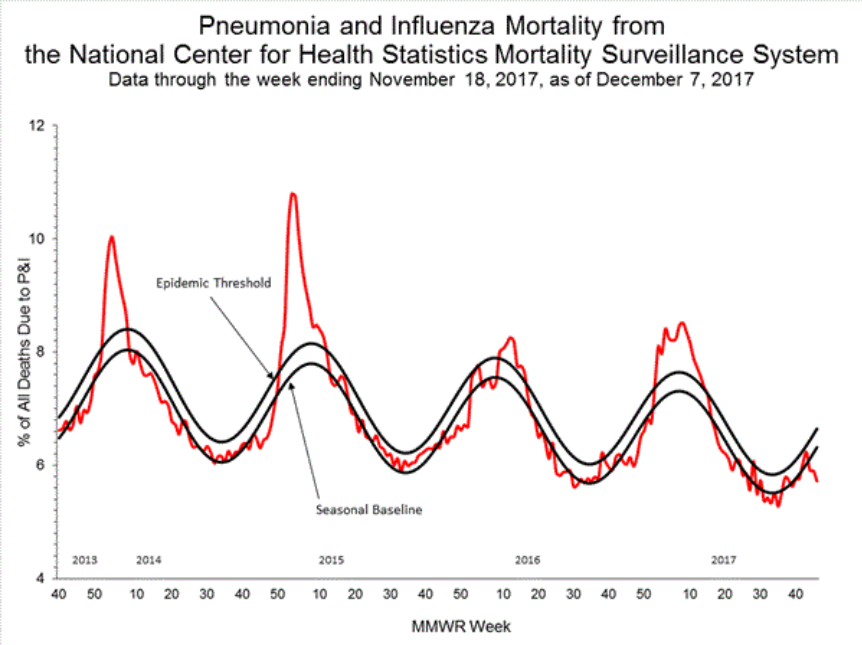
The majority of recently circulating influenza viruses are susceptible to the neuraminidase inhibitor antiviral medications, oseltamivir, zanamivir, and peramivir; however, rare sporadic instances of oseltamivir-resistant and peramivir-resistant influenza A(H1N1)pdm09 viruses and oseltamivir-resistant 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 December 7, 2017, 5.7% of the deaths occurring during the week ending November 18, 2017 (week 46) were due to P&I. This percentage is below the epidemic threshold of 6.6% for week 46.

Background: Weekly mortality surveillance data include a combination of machine coded and manually coded causes of death collected from death certificates. There is a backlog of data requiring manual coding within NCHS mortality surveillance data. The percentages of deaths due to P&I are higher among manually coded records than more rapidly available machine coded records and may result in initially reported P&I percentages that are lower than percentages calculated from final data. Efforts continue to reduce and monitor the number of records awaiting manual coding.

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



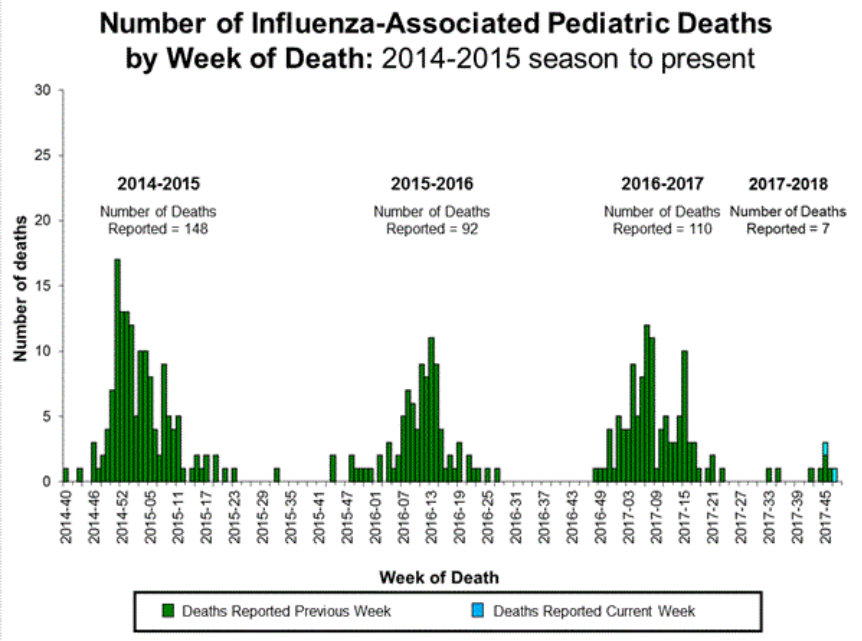
View Regional and State Level Data | View Chart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/data/NCHSData48.csv) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/NCHS48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

Influenza-Associated Pediatric Mortality:

Two influenza-associated pediatric deaths were reported to CDC during week 47. One death was associated with an influenza A (H3) virus and occurred during week 45 (the week ending November 11, 2017). One death was associated with an influenza B virus and occurred during week 47 (the week ending November 25, 2017).

A total of seven 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.



View Interactive Application | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/PedFlu48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

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).

