

FIGURE 1 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the breast cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

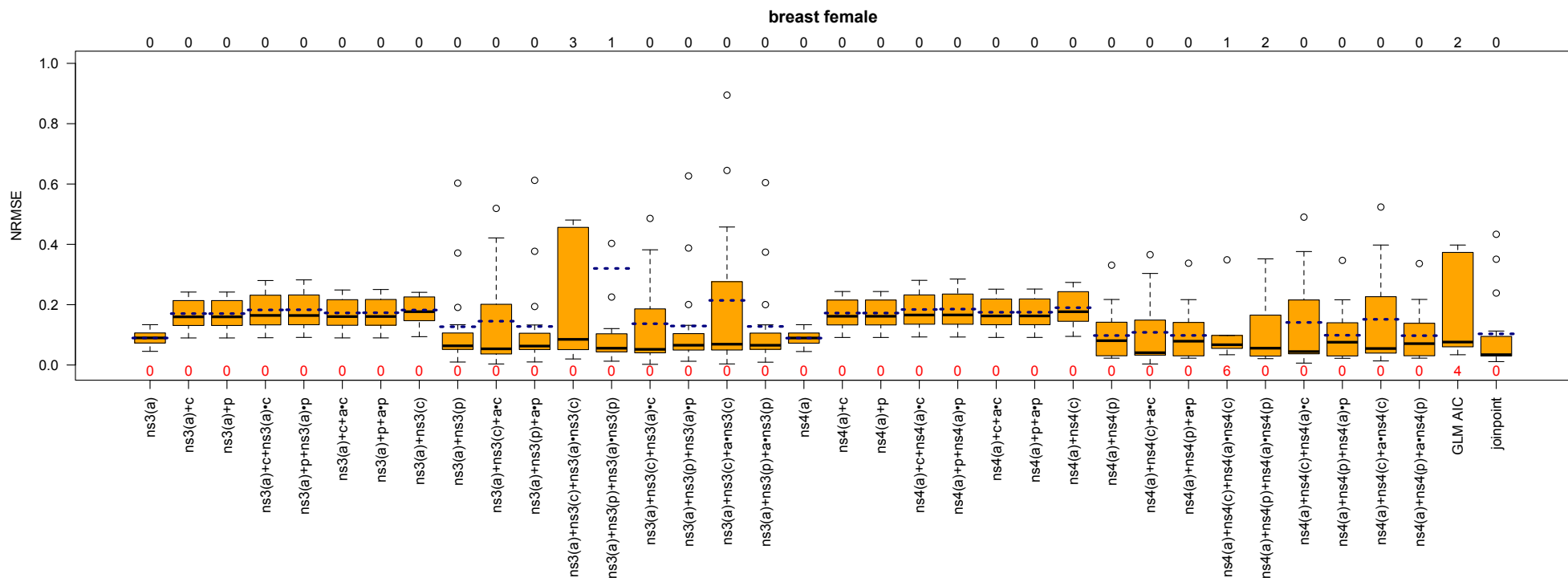


FIGURE 2 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and joinpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the breast cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

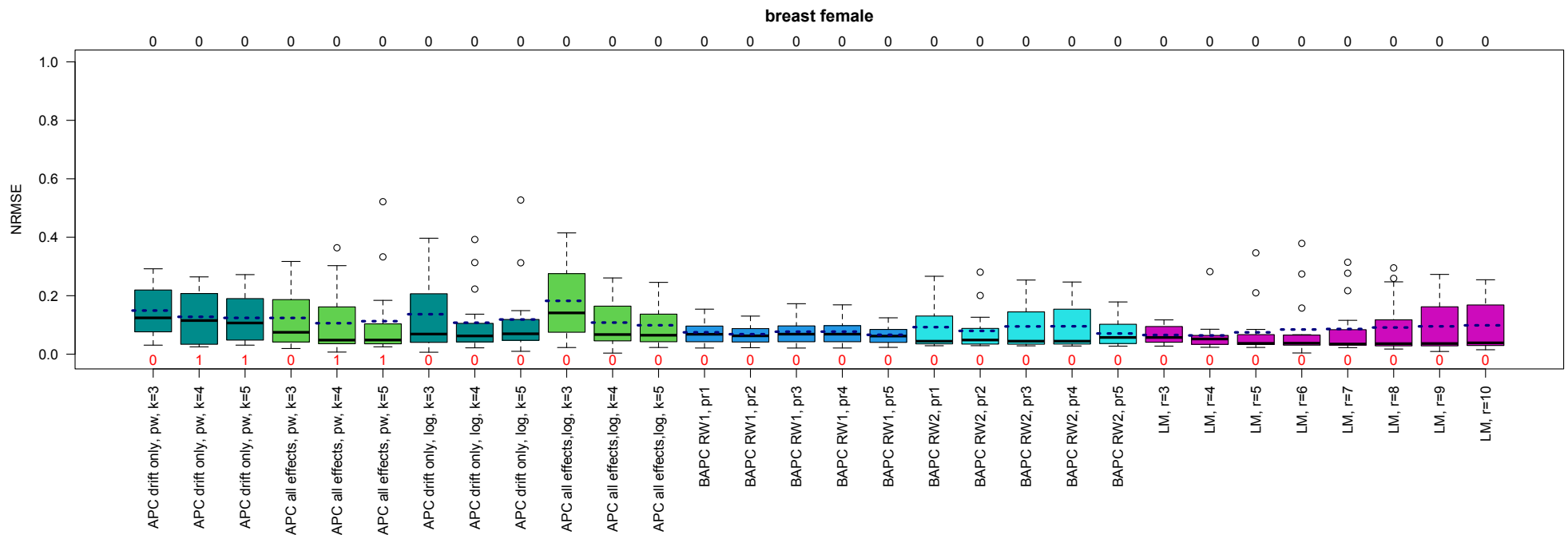


FIGURE 3 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the females and the breast cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\gamma(1, 9e-4)$ prior for the age effect and $\gamma(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\gamma(1, 5e-03)$, $\gamma(1, 5e-05)$, $\gamma(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

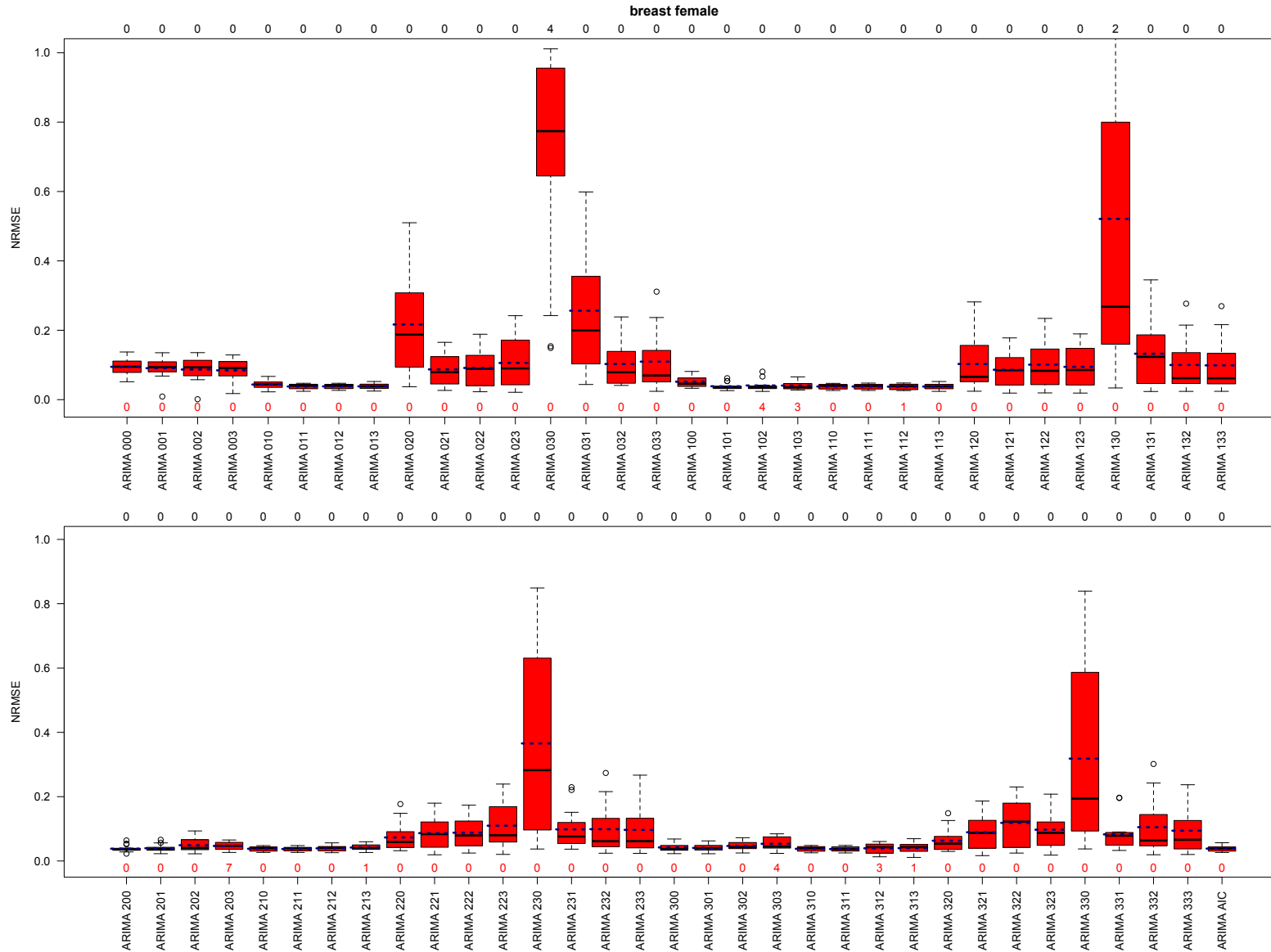


FIGURE 4 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the female and breast cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

