基于自适应深度射线树的 WLAN 室内目标入侵检测算法

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摘要 由于无线局域网 (wireless local area network, WLAN) 的广泛部署和智能终端对 WLAN 协议的普遍支持, 本文提出一种基于自适应深度射线树的 WLAN 室内目标入侵检测算法, 其利用现有 WLAN 基础设施即可实现未携带任何信号收发设备的室内目标的入侵检测. 为此, 首先建立基于自适应深度射线树的准三维射线追踪模型, 对室内静默和入侵状态下的接收信号强度 (received signal strength, RSS) 传播特性进行建模; 其次, 联合 RSS 均值、方差、最大值、最小值、极差值和中位值 6 种信号特征构建概率神经网络 (probabilistic neural network, PNN) 的训练数据库; 最后, 利用训练得到的 PNN 对新采集 RSS 数据进行多分类判决, 进而实现对室内目标的入侵检测与区域定位. 实验结果表明, 本文所提算法具有较高的入侵检测概率和较低的数据库构建开销.

关键词 无线局域网, 入侵检测, 射线追踪, 遗传算法, 神经网络

1 引言

现有室内目标入侵检测系统主要利用视频图像^[1]、全球定位系统 (global positioning system, GPS)^[2]、红外^[3]、超声波^[4]、压力传感器^[5]和无线传感网^[6]. 其中, 视频图像存在用户隐私泄露问题, 同时在夜晚或烟雾等光照条件恶劣的情况下无法使用; GPS、红外、超声波和压力传感器通常需要被检测目标携带特殊的硬件设备; 无线传感网往往要求在检测区域内部署大量的传感节点, 从而导致系统部署成本较高. 相较而言, 马里兰大学 (University of Maryland) 提出的无线局域网 (wireless local area network, WLAN) 室内目标入侵检测系统^[7]能够有效保护用户的位置隐私, 同时非视距且无需特殊硬件条件下具有稳定工作的优点. 基于此, 越来越多的国内外学者开始研究 WLAN 室内目标入侵检测算法, 较为典型的有: (1) 基于信号统计特征的入侵检测算法, 如运动均值 (moving average,

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MA) 和运动方差 (moving variance, MV) 检测算法^[8], 该算法仅需在离线阶段记录目标区域静默状态下的 WLAN 信号均值和方差特征, 然后根据在线阶段该特征相对于静默状态的变化规律进行目标入侵检测, 但这类算法不能实现对入侵目标的位置估计; (2) 基于被干扰链路几何位置推算的入侵检测算法, 该算法根据无线通信链路干扰变化特性推断被干扰链路, 然后通过被干扰链路的几何位置坐标估计入侵目标位置, 如文献^[9]中基于射频层析成像的入侵检测算法, 其根据射频链路变化与入侵目标位置之间的图像几何关系实现目标入侵检测, 但这类算法在多径衰落严重的室内环境下检测性能将急剧恶化; (3) 基于指纹学习的入侵检测算法, 该算法通过在离线阶段大量采集目标区域静默和不同入侵状态下的 WLAN 信号特征构建先验知识库, 然后根据在线阶段新观测链路干扰值与先验知识库的匹配结果估计入侵目标的位置, 如利用神经网络 (neural network, NN) 对目标区域内静默和入侵状态下的信号特征进行分类^[10], 但这类算法存在的主要问题是先验知识库的构建通常需要耗费大量的人力和时间开销. 比较上述算法, 本文所提基于自适应深度射线路径树的 WLAN 室内目标入侵检测算法系统整体流程如图 1 所示, 其具有如下特点: (1) 基于现有 WLAN 基础设施, 结合自适应深度射线树与概率神经网络 (probabilistic neural network, PNN) 来训练静默和入侵状态下的接收信号强度 (received signal strength, RSS) 特征, 相比于传统 RSS 特征数据库构建方法^[11]需要较小的人力开销; (2) 利用遗传算法 (genetic algorithm, GA) 自适应优化射线树的深度限制数, 相比于传统射线追踪方法^[12]在预测精度损失较小的情况下可以显著提高计算效率; (3) 联合 RSS 均值、方差、最大值、最小值、极差值和中位值 6 种信号特征构建 PNN 训练数据库, 使其具有更好的模式识别能力和学习收敛性^[13].

