Lung Screens (lung_screen) Data Dictionary

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Lung Screens (lung_screen): Data Dictionary
Section 1: Identifiers

Variable	Label	Description	Format Text
build	Build		Char, 30
build_cancers	Build Cancer Cohort	The source of the build data.	1="Trial Only"
build_incidence_cutoff	Build Incidence Cutoff	The censoring date for any cancer data associated with the dataset.	1="Cancers Through 2009"
plco_id	PLCO ID	PLCO ID	Char
study_yr	Study Year	XRY1-4 XRY2-3	Numeric

Section 2: XRY Date and Result

Variable	Label	Description	Format Text
xry_days	Days Until XRY	XRY1-1 XRY2-1 Days from randomization until Chest X-ray screen (XRY).	Numeric
xry_result	XRY Result	XRY1-C.1 XRY2-C.1	1="Negative" 2="Abnormal, suspicious" 3="Abnormal, not suspicious" 4="Inadequate"
xrydays_pvis1-3	Days Until XRY - Visit [X] (Screen)	XRY1-1 XRY2-1 Days from randomization until XRY protocol screen in visits 1-3.	Numeric .N="Not applicable"
xryres_pvis1-3	XRY Result - Visit [X] (Screen)	XRQ1-C.1 XRQ2-C.1 The result of Chest X-ray protocol screen in visits 1-3.	.N="Not Applicable" 1="NG" 2="AS" 3="AN" 4="IN"
xryres_qvis1-3	XRY Result - Visit [X] (QA)	XRQ1-C.1 XRQ2-C.1 The result of Chest X-ray QA screen in visits 1-3.	.F="No Form" .N="Not Applicable" 1="NG" 2="AS" 3="AN" 4="IN"
xry_assess_days_q	Day Until XRY Assessment (QA)	XRQ1-1 XRQ2-1 Days from randomization until Chest X-ray QA exam result was assessed.	Numeric .F="No Form"
xry_ref	XRY Referral Code	XRY2-C.3 The level of referral for the Chest X-ray Exam.	.M="Not answered" 1="Significant Abnormality, Referral" 2="Moderate Abnormality, Referral" 3="Slight Variation from Normal, No Referral" 4="Normal / Result Not Available, No Referral"

Section 3: XRY Findings

Variable	Label	Description	Format Text
as_mass	Y/N Mass?	Did screen report a mass abnormality?	0="No" 1="Yes"
as_mass_cnt	# of Masses	Number of mass abnormalities reported.	Numeric
as_mass_loc	Location of Mass	The location of the mass abnomality.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 5="Right lower" 6="Right upper lower" 8="Right diffuse" 11="Left upper" 13="Left middle" 14="Left middle lower" 15="Left lower" 16="Left upper lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 26="Left and right upper lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 30="Left diffuse right other comb" 31="Unknown location"
as_mass_loc_pos	Mass Location	The upper/middle/lower location of the mass abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_mass_loc_side	Mass Location	The left/right location of the mass abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
as_nodule	Y/N Nodule?	Did screen report a nodule abnormality?	0="No" 1="Yes"
as_nodule_cnt	# of Nodules	Number of nodule abnormalities reported.	Numeric

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as_nodule_loc	Location of Nodule	The location of the nodule abnomality.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 6="Right upper lower" 7="Right upper middle lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 16="Left upper lower" 17="Left upper middle lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 26="Left and right upper lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 29="Right diffuse left other comb" 30="Left diffuse right other comb" 31="Unknown location"
as_nodule_loc_pos	Nodule Location	The upper/middle/lower location of the nodule abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_nodule_loc_side	Nodule Location	The left/right location of the nodule abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
as_other	Y/N Other Abnormality?	Did screen report other abnormality, excluding mass or nodule?	0="No" 1="Yes"
as_other_cnt	# of Other Abnormalities	Number of other abnormalities reported, excluding masses or nodules.	Numeric
as_other_desc	Description of other abnormalities	Description of other abnormalities, exluding masses and nodules.	.N="Not Applicable" 1="Pleural Mass" 2="Hilar " 3="Atelectasis/collapse " 4="Infiltrate " 5="Multiple Other Abnormalities"