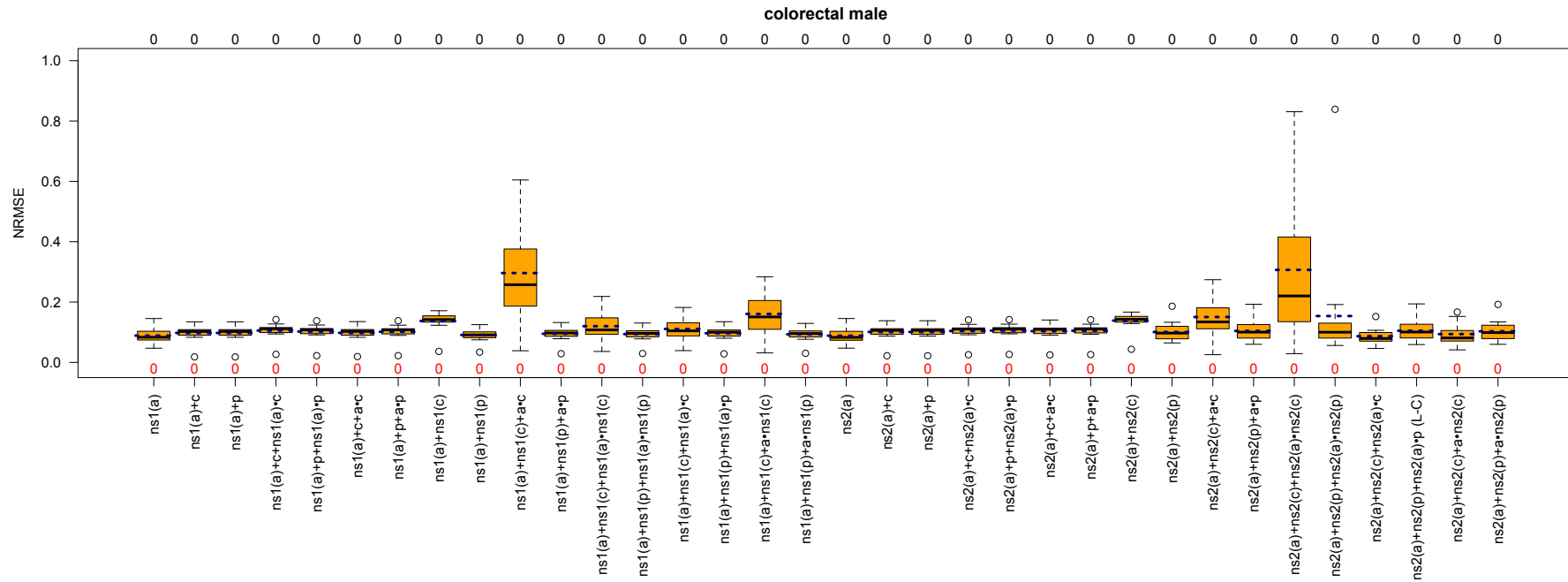


FIGURE 5 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

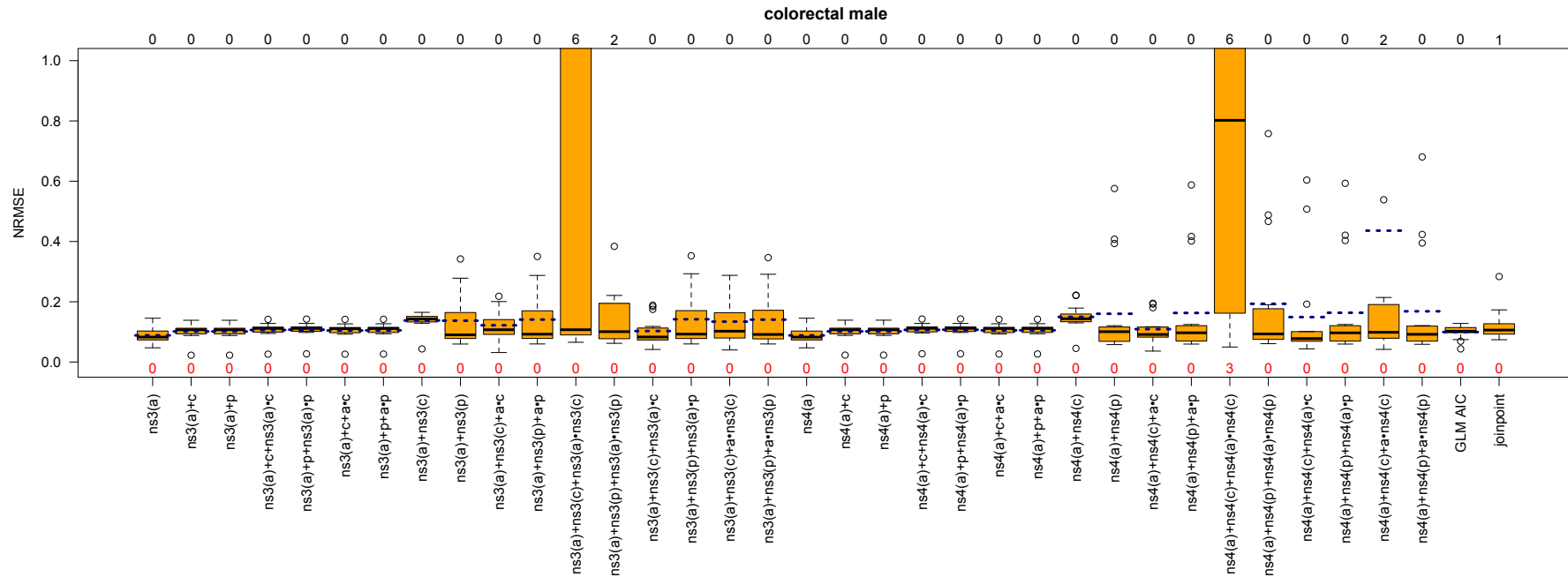


FIGURE 6 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

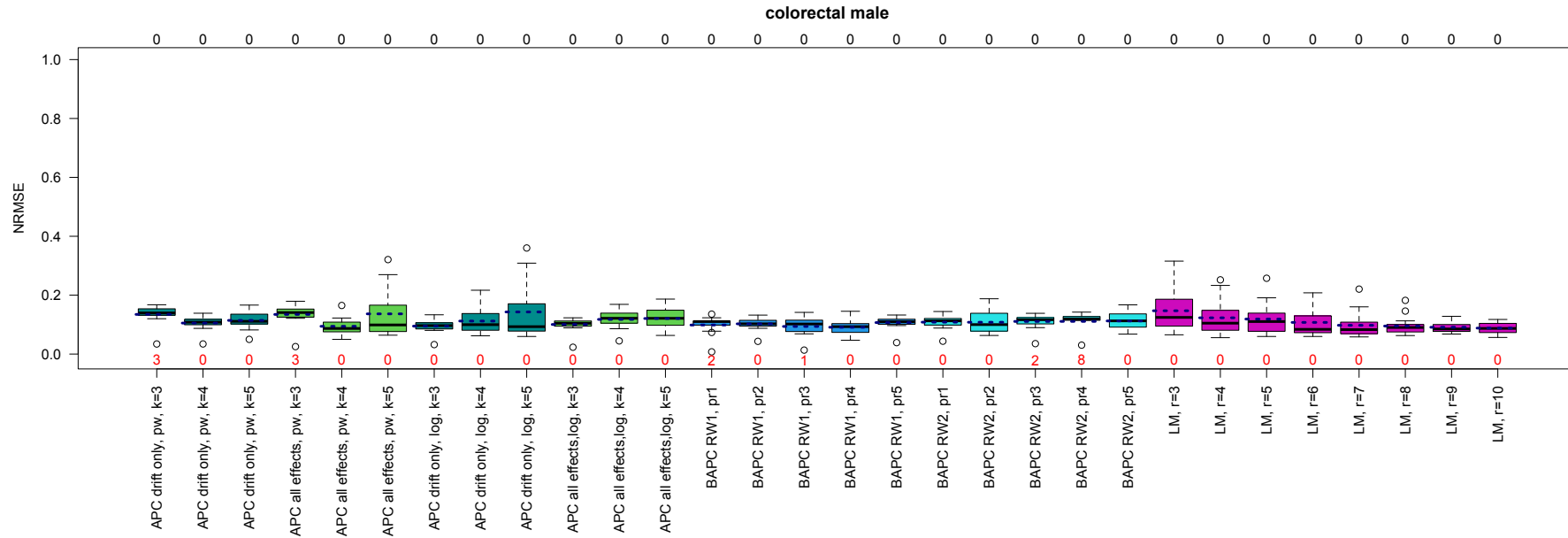


FIGURE 7 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the males and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\gamma(1, 9e-4)$ prior for the age effect and $\gamma(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\gamma(1, 5e-03)$, $\gamma(1, 5e-05)$, $\gamma(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

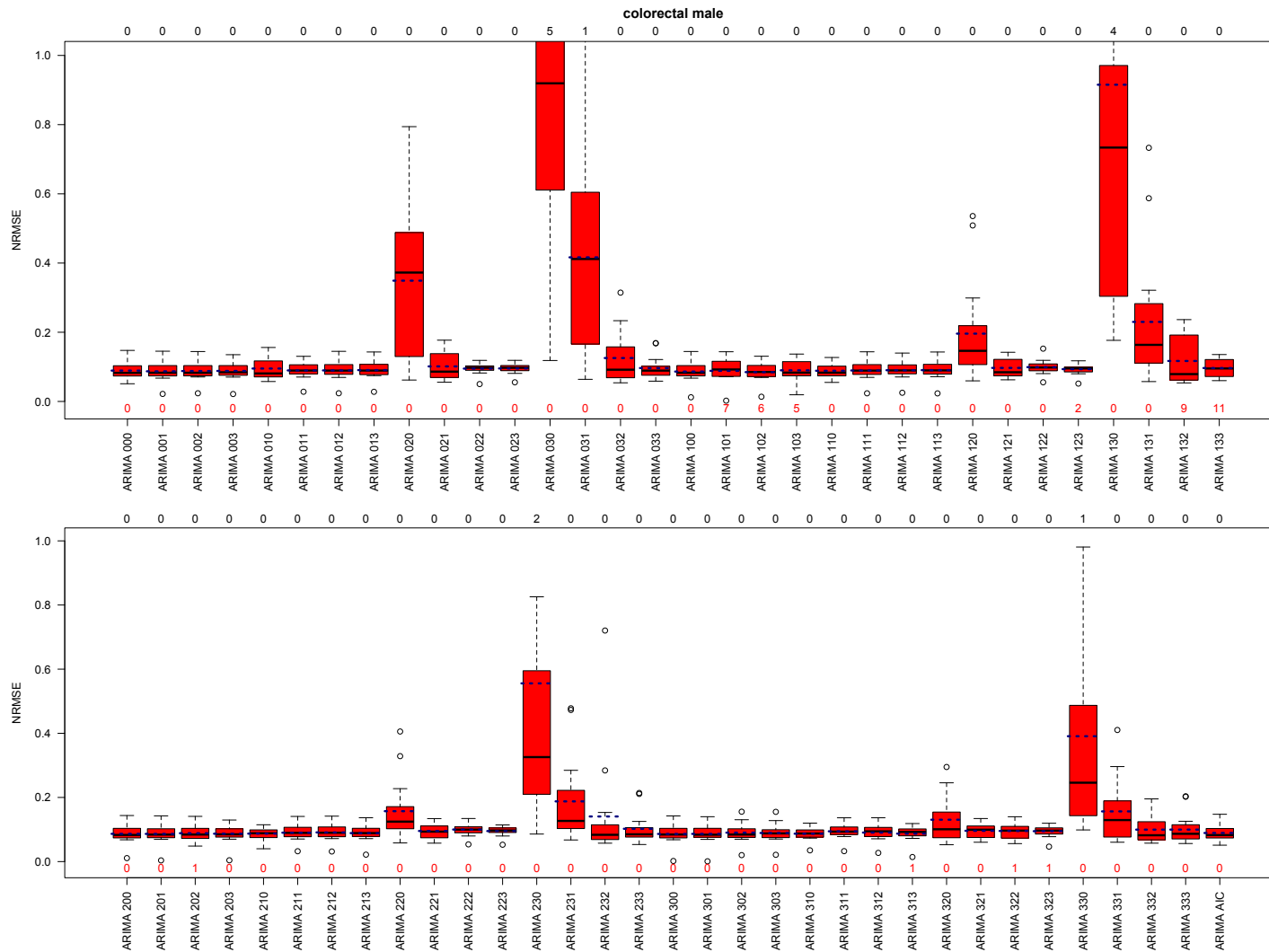


FIGURE 8 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the male and colorectal cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

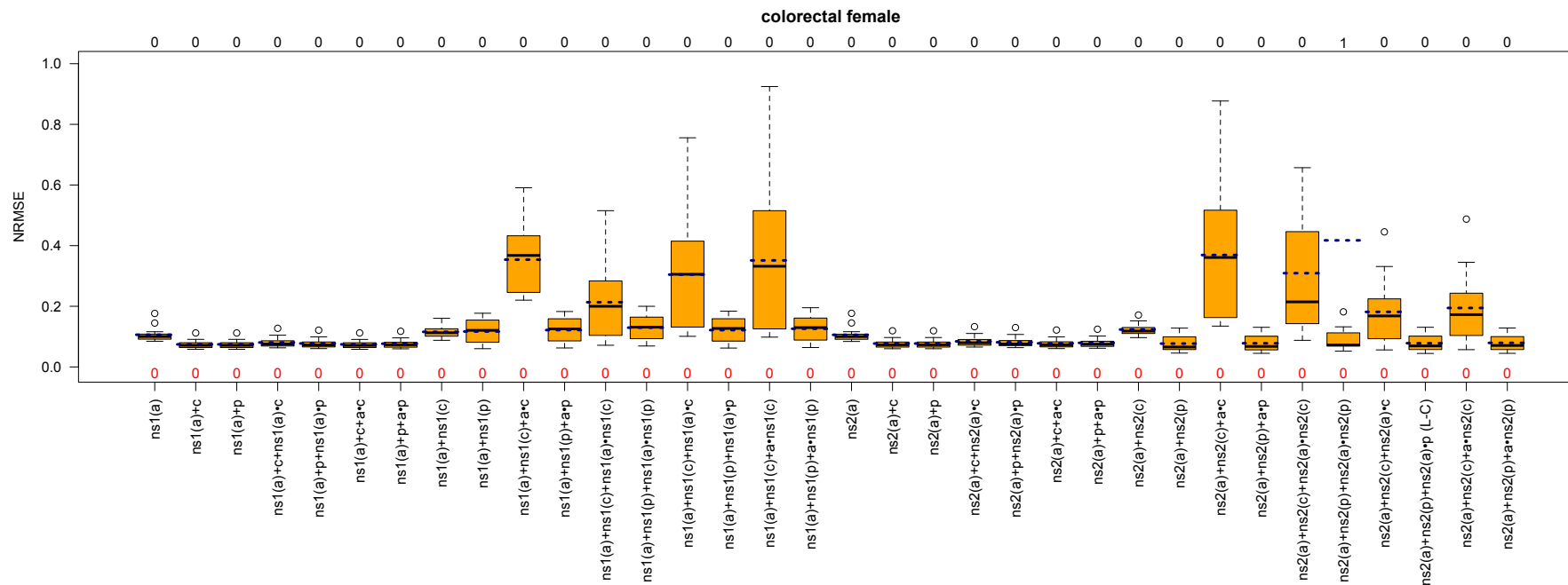


FIGURE 9 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

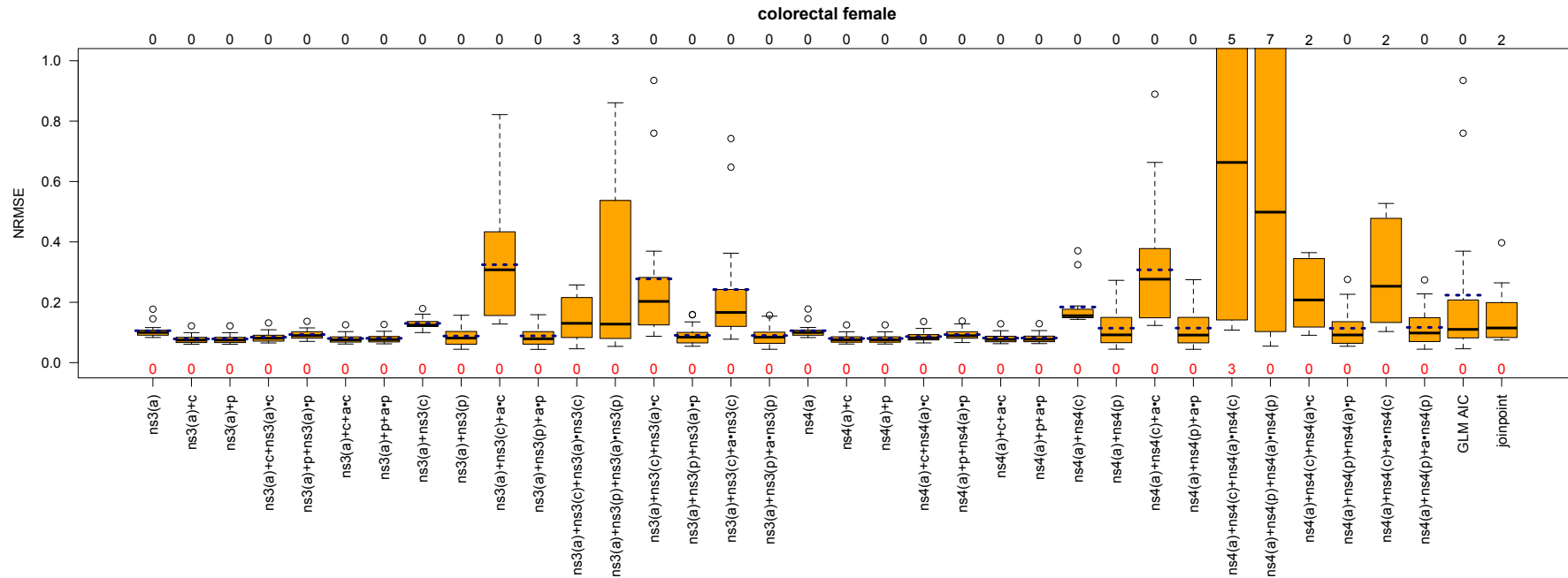


FIGURE 10 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

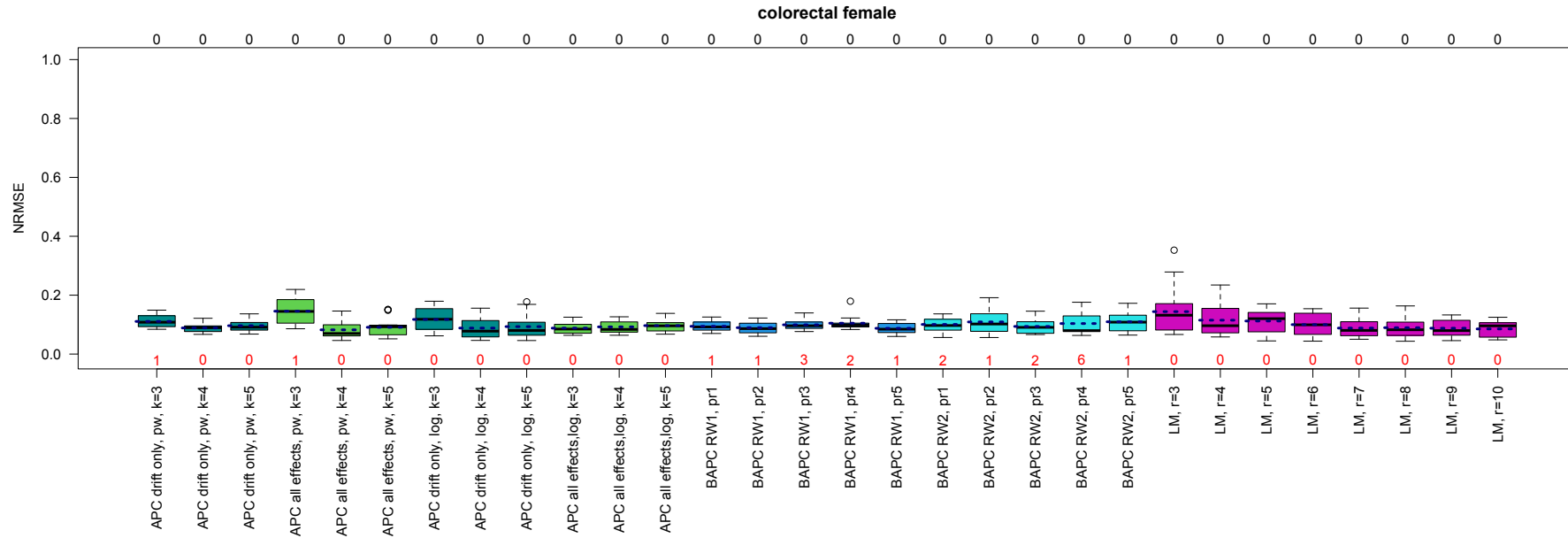


FIGURE 11 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the females and the colorectal cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\text{gamma}(1, 9e-4)$ prior for the age effect and $\text{gamma}(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\text{gamma}(1, 5e-03)$, $\text{gamma}(1, 5e-05)$, $\text{gamma}(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