1.1 信号预测

由于电波辐射遵循几何光学 (geometrical optics, GO)^[14] 和一致性绕射 (uniform theory of diffraction, UTD)^[15] 理论, 且考虑 WLAN 信号波长 (约为 125 mm) 通常小于环境中固定设施或建筑物尺寸, 于是, 当传播信号遇到表面平坦且自身尺寸远大于信号波长的遮挡物时信号将发生反射, 而当传播信号遇到尖锐的棱或劈时信号将发生绕射^[16]. 由此可见, 室内环境中的目标入侵将导致信号传播方向及电波能量分布的变化. 于是, 本文利用 WLAN 信号波动特性与标定目标位置的相关性来实现对入侵目标的检测与区域定位. 为了分析 WLAN 信号的波动特性, 一般采用正向射线跟踪法^[17] 和反向射线跟踪法^[18]. 前者通过追踪从无线接入点 (access point, AP) 均匀辐射的每条波束所遇反射和绕射的过程, 在无线检测点 (monitor point, MP) 处利用接收球模型计算到达射线的相干叠加结果来实现对接收信号场强的估计, 但该方法存在的主要问题是信号传播预测误差较大; 而后者则从 MP 出发, 反向追踪从 AP 到达 MP 的每条射线的场强、时延和到达角, 该方法相比于前者具有较高的信号传播预测精度, 但其所对应射线树的深度限制数通常由经验值确定, 从而导致系统稳定性较差. 具体而言, 当深度限制数过小时, 容易忽略某些对 MP 处场强贡献较大的射线从而影响模型精度; 而当深度限制数过大时, 容易引入过多的对 MP 处场强贡献较小的射线从而降低计算效率. 此外, 传统三维射线追踪模型^[12] 直接在三维空间上搜索从 AP 到达 MP 的射线路径, 其运算复杂度和对环境中固定设施或建筑物信息数据库的要求较高; 传统二维射线追踪模型^[18] 则忽略固定设施或建筑物顶部对射线路径的作用, 而以二维投影面代替三维空间进行射线跟踪, 其模型准确性受到限制. 因此, 考虑现有二维和三维射线跟踪模型分别在信号预测精度和算法复杂度上的局限性, 本文采用的准三维射线追踪模型首先在二维投影面内进行射线追踪, 然后将其转化为三维空间中的传播路径, 该过程在预测精度损失较小的情况下可以显著提高计算效率. 于是, 综合考虑模型精度与计算效率两方面因素, 本文提出一种基于自适应深度射线树的准三维射线追踪模型, 如图 2 所示.

图 1 系统整体流程
Figure 1 Overall system flowchart

图 2 基于准三维射线追踪模型的信号预测流程
Figure 2 Signal prediction flowchart based on quasi three-dimensional ray tracing model

1.1.1 环境信息导入

图 3 给出了某一简单环境的三维建模及对应的二维投影结果, 图中灰色和黑色部分分别表示环境和室内设施边界面. 此外, 为了保证环境信息导入的完整性, 将记录每个边界面的三维顶点坐标、高度信息, 以及对应材质的相对介电常数、电导率和磁导率.

1.1.2 深度限制数优化

为了在保证信号传播预测精度损失较小的情况下显著提高射线树的计算效率, 本文利用 GA 算法自适应优化不同环境下射线树的深度限制数. 具体而言, 首先, 将深度限制数初始化为 1; 然后, 对环境三维建模结果中所有铅锤面和铅垂线进行编号, 同时根据每条射线经过的作用部分 (即铅锤面或铅垂线) 编号按时序拼接成一条染色体, 并将每条射线到达 MP 处的场强值作为其对应染色体的适应度; 其次, 由算法 1 计算当前深度限制数条件下的射线对 MP 处场强的贡献率; 最后, 判断当前深度限制数条件下的射线贡献率是否大于预设的阈值, 若是, 则深度限制数加 1 并重复上述步骤, 否则将当前深度限制数记为最优深度限制数 (或称最优射线阶数).