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Variable	Label	Description	Format Text
as_other_loc	Location of Other Abnormalities	The location of all other abnormalities, excluding masses and nodules.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 6="Right upper lower" 7="Right upper middle lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 16="Left upper lower" 17="Left upper middle lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 26="Left and right upper lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 29="Right diffuse left other comb" 30="Left diffuse right other comb" 31="Unknown location"
as_other_loc_pos	Other Abnormality Location	The upper/middle/lower location of the other abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_other_loc_side	Other Abnormality Location	The left/right location of the other abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
an_bone	Had Bone/Soft Tissue Lesion?		0="No" 1="Yes"
an_cardiac	Had Cardiac Abnormality?		0="No" 1="Yes"
an_copd	Had COPD?		0="No" 1="Yes"
an_gran	Had Granuloma?		0="No" 1="Yes"
an_pleufibro	Had Pleural Fibrosis?		0="No" 1="Yes"
an_pleufluid	Had Pleural Fluid?		0="No" 1="Yes"
an_scar	Had Scarring?		0="No" 1="Yes"

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Variable	Label	Description	Format Text
as_atelect	Had Atelect?	Did screen report a atelect abnormality?	0="No" 1="Yes"
as_atelect_cnt	Number of Atelect	Number of atelect abnormalities reported.	Numeric
as_atelect_loc	Atelect Abnomality Location	Location of all the atelect/atelects reported.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 18="Left diffuse" 21="Left and right upper" 24="Left and right middle lower" 25="Left and right lower" 26="Left and right upper lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 29="Right diffuse left other comb" 30="Left diffuse right other comb"
as_atelect_loc_pos	Atelect Abnomality Location	The upper/middle/lower location of the atelect abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse"
as_atelect_loc_side	Atelect Abnomality Location	The left/right location of the atelect abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both"
as_hilar	Had Hilar?	Did screen report a hilar abnormality?	0="No" 1="Yes"
as_hilar_cnt	Number of Hilar	Number of hilar abnormalities reported.	Numeric

Variable	Label	Description	Format Text
as_hilar_loc	Hilar Abnomality Location	Location of all the hilar reported.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 31="Unknown location"
as_hilar_loc_pos	Hilar Abnomality Location	The upper/middle/lower location of the hilar abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_hilar_loc_side	Hilar Abnomality Location	The left/right location of the hilar abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
as_infiltrate	Had Infiltrate?	Did screen report a infiltrate abnormality?	0="No" 1="Yes"
as_infiltrate_cnt	Number of Infiltrate	Number of infiltrate abnormalities reported.	Numeric

Variable	Label	Description	Format Text
as_infiltrate_loc	Atelect Abnomality Location	Location of all the infiltrate reported.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 6="Right upper lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 16="Left upper lower" 17="Left upper middle lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 26="Left and right upper lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 29="Right diffuse left other comb" 30="Left diffuse right other comb" 31="Unknown location"
as_infiltrate_loc_pos	Infiltrate Abnomality Location	The upper/middle/lower location of the infiltrate abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_infiltrate_loc_side	Infiltrate Abnomality Location	The left/right location of the infiltrate abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
as_pleural	Had Pleural?	Did screen report a pleural abnormality?	0="No" 1="Yes"
as_pleural_cnt	Number of Pleural	Number of pleural abnormalities reported.	Numeric