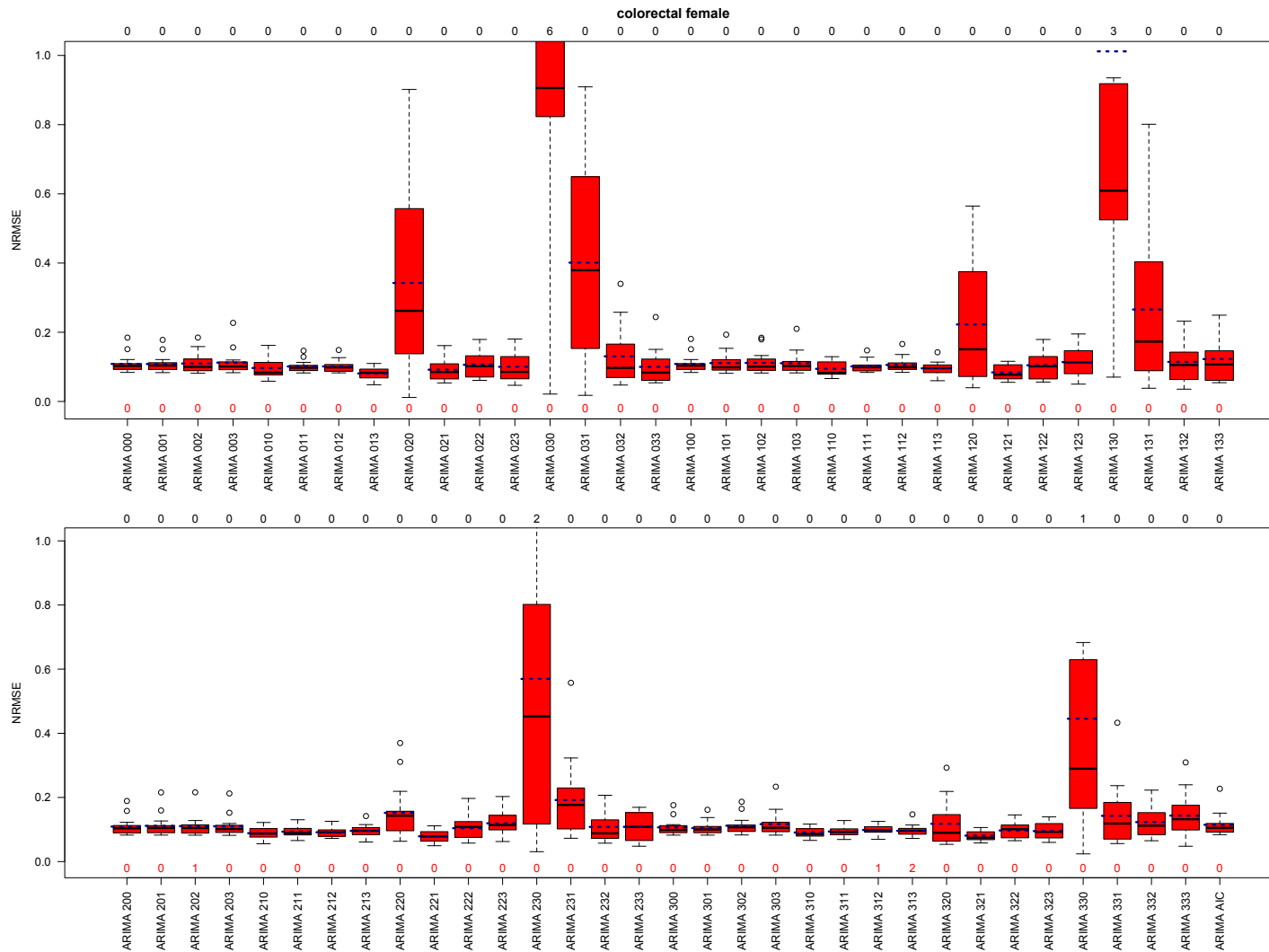


FIGURE 12 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the female and colorectal cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

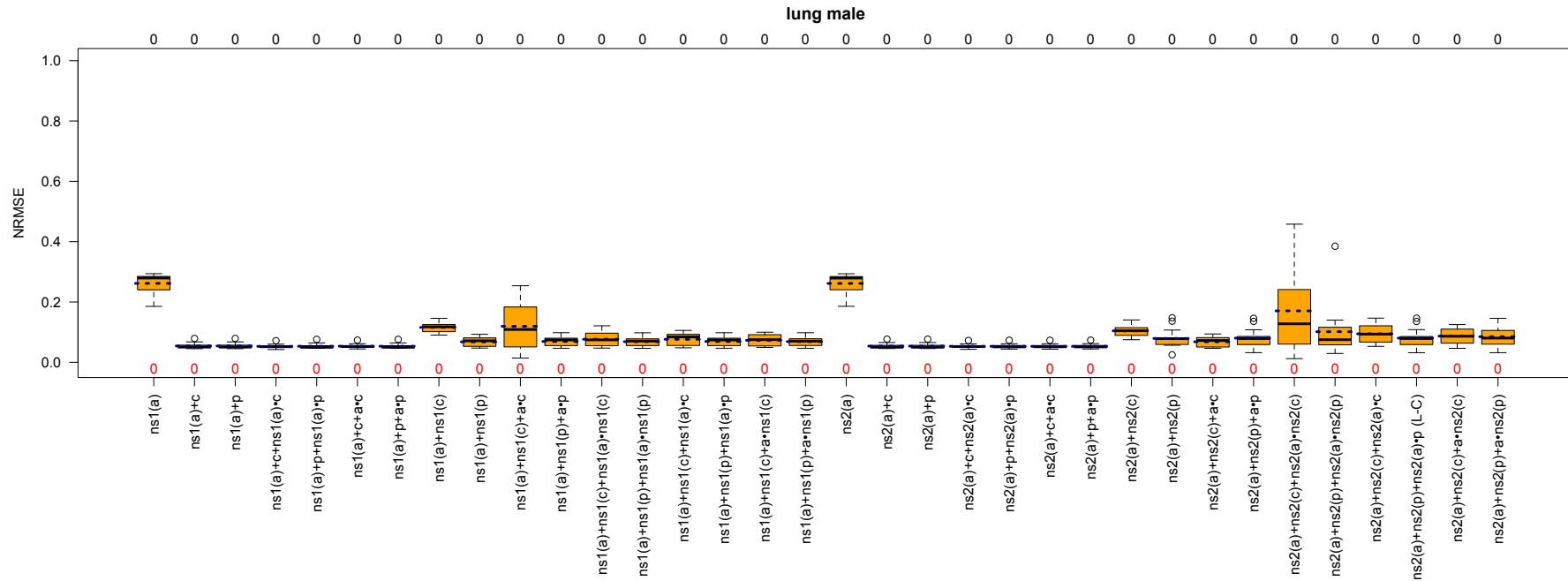


FIGURE 13 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE $>$ 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

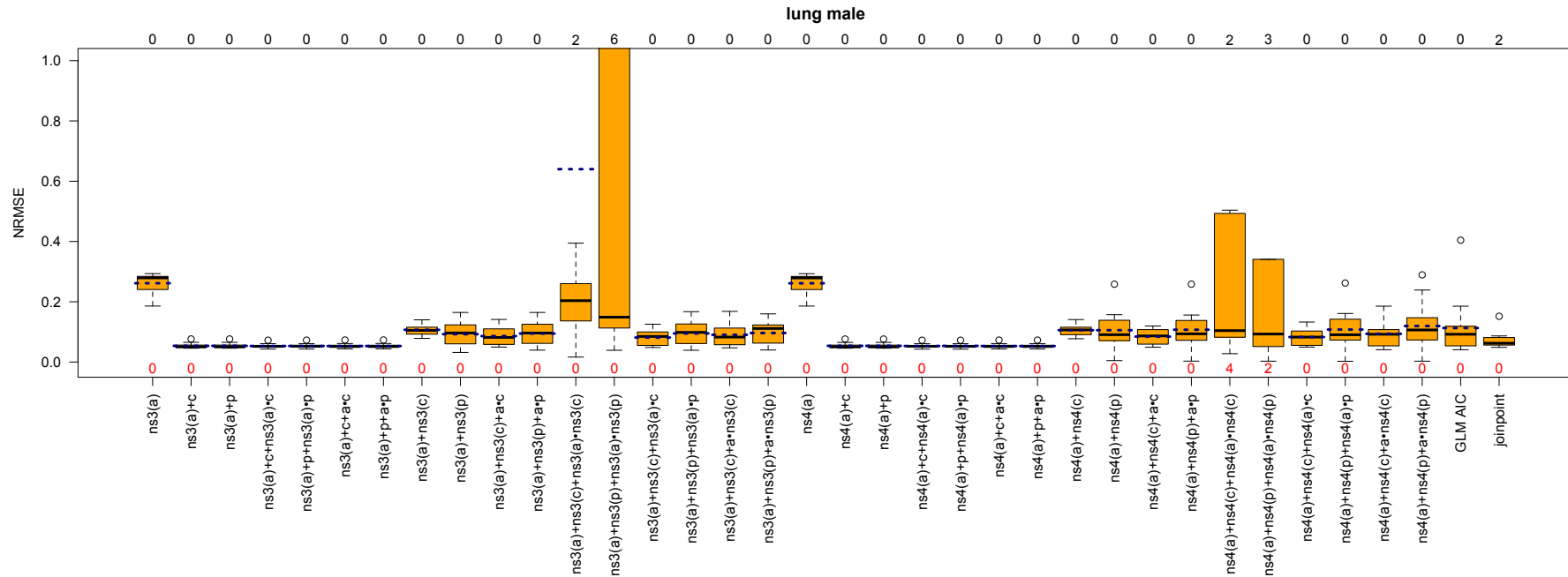


FIGURE 14 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

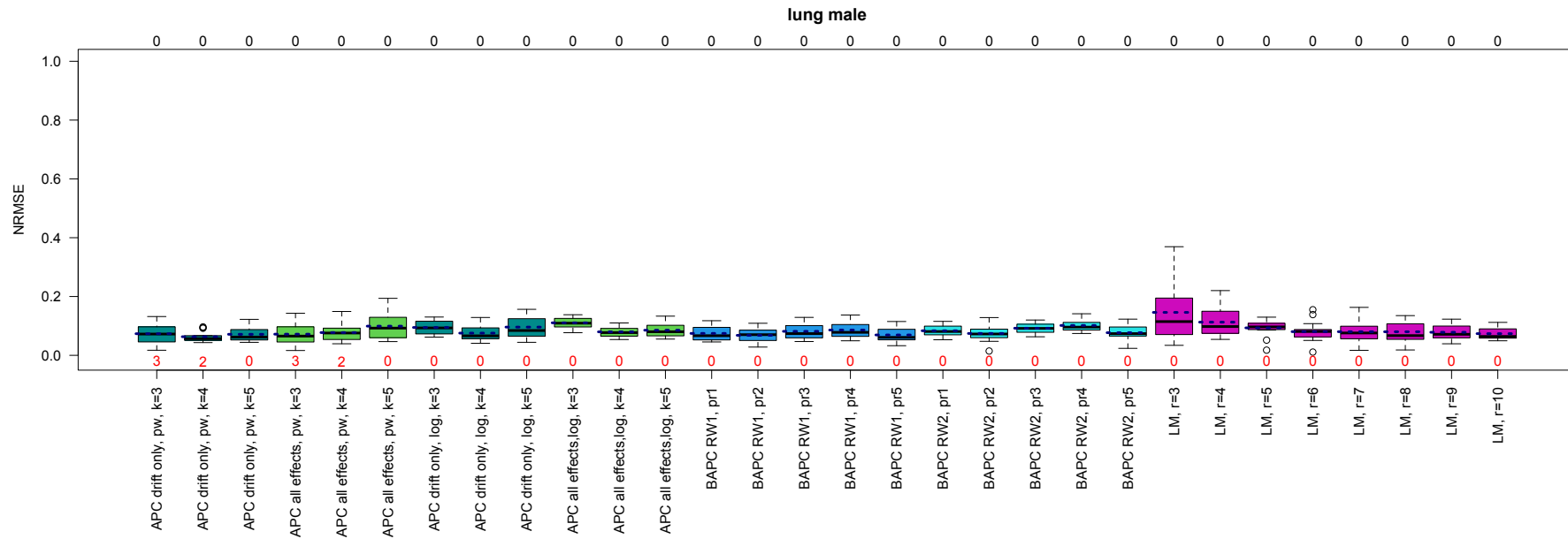


FIGURE 15 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the males and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\gamma(1, 9e-4)$ prior for the age effect and $\gamma(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\gamma(1, 5e-03)$, $\gamma(1, 5e-05)$, $\gamma(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

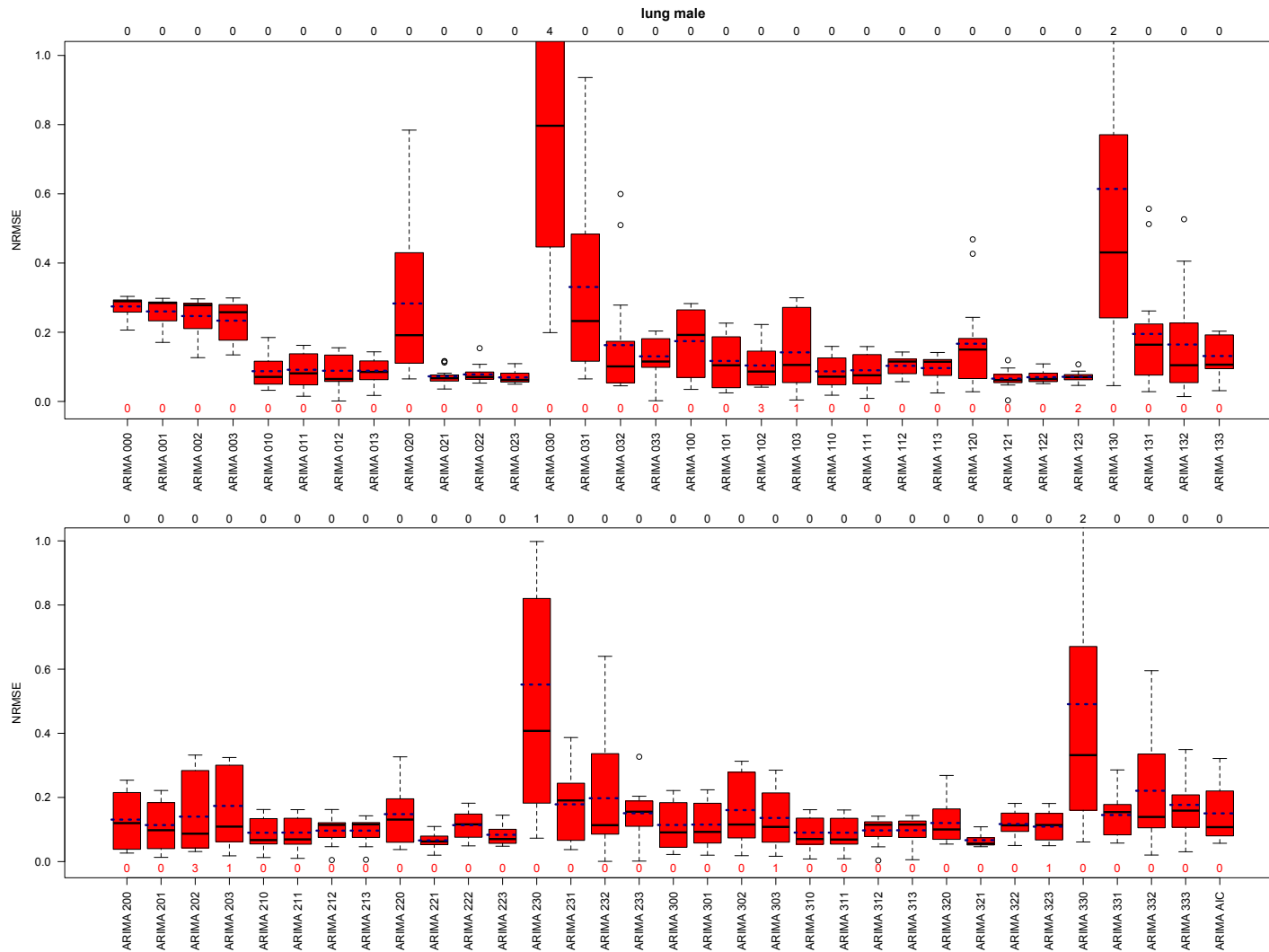


FIGURE 16 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the male and lung cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE >1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