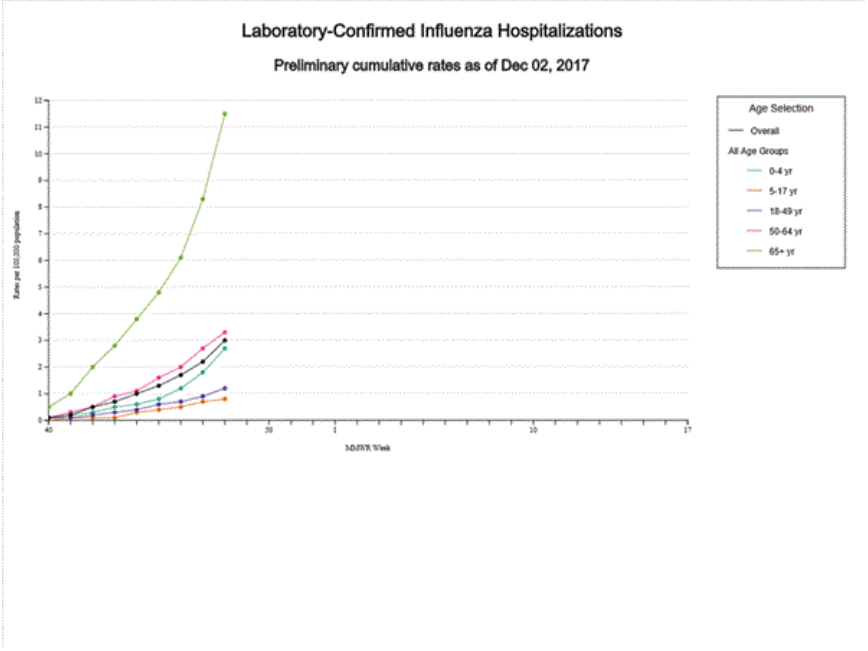
The FluSurv-NET covers more than 70 counties in the 10 Emerging Infections Program (EIP) states (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN) and additional Influenza Hospitalization Surveillance Project (IHSP) states. The IHSP began during the 2009-2010 season to enhance surveillance during the 2009 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 856 laboratory-confirmed influenza-associated hospitalizations were reported between October 1, 2017 and December 2, 2017. The overall hospitalization rate was 3.0 per 100,000 population. The highest rate of hospitalization was among adults aged ≥65 years (11.5 per 100,000 population), followed by adults aged 50-64 (3.3 per 100,000 population), and children aged 0-4 years (2.7 per 100,000 population). Among 856 hospitalizations, 735 (85.9%) were associated with influenza A virus, 116 (13.6%) with influenza B virus, 3 (0.4%) with influenza A virus and influenza B virus co-infection, and 2 (0.2%) with influenza virus for which the type was not determined. Among those with influenza A subtype information, 189 (85.9%) were A(H3N2) and 31 (14.1%) were A(H1N1)pdm09 virus.

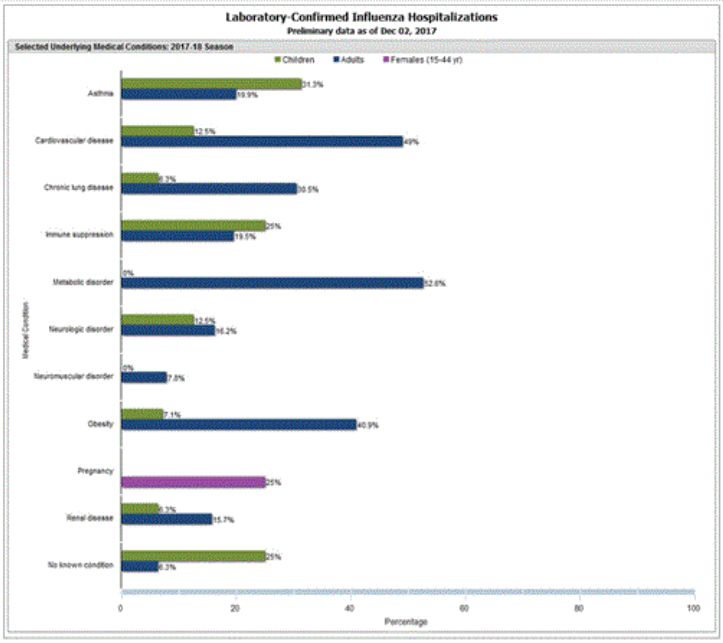
Among 160 hospitalized adults with information on underlying medical conditions, 150 (93.8%) had at least one reported underlying medical condition; the most commonly reported were metabolic disorder, cardiovascular disease, and obesity. Among 16 hospitalized children with information on underlying medical conditions, 12 (75.0%) had at least one underlying medical condition; the most commonly reported were asthma and immunocompromised conditions. Among 8 hospitalized women of childbearing age (15-44 years) with information on pregnancy status, 2 (25.0%) 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.



Data 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. Cumulative incidence rates are calculated using the National Center for Health Statistics' (NCHS) population estimates for the counties included in the surveillance catchment area.