图 3 环境三维建模及对应的二维投影结果

Figure 3 Three-dimensional modeling of environment and the corresponding two-dimensional projection result

Algorithm 1 Calculation of the contribution degree of ray tree to the field strength at the MP

Input: n (limited number of depth of ray tree); D_k ($k = 1, \dots, N$) (number of the k -th functional part); N (number of functional parts); P_c (crossover probability); P_m (mutation probability); M (population size); ρ_{th} (threshold of calculation rate); e_{n-1} (maximum field strength with respect to the $(n-1)$ -th order of ray tree);

Output: C_n (contribution degree of the n -th order ray tree to the field strength at the MP);

- 1: Initialize the population T_1 from the M random chromosomes with the length of n , and then set the current population $T = T_1$;
 - 2: **repeat**
 - 3: Use the inverse ray-tracing approach to calculate the fitness of each chromosome in T , notated as $e_1, \dots, e_M$ (described in Algorithm 2);
 - 4: **repeat**
 - 5: Select two chromosomes in T according to the fitness ratio selection algorithm [19];
 - 6: **if** $\text{random}(0,1) < P_c$ **then**
 - 7: Conduct crossover operation on the two selected chromosomes;
 - 8: **end if**
 - 9: **if** $\text{random}(0,1) < P_m$ **then**
 - 10: Conduct mutation operation on the two selected chromosomes;
 - 11: **end if**
 - 12: Add the two new chromosomes obtained from crossover or mutation operation into the updated population T_{new} ;
 - 13: **until** obtain M different chromosomes;
 - 14: $T \leftarrow T_{new}$;
 - 15: Compute the calculation rate $\rho = N_C/N^n$, where N_C is the number of different chromosomes which have appeared from the initial to current populations;
 - 16: **until** $\rho > \rho_{th}$;
 - 17: Compute $T_f = e_{n-1}/2$;
 - 18: Count the number of chromosomes with the fitness larger than T_f in T , m ;
 - 19: Compute $C_n = m/M$.
-

关于算法 1 中利用反向射线跟踪法计算当前种群中每个染色体的适应度, 其计算过程如算法 2 所述.

为了实现算法 2 中二维射线投影的三维拓展, 假设任意射线在多次反射或绕射作用下均按最短路径传播, 同时考虑实际三维射线由若干段折线连接得到, 且各段折线相对于每条铅垂线的夹角 (即射线俯角) 均相等, 于是, 若将任意不经水平面作用的射线二维投影沿其经过的作用部分进行三维拓展, 则拓展后射线的二维展开结果为对应 AP 与 MP 的连线. 图 4 给出了某条不经水平面作用的 1 次绕

Algorithm 2 Calculation of the fitness of each chromosome by using the reverse ray-tracing approach

Input: D_k ($k = 1, \dots, N$); P_k and H_k ($k = 1, \dots, N_1$) (vertex coordinate and height of the k -th vertical line); N_1 (number of vertical lines); c_k , ε_k and μ_k ($k = 1, \dots, N_2$) (permittivity, conductivity, and permeability of the k -th vertical face); N_2 (number of vertical faces); λ (signal wavelength); P_t (transmitting power of each AP). (For simplicity and without losing generality, we assume that the transmitting power of each AP is the same);

Output: e_i (fitness of the i -th n chromosome);