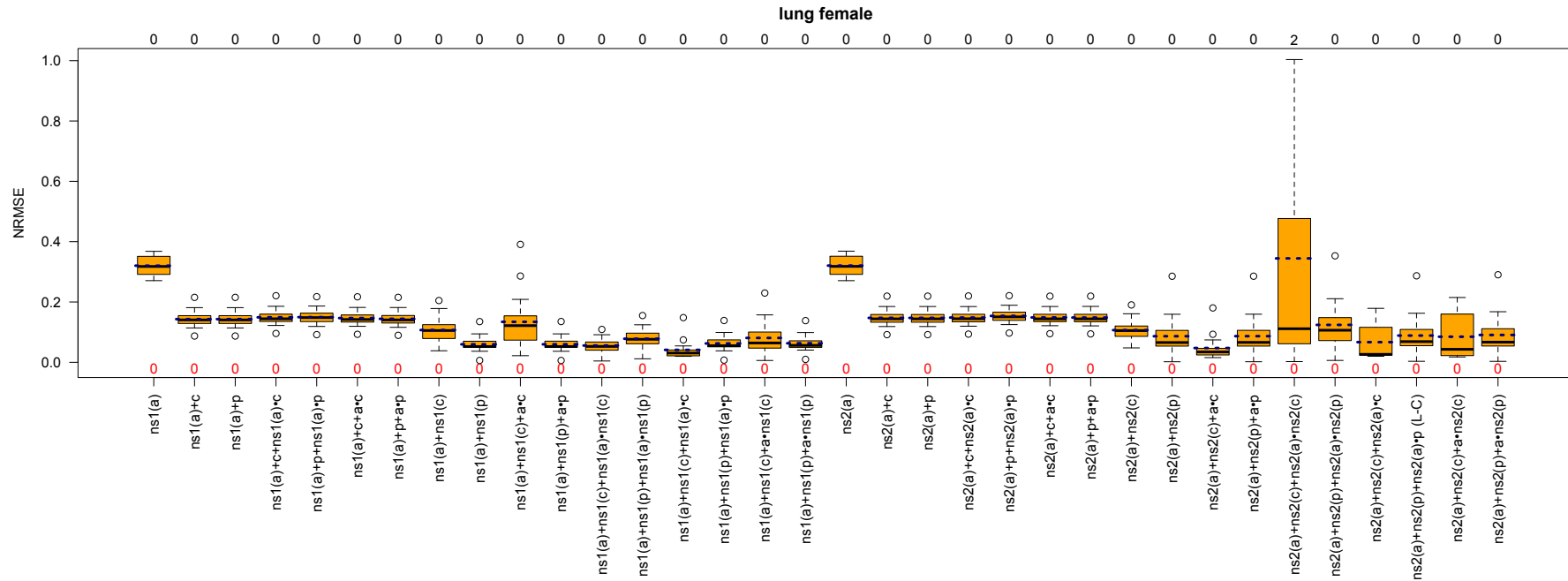


FIGURE 17 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE >1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

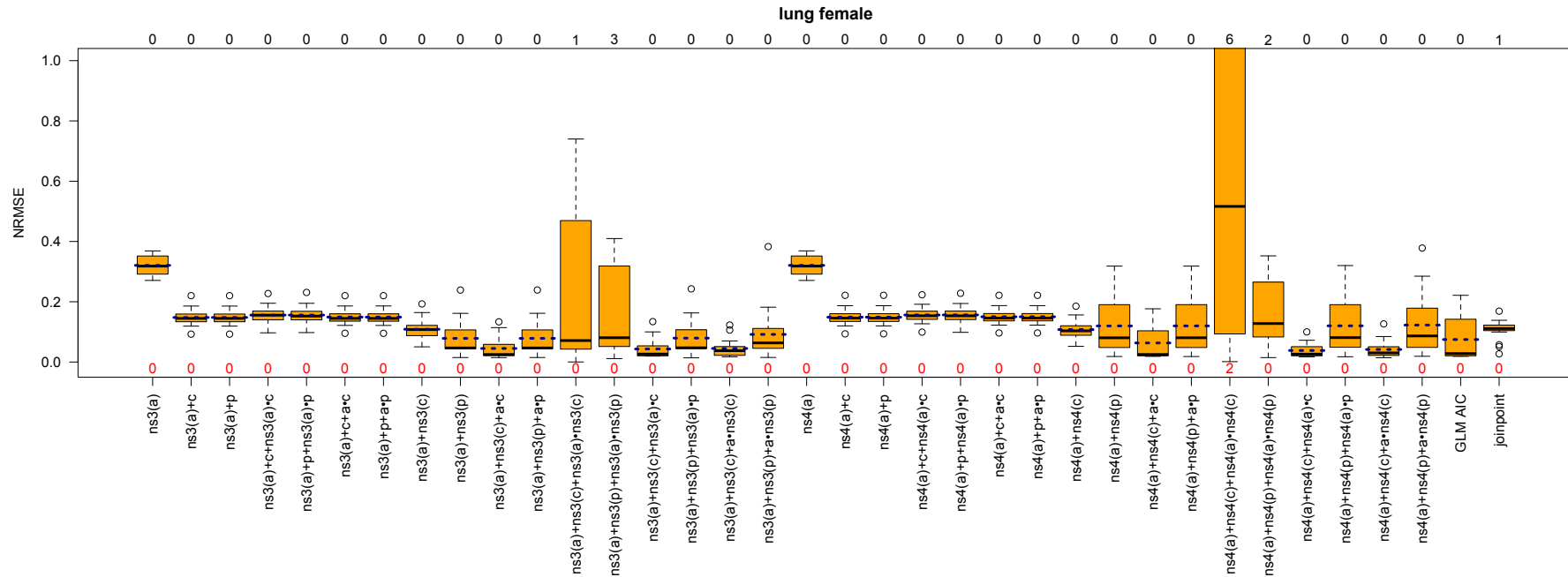


FIGURE 18 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

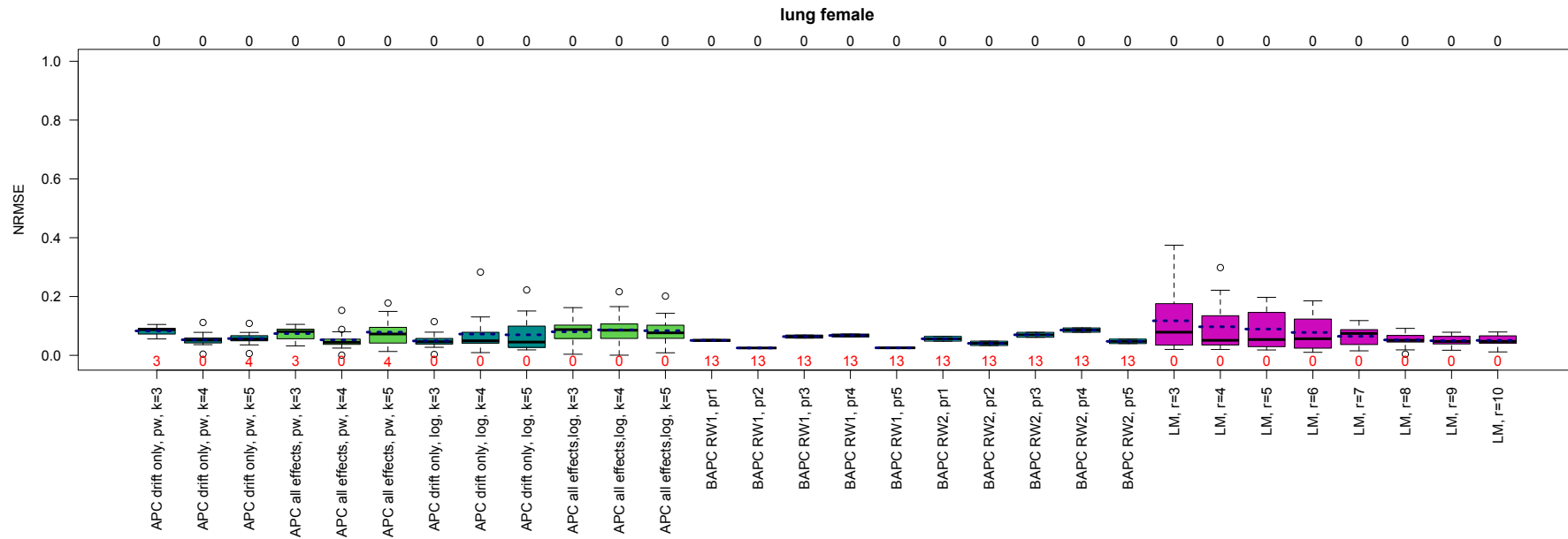


FIGURE 19 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the females and the lung cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates gamma(1, 9e-4) prior for the age effect and gamma(1, 2.5e-4) prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate gamma(1, 5e-03), gamma(1, 5e-05), gamma(1, 5e-07) and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

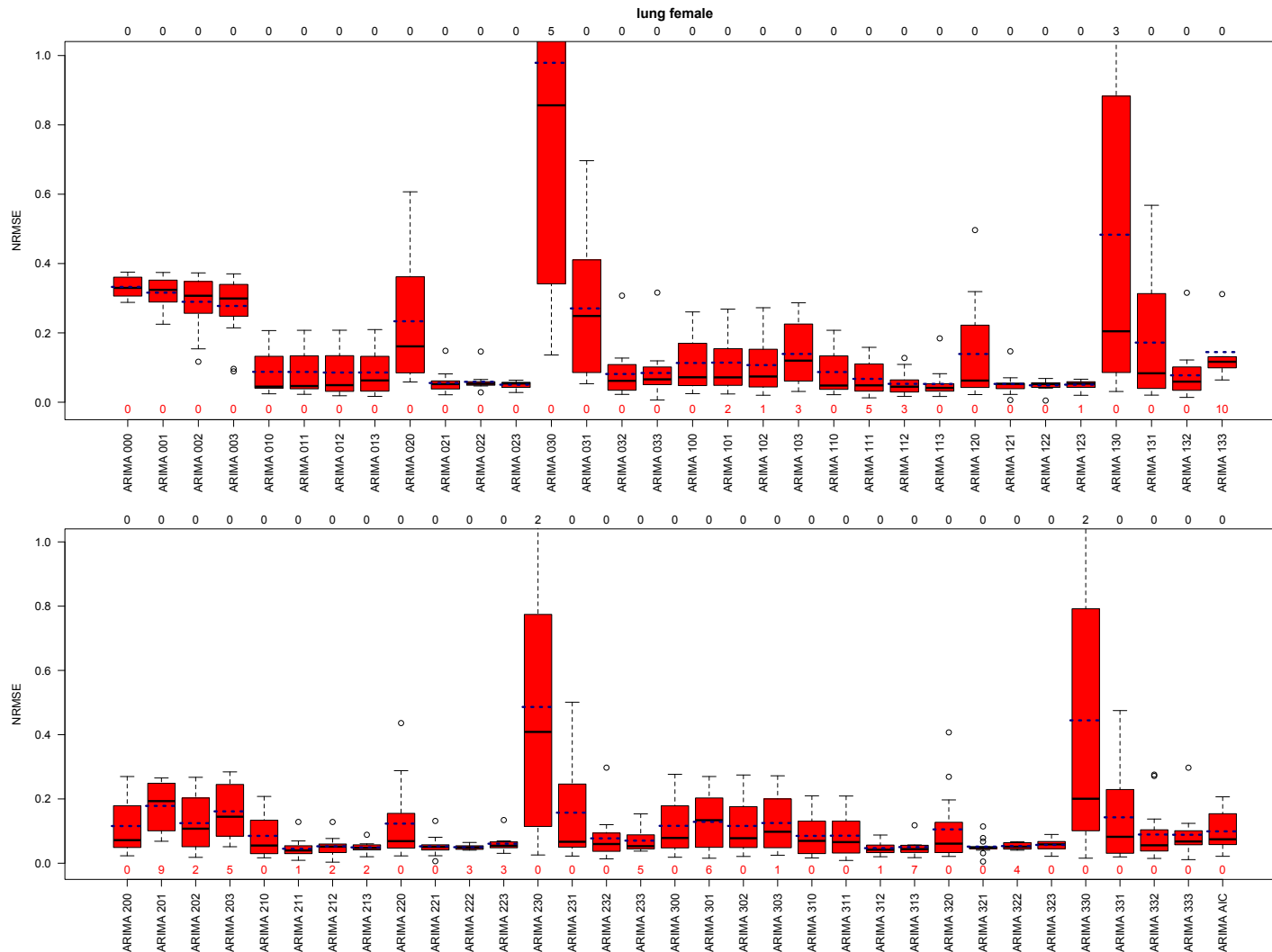


FIGURE 20 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the female and lung cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