View Interactive Application | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/EIPrates48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)



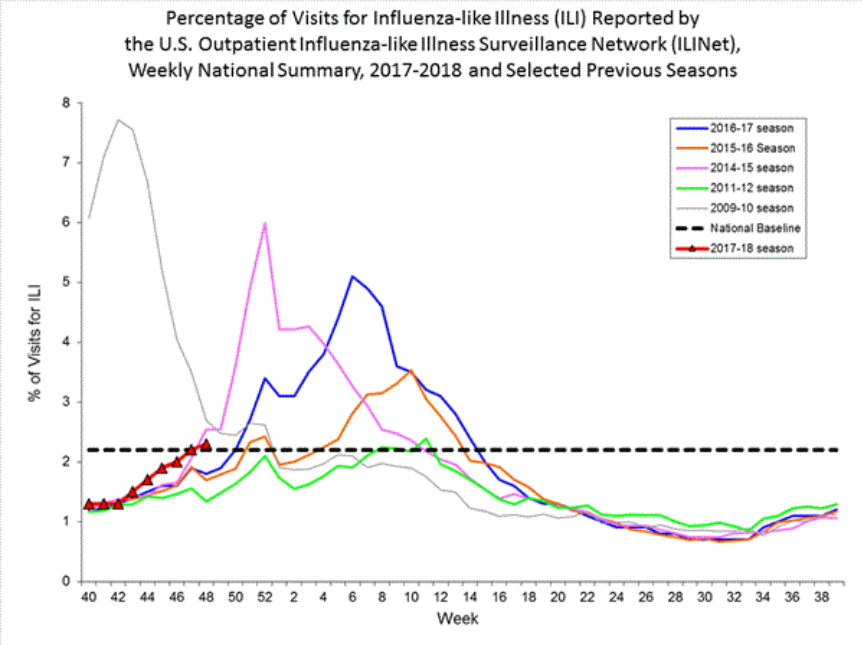
FluSurv-NET data are preliminary and displayed as they become available. Therefore, figures are based on varying denominators as some variables represent information that may require more time to be collected. Data are refreshed and updated weekly. Asthma includes a medical diagnosis of asthma or reactive 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 female cases 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 case did not have any known high risk medical condition indicated in medical chart at the time of hospitalization.

View Interactive Application | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/EIPConditions48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

Outpatient Illness Surveillance:

Nationwide during week 48, 2.3% 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.



View National and Regional Level Graphs and Data | ViewChart Data(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/data/senAllregt48.html) | View Full Screen(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/ILI48.html) | View PowerPoint Presentation(https://www.cdc.gov/flu/weekly/weeklyarchives2017-2018/FluView48.ppt)

On a regional level, the percentage of outpatient visits for ILI ranged from 1.0% to 4.7% during week 48. Regions 1, 4, 6 and 7 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 48, the following ILI activity levels were experienced:

- Three states experienced high activity (Louisiana, Mississippi, and South Carolina)
- Puerto Rico and three states experienced moderate ILI activity (Georgia, Hawaii, and Texas)
- The District of Columbia and six states experienced low ILI activity (Alabama, Alaska, Arkansas, Oklahoma, South Dakota, and Virginia).
- New York City and 38 states experienced minimal ILI activity (Arizona, California, Colorado, Connecticut, Delaware, Florida, Idaho, Illinois, Indiana, Iowa, Kansas, Kentucky, Maine, Maryland, Massachusetts, Michigan, Minnesota, Missouri, Montana, Nebraska, Nevada, New Hampshire, New Jersey, New Mexico, New York, North Carolina, North Dakota, Ohio, Oregon, Pennsylvania, Rhode Island, Tennessee, Utah, Vermont, Washington, West Virginia, Wisconsin, and Wyoming).

Click on map to launch interactive tool

*This map uses the proportion of outpatient visits to health care providers for ILI 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 disproportionally 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 are 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 48, the following influenza activity was reported::

- Widespread influenza activity was reported by seven states (Arkansas, Georgia, Louisiana, Massachusetts, Mississippi, Oklahoma, and Virginia).
- Regional influenza activity was reported by Puerto Rico and 18 states (Alabama, Alaska, Arizona, California, Colorado, Connecticut, Florida, Illinois, Kentucky, Maine, Missouri, New Hampshire, New York, North Dakota, Ohio, South Carolina, Texas, and Washington).
- Local influenza activity was reported by 18 states (Hawaii, Idaho, Indiana, Kansas, Maryland, Michigan, Minnesota, Montana, Nebraska, New Jersey, New Mexico, North Carolina, Oregon, Pennsylvania, South Dakota, Tennessee, Wisconsin, and Wyoming).
- Sporadic influenza activity was reported by the District of Columbia, the U.S. Virgin Islands and seven states (Delaware, Iowa, Nevada, Rhode Island, Utah, Vermont, and West Virginia).
- Guam did not report.

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 and local influenza surveillance: Click on a jurisdiction below to access the latest local influenza information.

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 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.