Variable	Label	Description	Format Text
as_pleural_loc	Pleural Abnomality Location	Location of all the pleural reported.	.N="Not Applicable" 1="Right upper" 2="Right upper middle" 3="Right middle" 4="Right middle lower" 5="Right lower" 8="Right diffuse" 11="Left upper" 12="Left upper middle" 13="Left middle" 14="Left middle lower" 15="Left lower" 16="Left upper lower" 17="Left upper middle lower" 18="Left diffuse" 21="Left and right upper" 22="Left and right upper middle" 23="Left and right middle" 24="Left and right middle lower" 25="Left and right lower" 27="Left and right upper middle lower" 28="Left and right diffuse" 29="Right diffuse left other comb" 31="Unknown location"
as_pleural_loc_pos	Pleural Abnomality Location	The upper/middle/lower location of the pleural abnormality.	.N="Not Applicable" 1="Upper" 2="Upper & Middle" 3="Middle" 4="Lower & Middle" 5="Lower" 6="Multiple" 7="Diffuse" 9="Unknown, N/A"
as_pleural_loc_side	Pleural Abnomality Location	The left/right location of the pleural abnomality.	.N="Not Applicable" 1="Right" 2="Left" 3="Both" 9="Unknown, N/A"
radiographic_abnorm	Radiographic Abnormality noted?		.M="Not answered" 0="No" 1="Yes"

Section 4: XRY Form and Procedural Details

Variable	Label	Description	Format Text
adeqfilm	Adequate films obtained (QA)	Are adequate films obtained from X-Ray QA exam?	.M="Not answered" 0="No" 1="Yes"
examinerid	Examiner ID		Char, 8
inad_lost	Reason for Inadequate Exam: Film Lost		.M="Not answered" 1="Yes"
inad_mal	Reason for Inadequate Exam: Equipment Malfunction		.M="Not answered" 1="Yes"
inad_oth	Reason for Inadequate Exam: Other Specify		.M="Not answered" 1="Yes"
inad_quality	Reason for Inadequate Exam: Poor Film Quality		.M="Not answered" 1="Yes"
inadfilm_oth	Reason for Inadequate Film: other specify		.M="Not answered" 1="Yes"
inadfilm_poor	Reason for Inadequate Film: Poor Film Quality		.M="Not answered" 1="Yes"
inadfilm_ref	Reason for Inadequate Film: Participant Refusal		.M="Not answered" 1="Yes"
examinerid_pvis1-3	Center-Examiner ID - Visit [X] (Screen)	XRY1-2 + C.4 XRY2-2 + C.5 The examiner ID for the XRY protocol exam made by concatenating center and exam ID. Collects up to 3 visits.	Char, 8 " "="Missing"
examinerid_qvis1-3	Center-Examiner ID - Visit [X] (QA)	XRQ1-2 + C.4 XRQ2-2 + C.5 The examiner ID for the XRY QA exam made by concatenating center and exam ID. Collects up to 3 visits.	Char, 8 " "="Missing"
inad_lost_p1-3	Reason for Inadequate Exam - Visit [X]: Film Lost (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inad_lost_q1-3	Reason for Inadequate Exam - Visit [X]: Film Lost (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable"
inad_mal_p1-3	Reason for Inadequate Exam - Visit [X]: Equipment Malfunction: (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inad_mal_q1-3	Reason for Inadequate Exam - Visit [X]: Equipment Malfunction (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable"
inad_oth_p1-3	Reason for Inadequate Exam - Visit [X]: Other Specify (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"

Variable	Label	Description	Format Text
inad_oth_q1-3	Reason for Inadequate Exam - Visit [X]: Other Specify (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable" 1="Yes"
inad_quality_p1-3	Reason for Inadequate Exam - Visit [X]: Poor Film Quality (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inad_quality_q1-3	Reason for Inadequate Exam - Visit [X]: Poor Film Quality (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable" 1="Yes"
inadfilm_oth_p1-3	Reason for Inadequate Film - Visit [X]: Other Specify (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inadfilm_oth_q1-3	Reason for Inadequate Film - Visit [X]: Other Specify (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable"
inadfilm_poor_p1-3	Reason for Inadequate Film - Visit [X]: Poor Film Quality (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inadfilm_poor_q1-3	Reason for Inadequate Film - Visit [X]: Poor Film Quality (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable"
inadfilm_ref_p1-3	Reason for Inadequate Film - Visit [X]: Participant Refusal (Screen)	XRQ1-C.2 XRQ2-C.2	.N="Not Applicable" 1="Yes"
inadfilm_ref_q1-3	Reason for Inadequate Film - Visit [X]: Participant Refusal (QA)	XRQ1-C.2 XRQ2-C.2	.F="No Form" .N="Not Applicable"
num_attem	Number of Attempts	Number of attempts.	.M="Not answered" 1="One" 2="Two"
techid	Technician ID		Numeric .M="Missing"