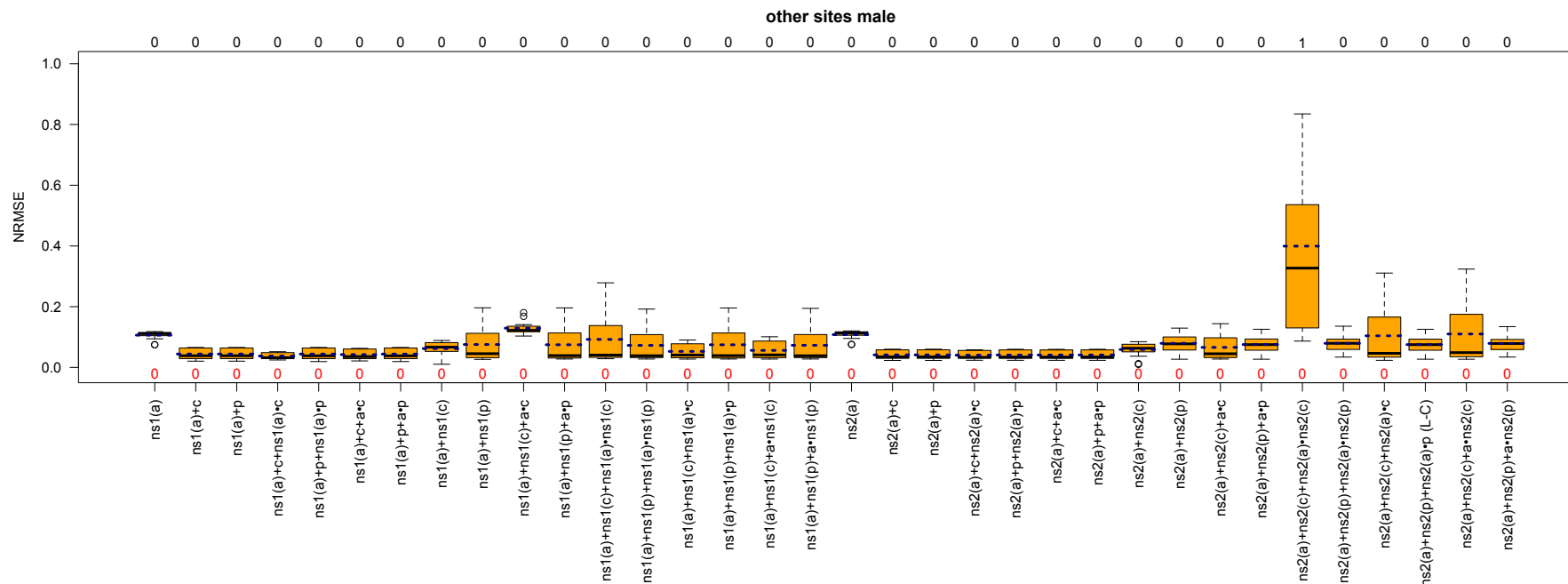


FIGURE 21 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

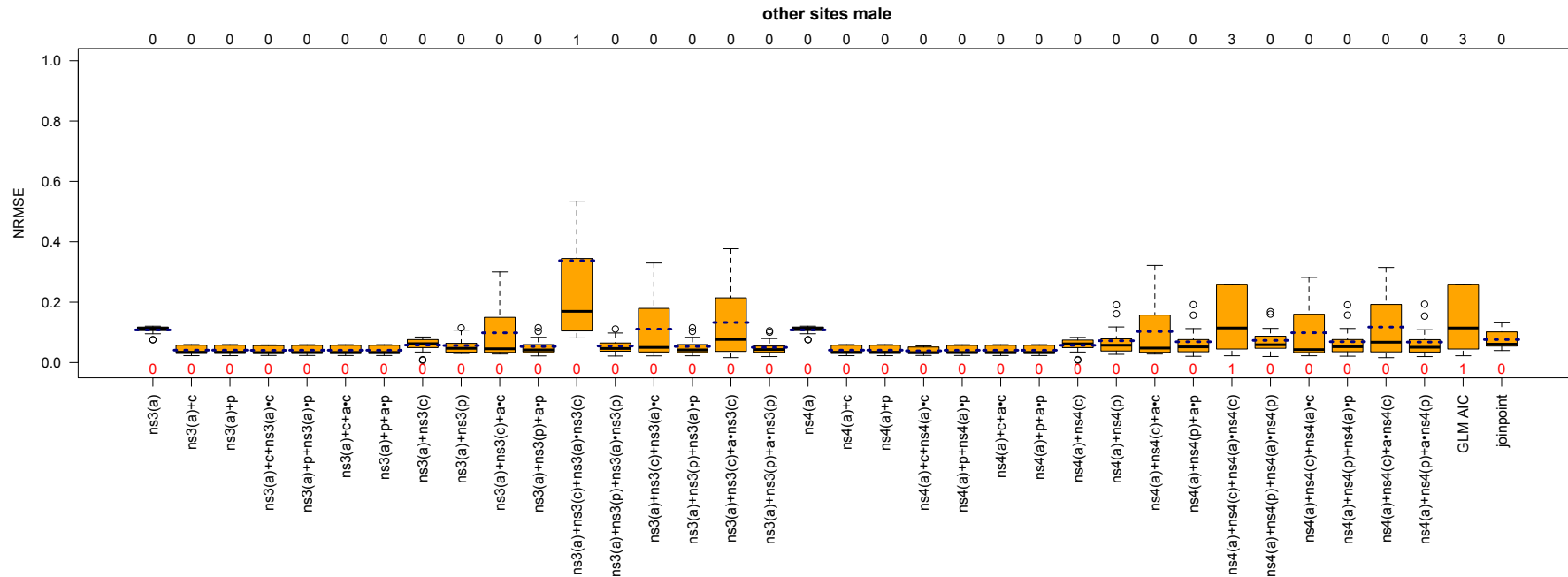


FIGURE 22 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

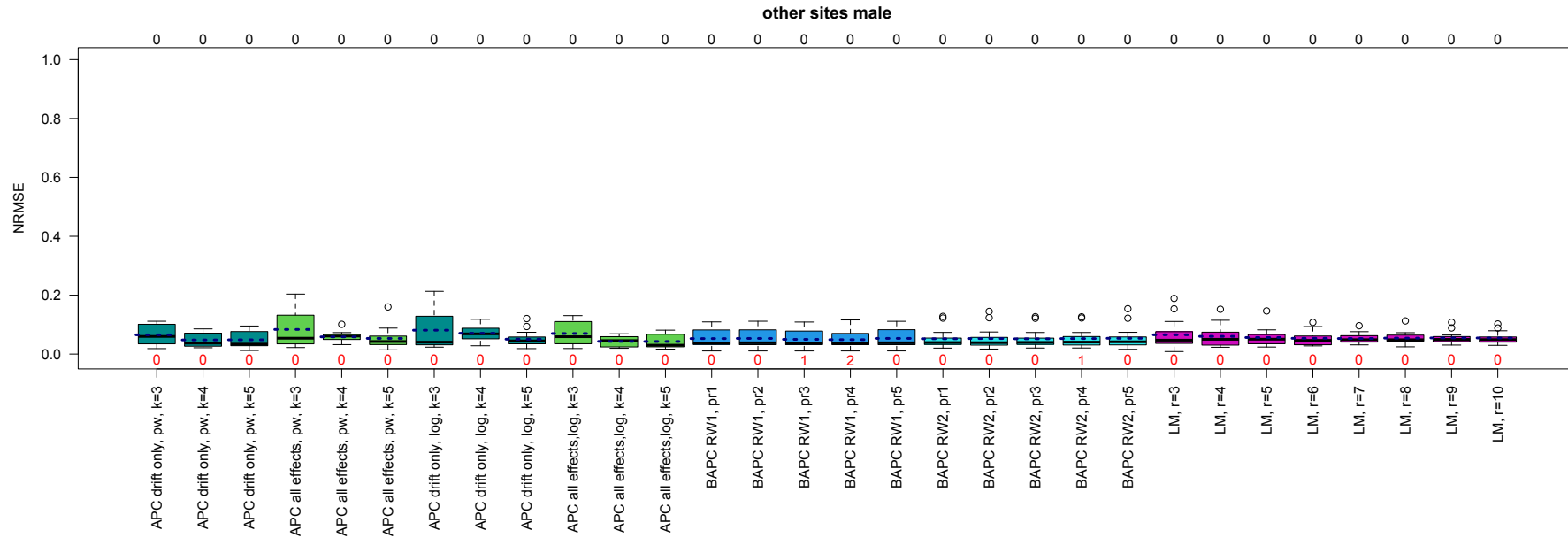


FIGURE 23 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the males and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\text{gamma}(1, 9e-4)$ prior for the age effect and $\text{gamma}(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\text{gamma}(1, 5e-03)$, $\text{gamma}(1, 5e-05)$, $\text{gamma}(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

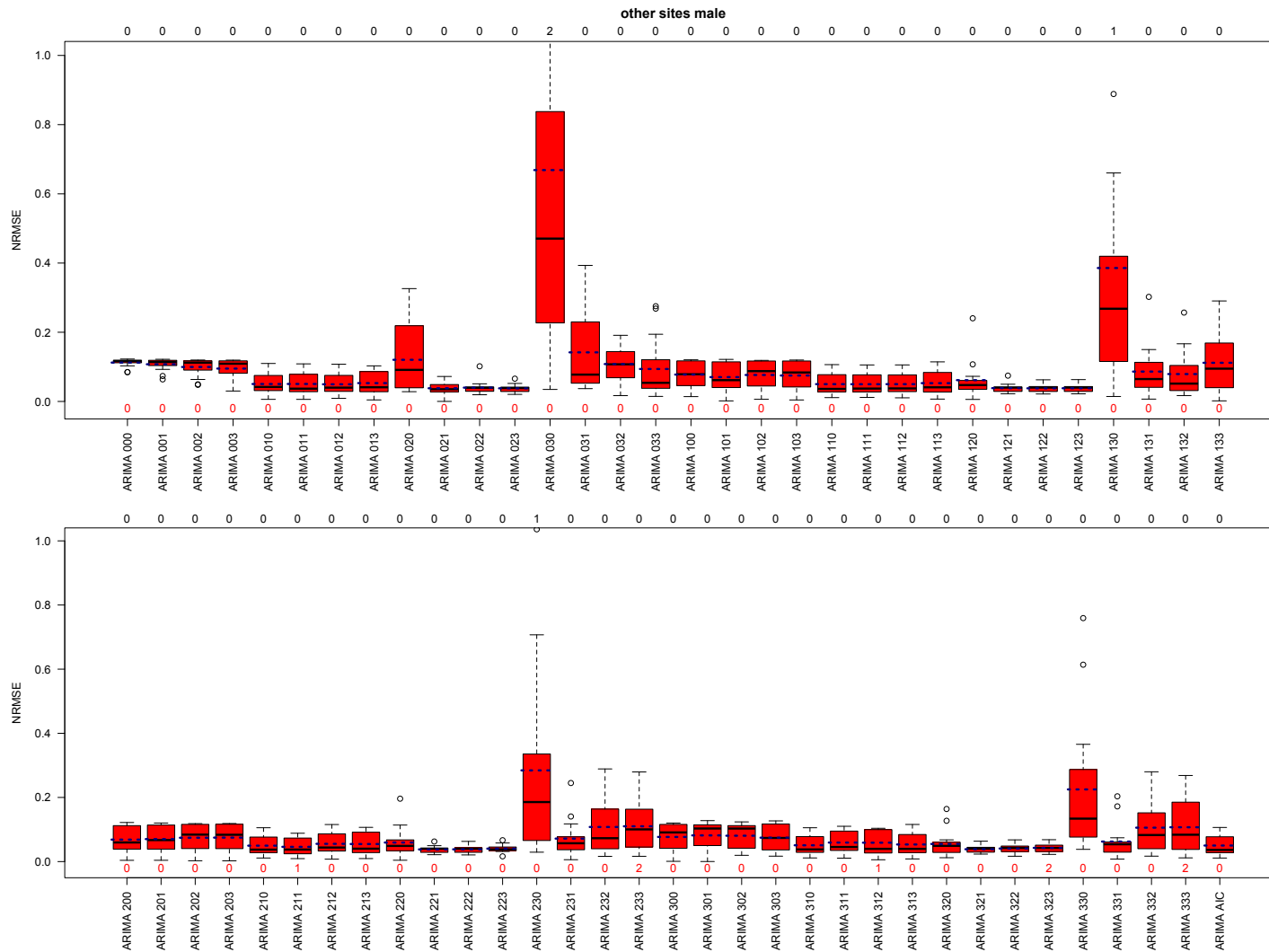


FIGURE 24 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the male and other sites cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

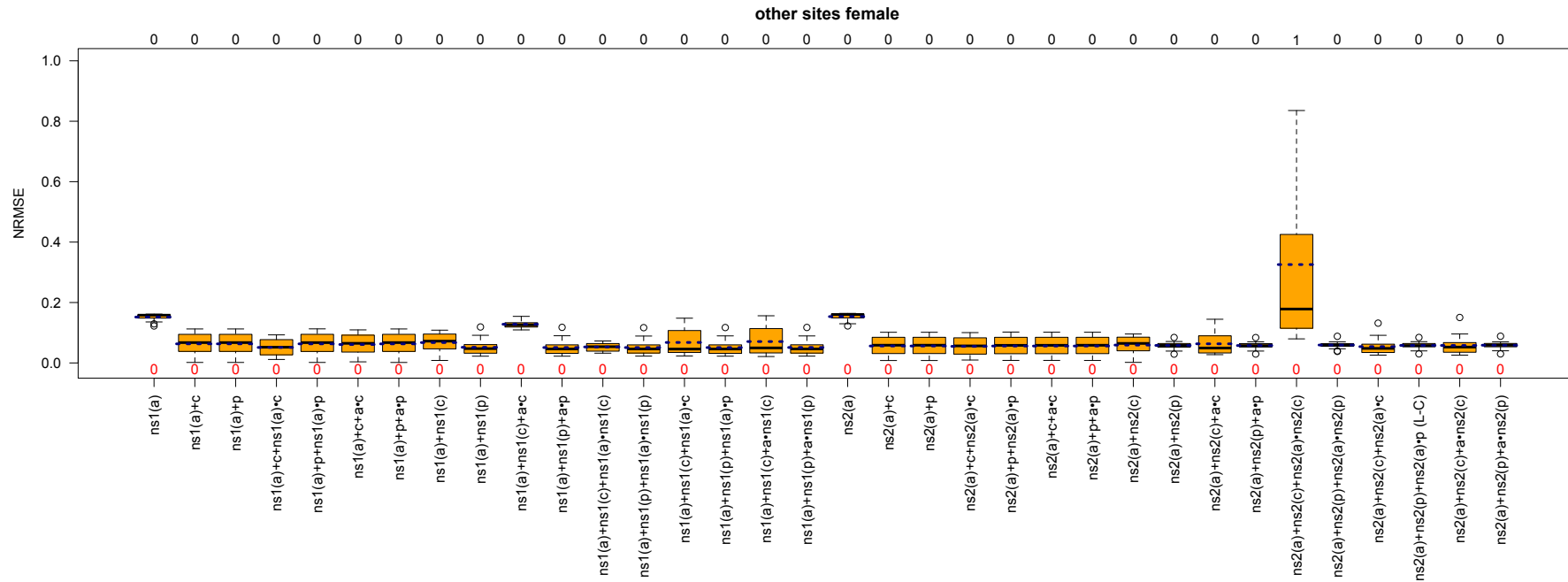


FIGURE 25 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

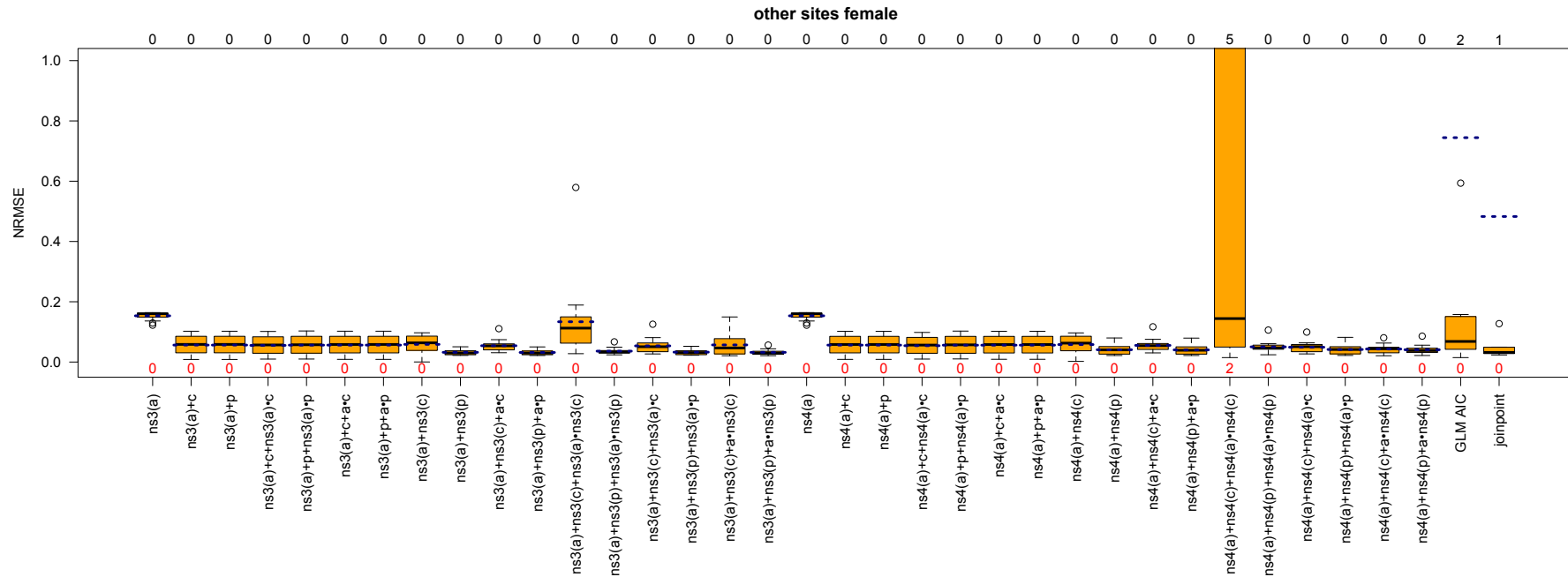


FIGURE 26 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

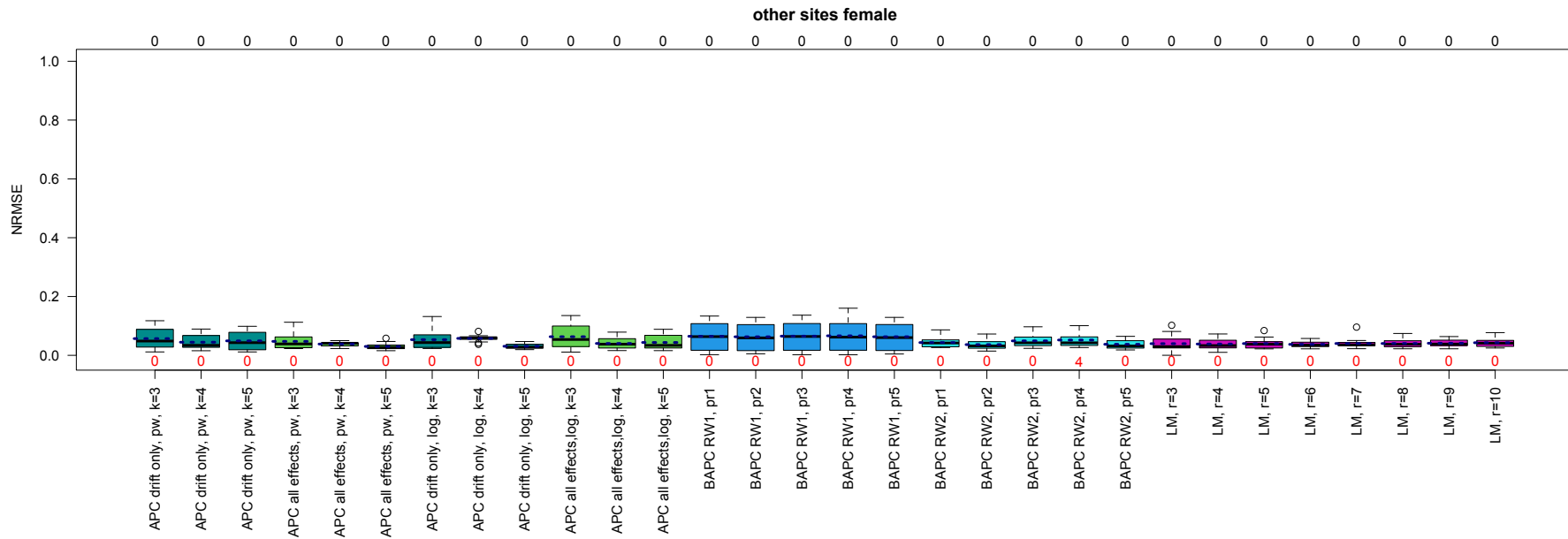


FIGURE 27 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the females and the other sites cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\gamma(1, 9e-4)$ prior for the age effect and $\gamma(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\gamma(1, 5e-03)$, $\gamma(1, 5e-05)$, $\gamma(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

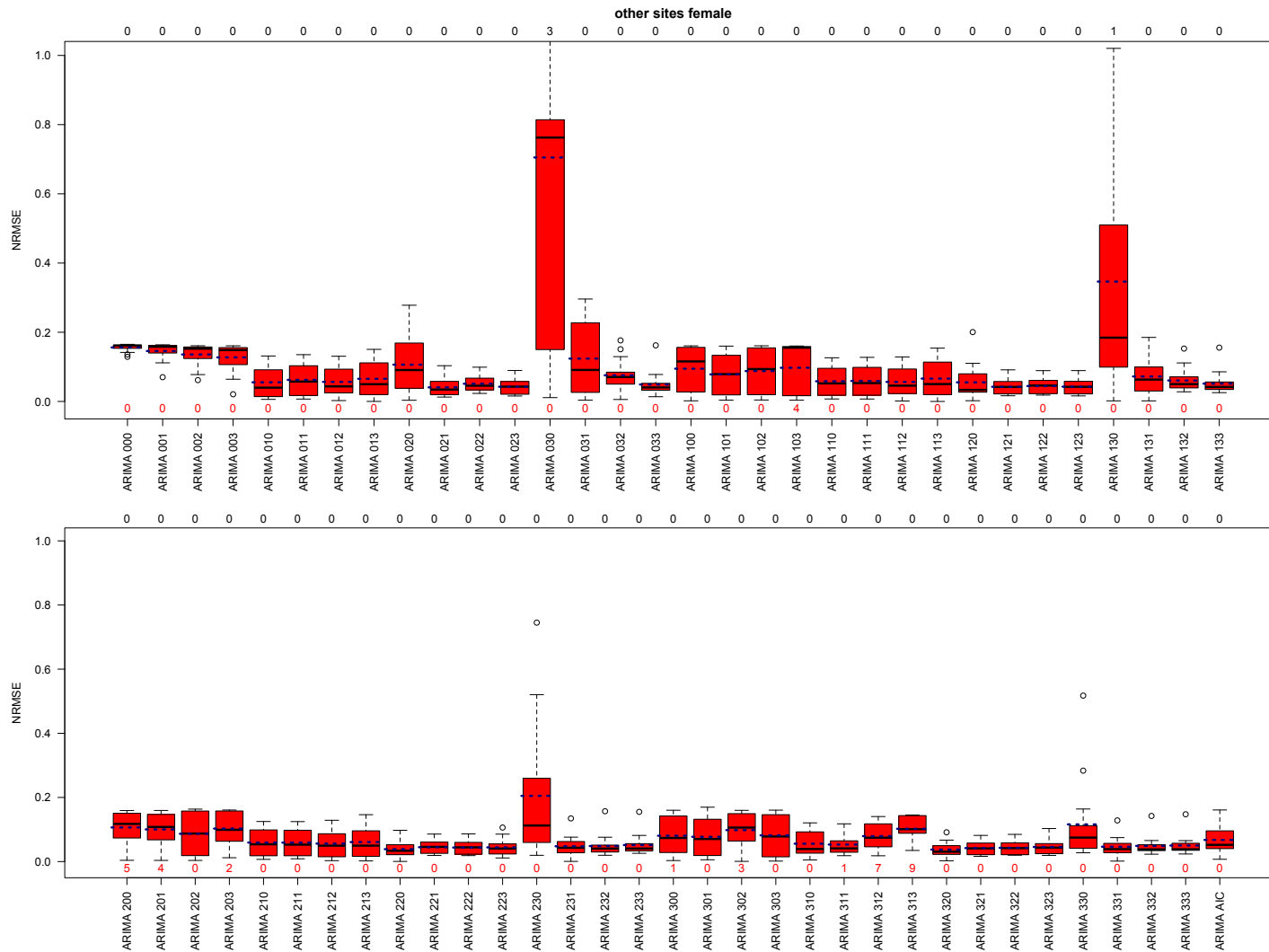


FIGURE 28 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the female and other sites cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

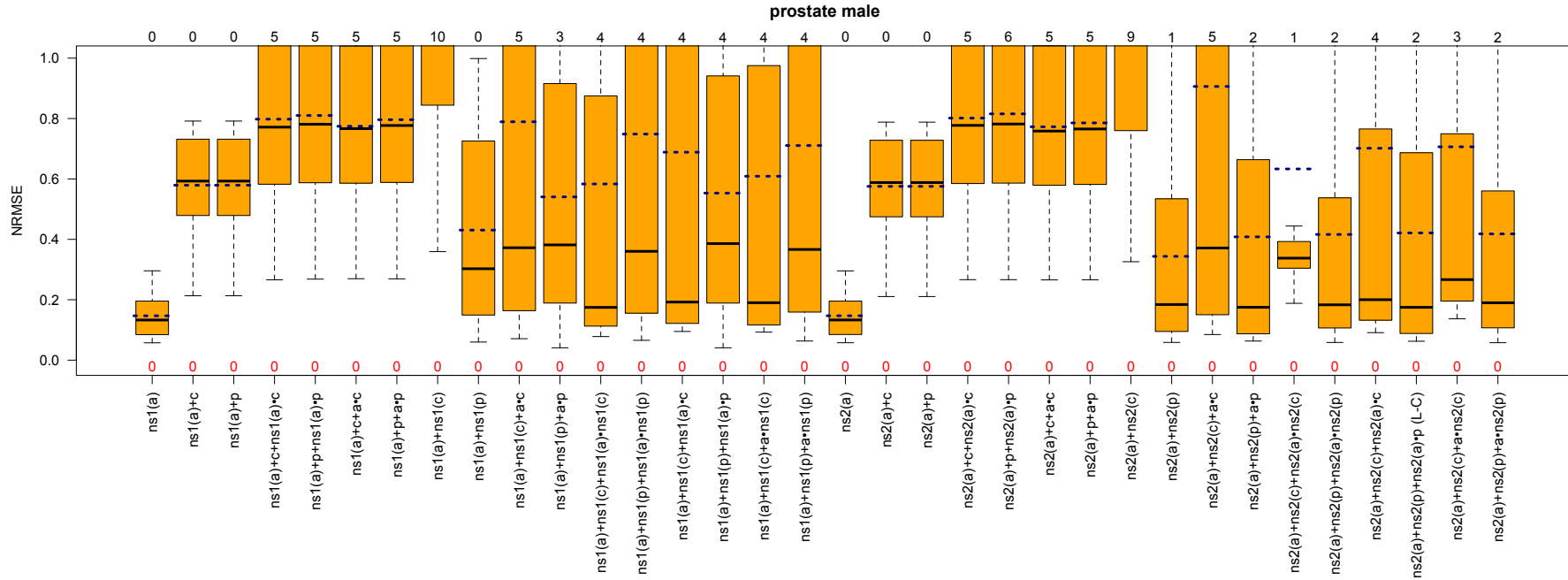


FIGURE 29 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the prostate cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

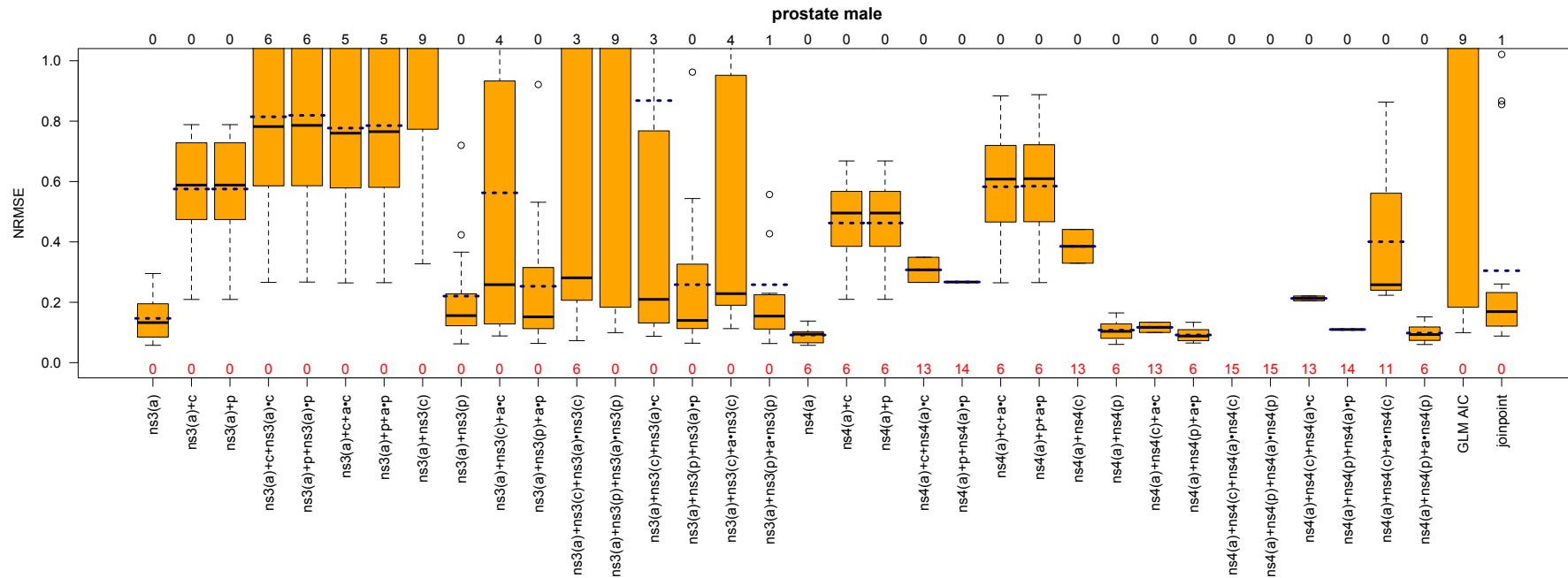


FIGURE 30 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the prostate cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

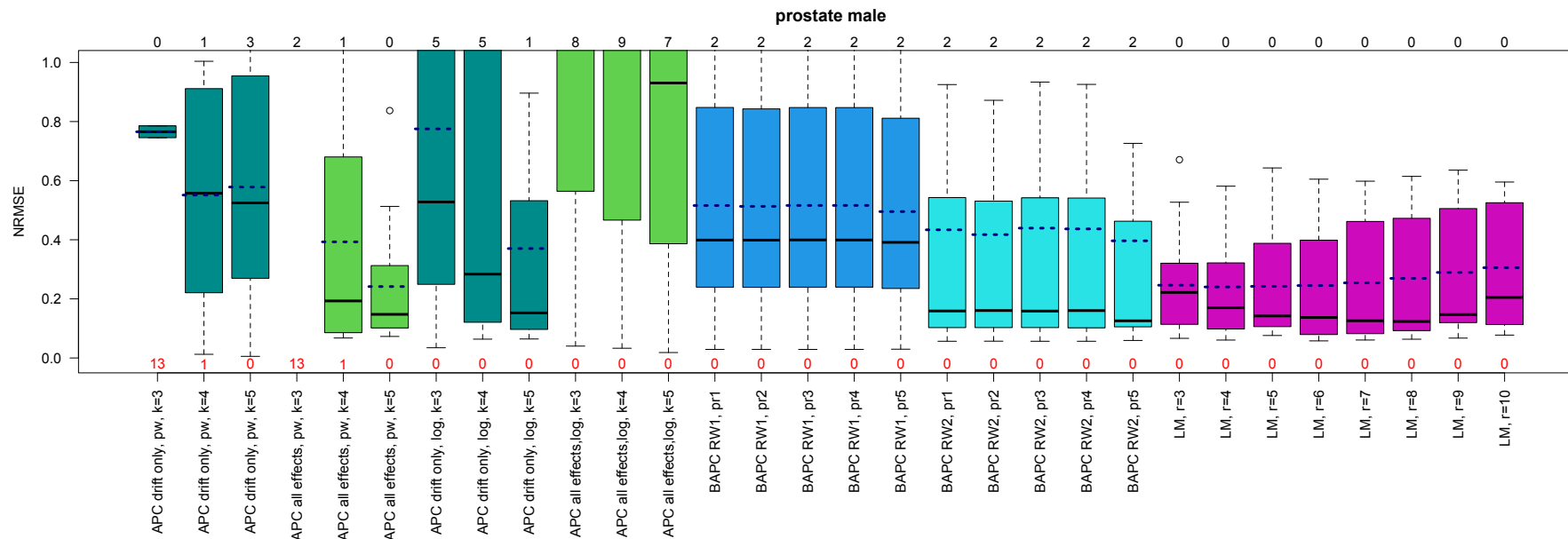


FIGURE 31 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the males and the prostate cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates $\gamma(1, 9e-4)$ prior for the age effect and $\gamma(1, 2.5e-4)$ prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate $\gamma(1, 5e-03)$, $\gamma(1, 5e-05)$, $\gamma(1, 5e-07)$ and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