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Section 5: XRY Images

Variable	Label	Description	Format Text
ccsub_caseset	Case/Control Group For The Screen	Identifies the case/control group for the screen. Each case has a total of 15 matched controls. The Case/Control Subset is a selection of x-ray images designed for the analysis of lung cancer that is available on CDAS as a manageable download. The subset was constructed with screen-detected and interval cancers matched to cancer-free controls.	Numeric .N="Not Applicable"
in25k_ccsub_eligible	Eligible To Be Selected As A Case Or Control In The Case/Control Subset	Eligible To Be Selected As A Case Or Control In The Case/Control Subset The Case/Control Subset is a selection of x-ray images designed for the analysis of lung cancer that is available on CDAS as a manageable download. The subset was constructed with screen-detected and interval cancers matched to cancer-free controls.	0="Not Eligible" 1="Eligible"
in_ccsub_selection	Screen Was Selected In The Case/Control Subset	Screen was selected in the Case/Control Subset The Case/Control Subset is a selection of x-ray images designed for the analysis of lung cancer that is available on CDAS as a manageable download. The subset was constructed with screen-detected and interval cancers matched to cancer-free controls.	0="Not Selected" 1="Selected"
selected_25k_2020	Selected For 2020 25K Population	Participant is part of the standard 25k selection. The Standard 25k Selection is a selection of 25,000 PLCO participants with X-ray images that is available for download from CDAS. It includes all participants with T0-T5 lung cancer or non-target cancer, all participants with any abnormal/suspicious screens, a random selection of participants with any abnormal/not suspicious screens, and a random selection of participants with all negative screens.	0="Not Selected" 1="Selected"

Variable	Label	Description	Format Text
selected_25k_2020_batch	Download Batch For Standard 25k Images	Image download batch associated with images in Standard 25k Selection. The Standard 25k Selection is a selection of 25,000 PLCO participants with X-ray images that is available for download from CDAS. It includes all participants with T0-T5 lung cancer or non-target cancer, all participants with any abnormal/suspicious screens, a random selection of participants with any abnormal/not suspicious screens, and a random selection of participants with all negative screens.	.N="Not Applicable" 1="Batch A" 2="Batch B" 3="Batch C" 4="Batch D" 5="Batch E" 6="Batch F"
selected_25k_2020_set	Set For Standard 25k Selection Images	Image download set associated with images in Standard 25k Selection. The Standard 25k Selection was divided into two equally-distributed sets that were intended to be used as training and test sets. The Standard 25k Selection is a selection of 25,000 PLCO participants with X-ray images that is available for download from CDAS. It includes all participants with T0-T5 lung cancer or non-target cancer, all participants with any abnormal/suspicious screens, a random selection of participants with any abnormal/not suspicious screens, and a random selection of participants with all negative screens.	.N="Not Applicable" 1="Set 1" 2="Set 2"
weight_ccsub_to_elig	Weight For Study Year Selected In The Case/Control Subset	Sampling weight for study year selected in the case/control subset. Variable is used to weight the population to the total eligible population to be selected in the standard 25k selection. The Case/Control Subset is a selection of x-ray images designed for the analysis of lung cancer that is available on CDAS as a manageable download. The subset was constructed with screen-detected and interval cancers matched to cancer-free controls. The Standard 25k Selection is a selection of 25,000 PLCO participants with X-ray images that is available for download from CDAS. It includes all participants with T0-T5 lung cancer or non-target cancer, all participants with any abnormal/suspcious screens, a random selection of participants with any abnormal/not suspicious screens, and a random selection of participants with all negative screens.	Numeric .M="Missing" .N="Not Applicable"