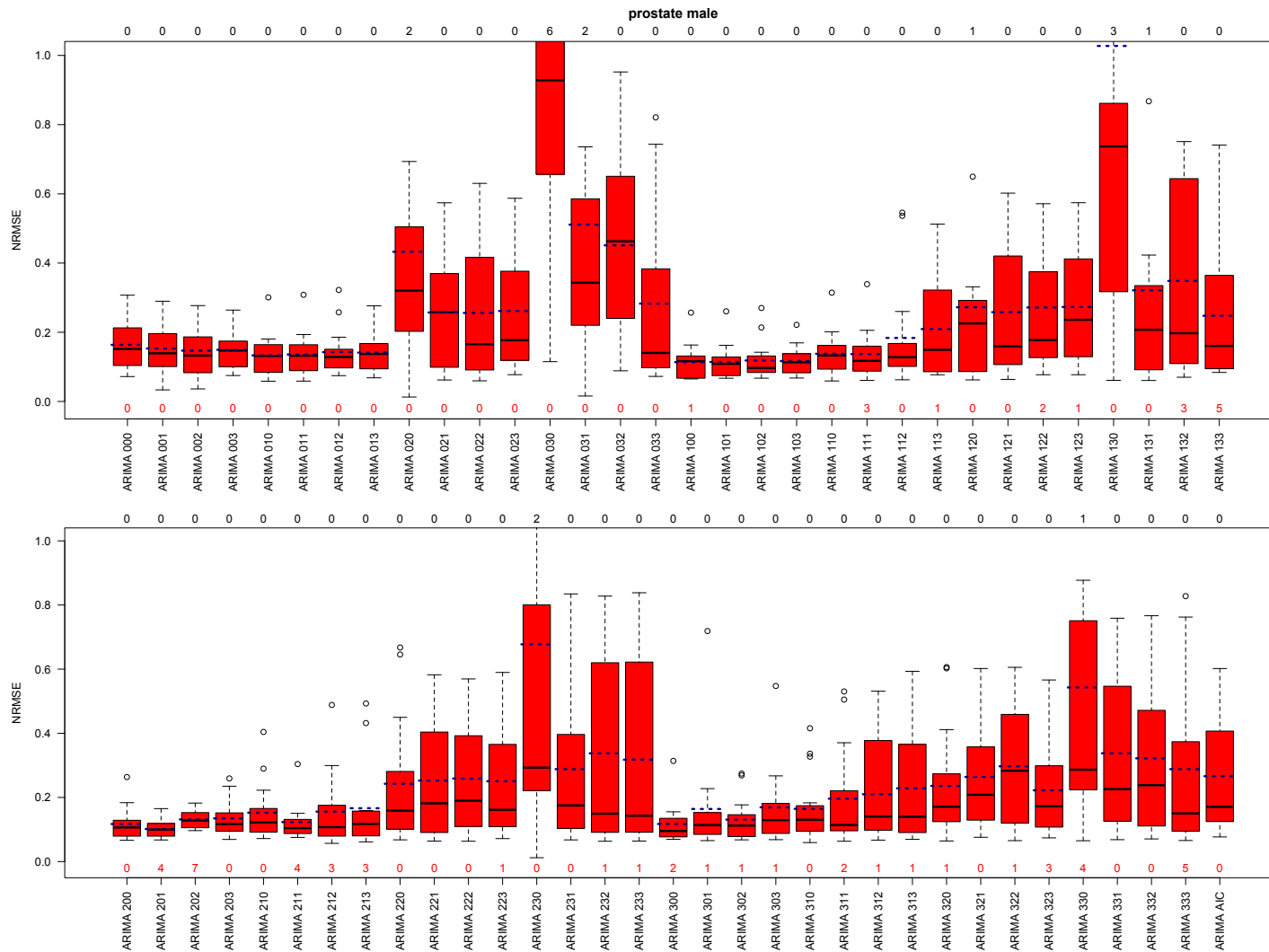


FIGURE 32 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the male and prostate cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

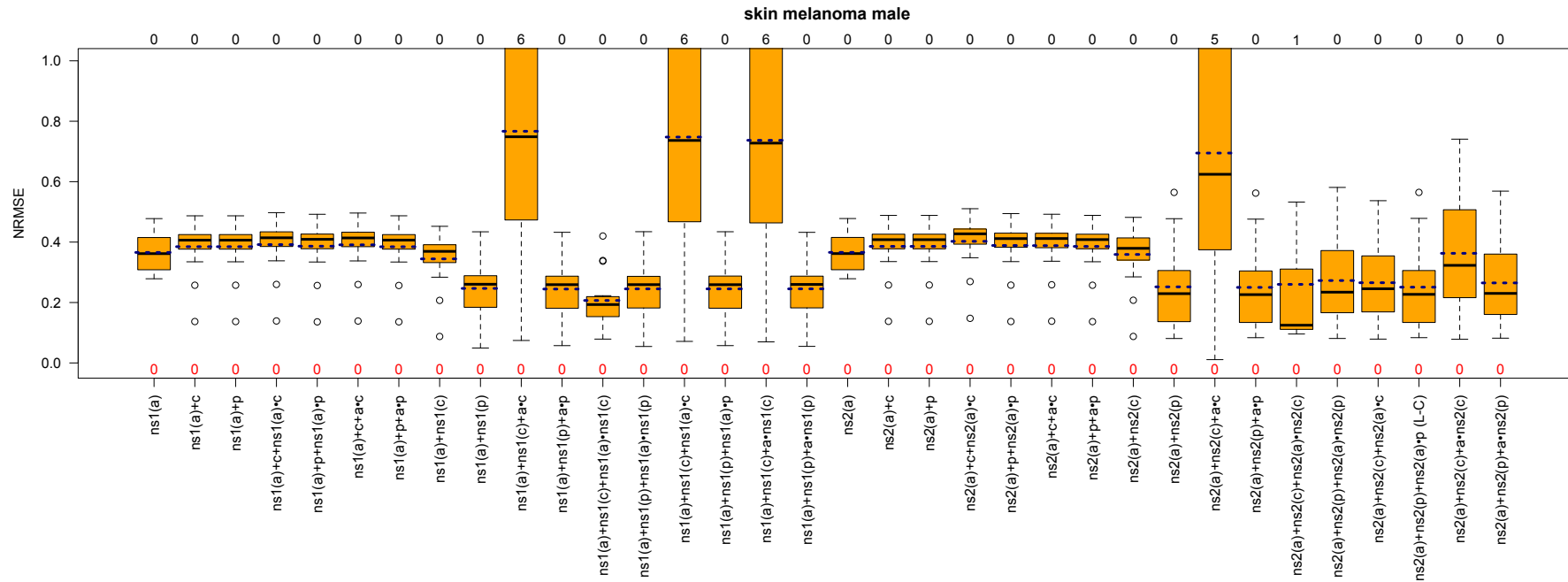


FIGURE 33 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

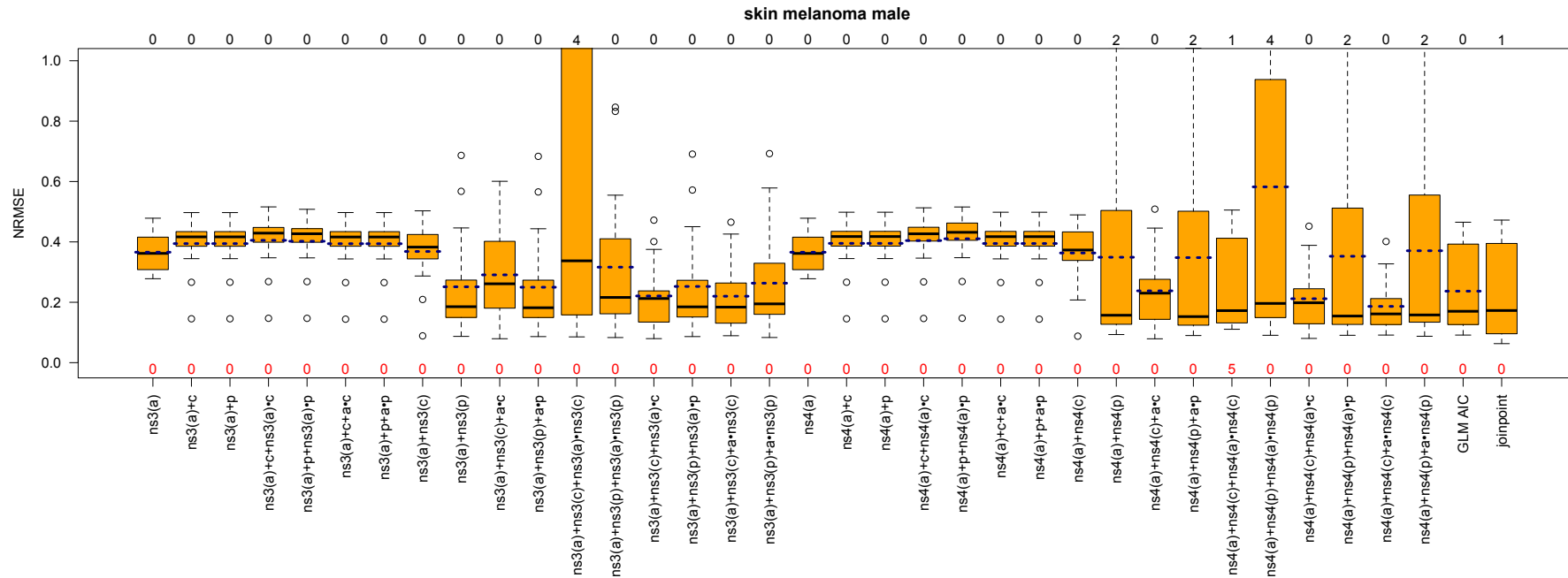


FIGURE 34 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the males and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE > 1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

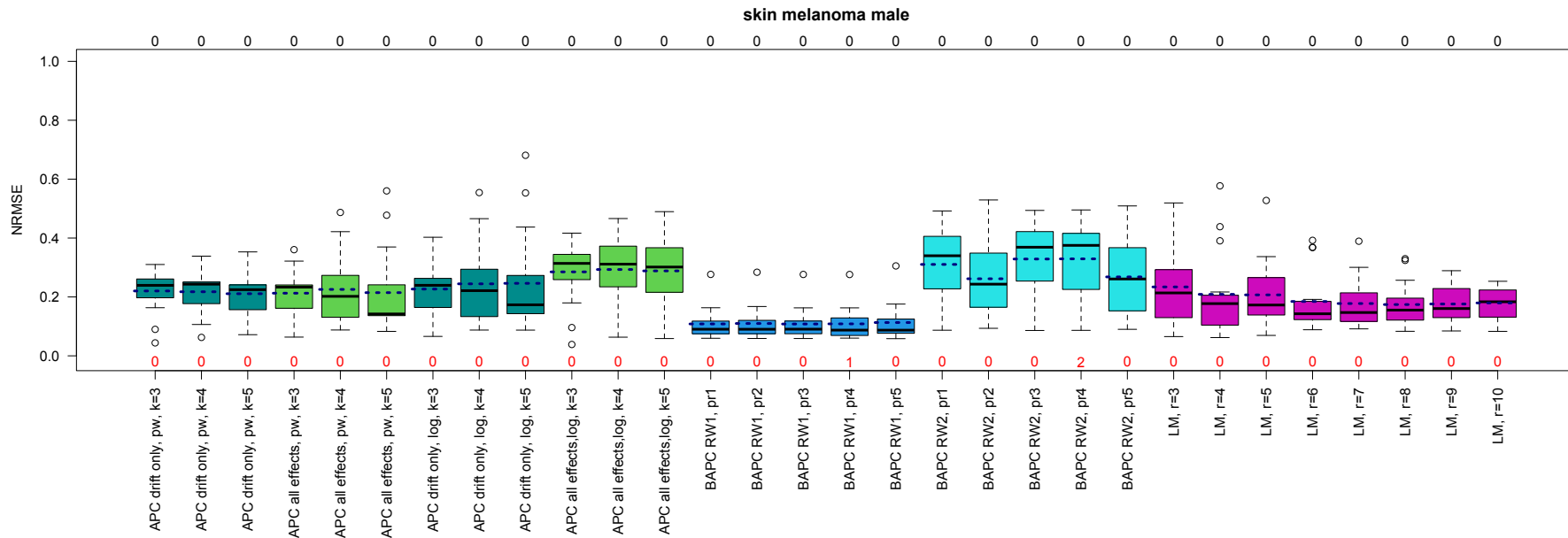


FIGURE 35 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the males and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates gamma(1, 9e-4) prior for the age effect and gamma(1, 2.5e-4) prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate gamma(1, 5e-03), gamma(1, 5e-05), gamma(1, 5e-07) and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

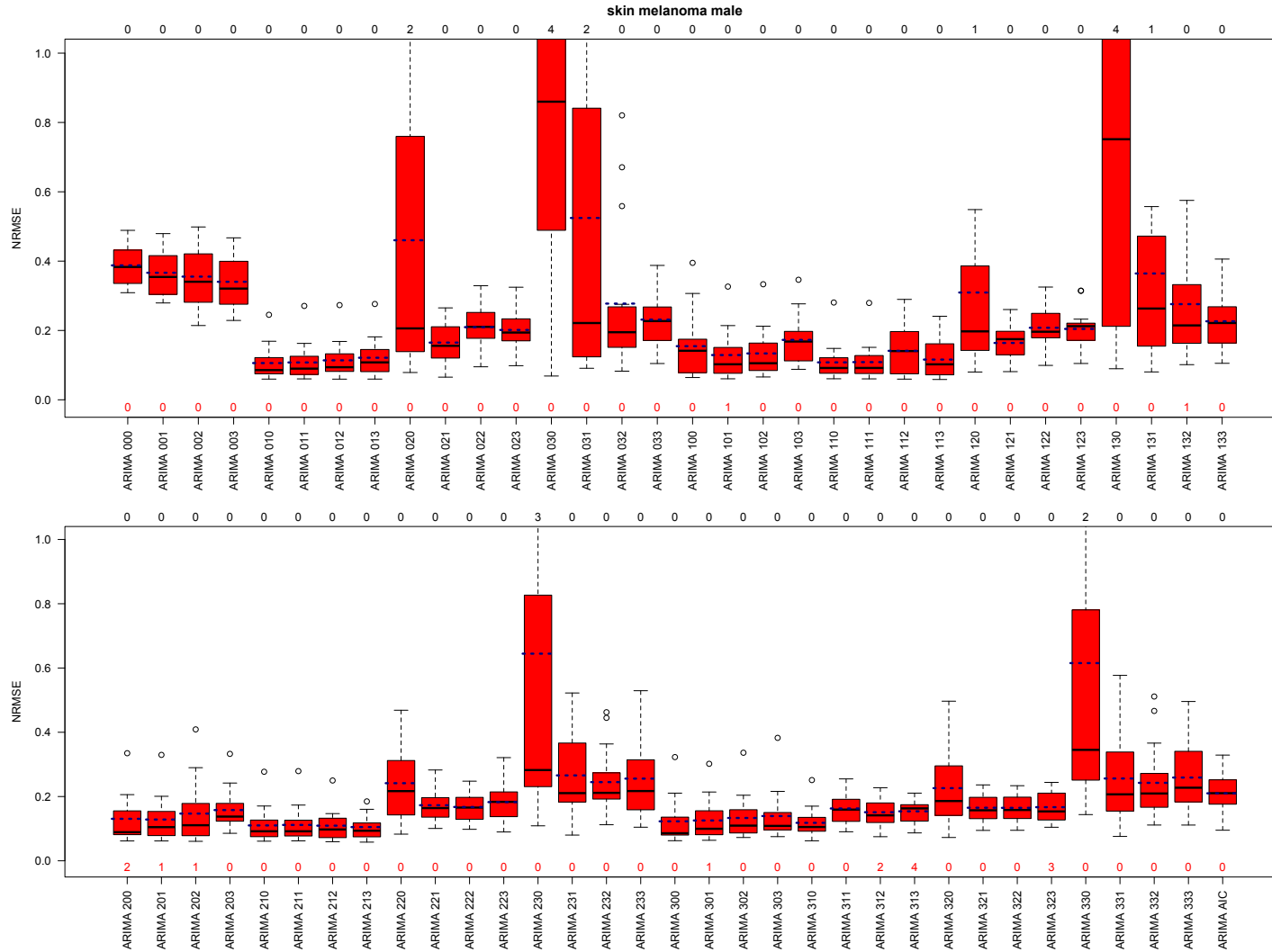


FIGURE 36 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the male and skin melanoma cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE >1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

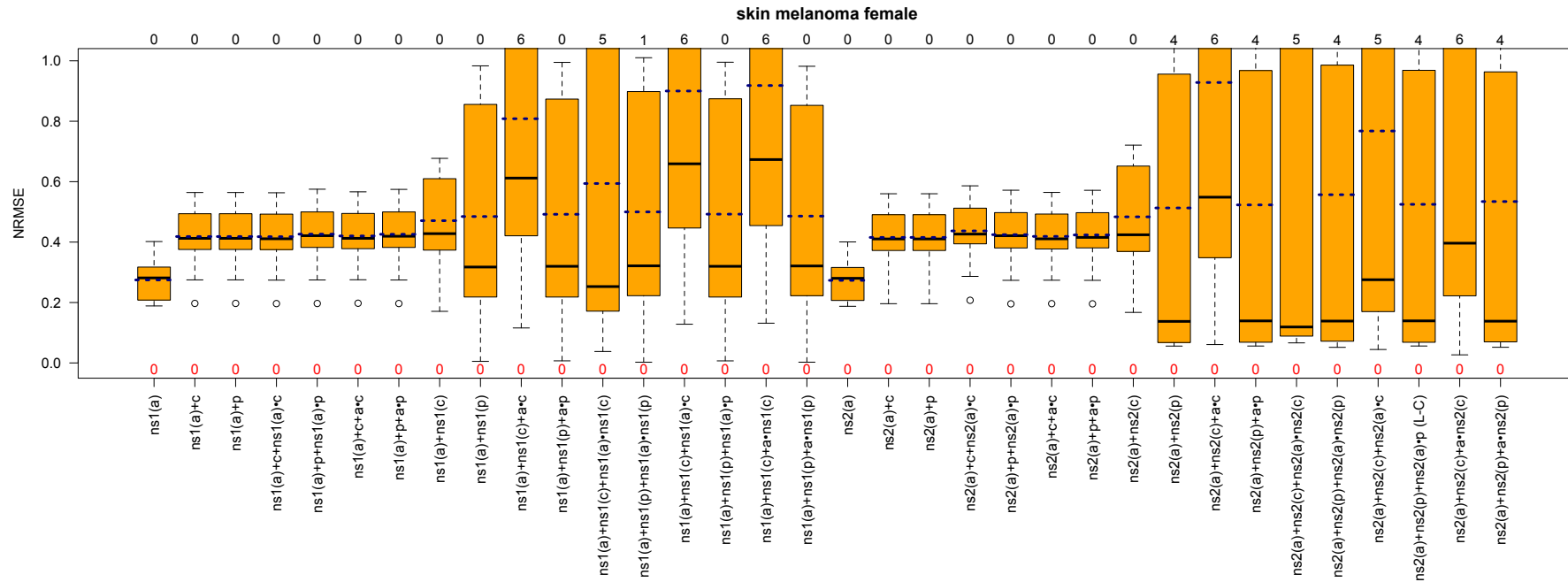


FIGURE 37 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 1$ and $k = 2$) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NRMSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region ($NRMSE > 1$). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge. The Lee-Carter (L-C) model is one of these models.

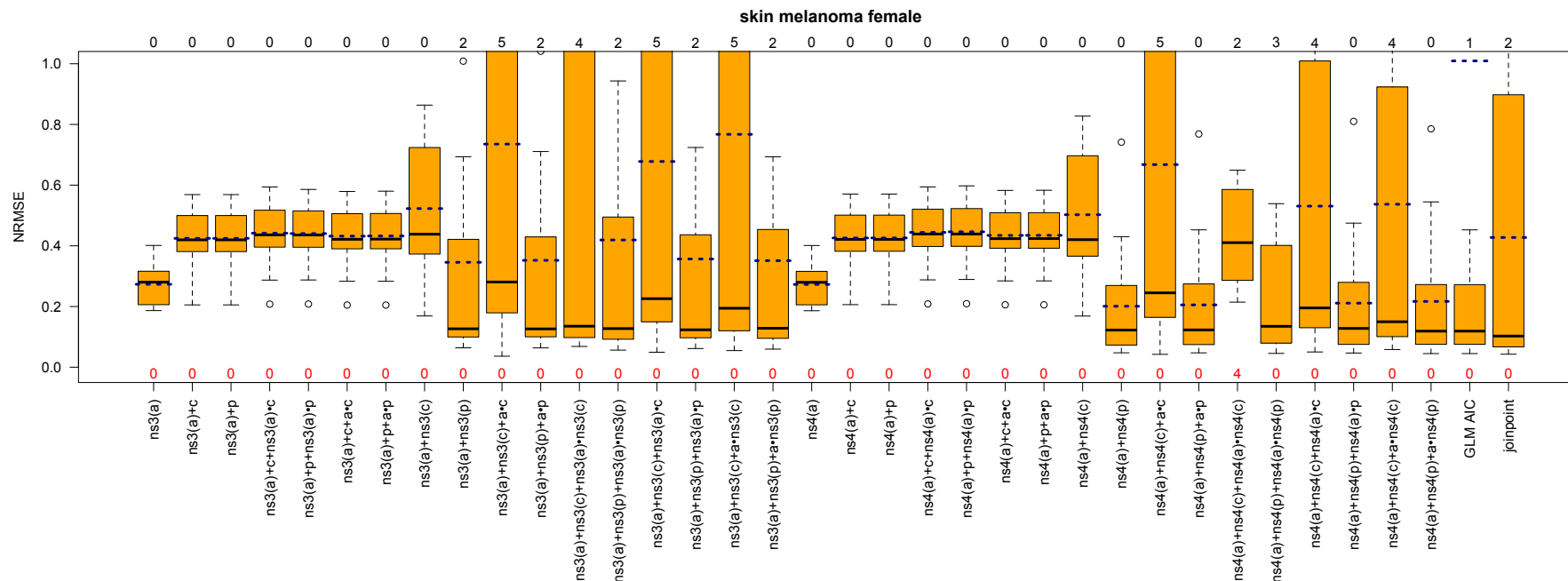


FIGURE 38 – Normalized Root Mean Square Error (NRMSE) distribution for 34 GLM (number of knots $k = 3$ and $k = 4$), a GLM AIC (35th model) and jointpoint regression (36th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the females and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. In the labels, “a”, “p”, and “c” refer to age, period and cohort, and nsk to natural splines with k knots. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

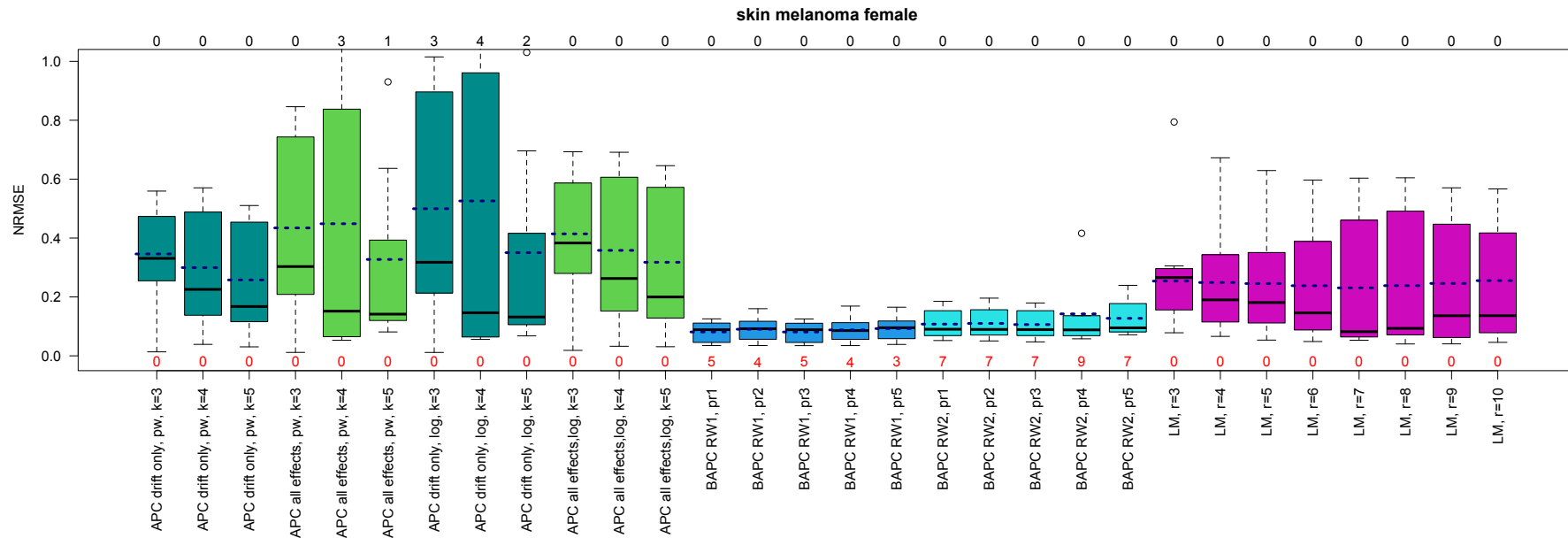


FIGURE 39 – Normalized Root Mean Square Error (NRMSE) distribution for 12 APC, 10 BAPC, and 8 LM across 15 scenarios (15 leave-future-out cross-validation scenarios the females and the skin melanoma cancer) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. For APC, “drift only” and “all effects” refer to prediction strategies extrapolating only the drift, respectively the drift + all non linear effects, “log” indicates the logarithmic link, “pw” the 1/5 power link, and k the number of knots used. For BAPC, RW1 and RW2 refer to first and second-order random walk, “p1” indicates gamma(1, 9e-4) prior for the age effect and gamma(1, 2.5e-4) prior for the period and cohort effects, “p2”, “p3”, “p4”, and “p5” indicate gamma(1, 5e-03), gamma(1, 5e-05), gamma(1, 5e-07) and PC priors for all effects, respectively. For LM, “r” is the number of past periods included in the regression. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE>1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.

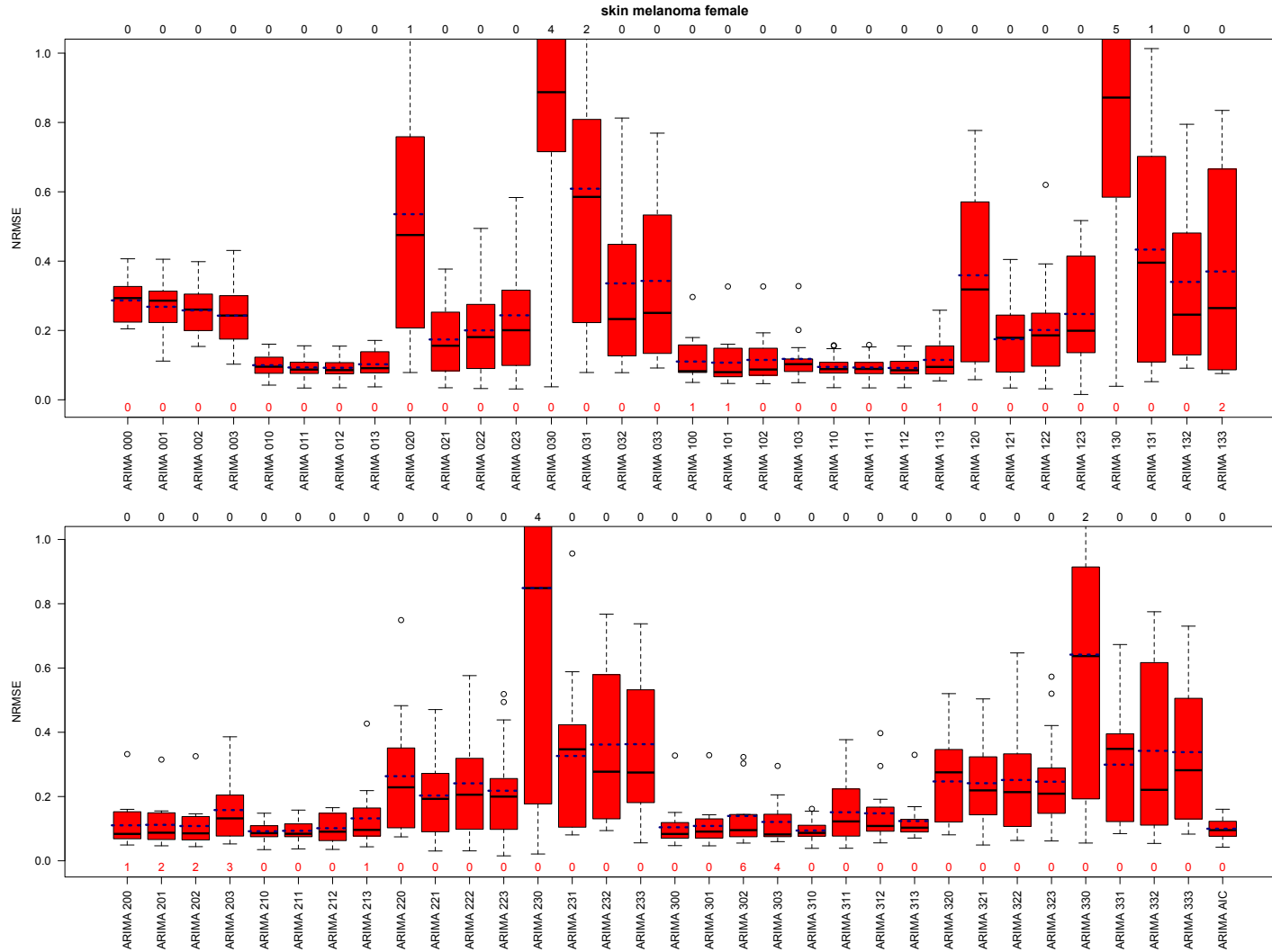


FIGURE 40 – Normalized Root Mean Square Error (NRMSE) distribution for 64 ARIMA with orders of each component (AR, I and MA) between 0 and 3, and an ARIMA AIC (65th model) across 15 scenarios (15 leave-future-out cross-validation scenarios for the female and skin melanoma cancer site) obtained on combined data from the Swiss registries of Vaud, Geneva and Neuchatel, 1982-2016. The mean NRMSE (M-NMRSE) is indicated with a dotted horizontal line. The numbers on the top of the graph give for each model the number of scenarios outside the plotted region (NRMSE >1). The number on the bottom is the number of scenarios for which the fitting algorithm of a method did not converge.