- 1: Set the values of B_k ($k = 1, \dots, n+2$) for each chromosome based on the criteria that $B_1 = 1$ and $B_{n+2} = 1$ are for the AP and MP respectively, and $B_k = 0$ and 1 ($k = 2, \dots, n+1$) are for the signal reflection and diffraction on the k -th functional part respectively;
- 2: Denote the coordinates of AP and MP in the 2D projection plane as L_1 and L_{n+2} respectively;
- 3: **for** $k = 2 : n+1$ **do**
- 4: **if** $B_k = 0$ **then**
- 5: $L_k \leftarrow$ Coordinate of the mirror point of L_{k-1} with respect to the k -th vertical face in the 2D projection plane;
- 6: **else if** $B_k = 1$ **then**
- 7: $L_k \leftarrow$ Coordinate of the k -th vertical line in the 2D projection plane;
- 8: **end if**
- 9: **end for**
- 10: **repeat**
- 11: **if** $B_k = 0$ and $B_{k+1} = 1$ **then**
- 12: $L_k \leftarrow$ Coordinate of the intersection point of the connection between L_k and L_{k+1} and k -th vertical face;
- 13: $B_k \leftarrow 1$;
- 14: **end if**
- 15: **until** $B_i = 1$ ($i = 1, \dots, n$);
- 16: **for** $k = 1 : n+1$ **do**
- 17: Denote $T_{k,k+1}$ as the connection between L_k and L_{k+1} ;
- 18: **if** the intersection point of $T_{k,k+1}$ and a certain functional part exists **then**
- 19: $e_i \leftarrow 0$;
- 20: **break**;
- 21: **end if**
- 22: **end for**
- 23: **if** $e_i \neq 0$ **then**
- 24: Extend the i -th ray from the 2D projection plane to raw 3D space by the Fermat principle [20], and then select the field strength at the MP as the fitness of the i -th chromosome, e_i ;
- 25: **end if**

射加 1 次反射射线的三维拓展结果, 图中, P1 和 P2 分别为绕射点和反射点. 图 5 为该拓展后射线的二维展开结果, 图中, H_{AP} , H_{MP} , H_{P1} 和 H_{P2} 分别为 AP, MP, P1 和 P2 高度, L , d_1 , d_2 和 d_3 分别为二维展开结果中 AP 与 MP, AP 与 P1, P1 与 P2 和 P2 与 MP 的连线二维投影距离, θ 为射线俯角. 由几何关系可知

$$\theta = \arctan \frac{L}{(H_{AP} - H_{MP})}, \quad (1)$$

$$\begin{cases} H_{P1} = H_{AP} - \frac{d_1}{\tan \theta}, \\ H_{P2} = H_{AP} - \frac{d_1 + d_2}{\tan \theta}. \end{cases} \quad (2)$$

为了考虑室内天花板和地板作用部分对本文所提射线追踪模型的影响, 图 6 给出了某条经水平面作用的 1 次绕射加 2 次反射射线的三维拓展结果, 其对应的二维展开结果如图 7 所示, 图中, AP' 为

图 4 (网络版彩图) 某条不经水平面作用的射线三维拓展结果

Figure 4 (Color online) Three-dimensional development of a ray without the effect of the horizontal surface

图 5 某条不经水平面作用的射线二维展开结果

Figure 5 Two-dimensional expansion of a ray without the effect of the horizontal surface

图 6 (网络版彩图) 某条经水平面作用的射线三维拓展结果

Figure 6 (Color online) Three-dimensional development of a ray with the effect of the horizontal surface

AP 关于水平面的镜像点, P3 为水平面反射点. 由几何关系可知

$$\theta = \arctan \left(\frac{L}{H_{AP} + H_{MP}} \right), \quad (3)$$

$$\begin{cases} H_{P1} = H_{AP} - \frac{d_1}{\tan \theta}, \\ H_{P2} = H_{MP} - \frac{d_3}{\tan \theta}. \end{cases} \quad (4)$$

1.1.3 接收信号功率计算

为了计算 MP 处的接收信号功率, 分别考虑直达和非直达射线. 对于直达射线, 由文献 [21] 可计

图 7 某条经水平面作用的射线二维展开结果

Figure 7 Two-dimensional expansion of a ray with the effect of the horizontal surface

算其到达信号场强 E_{LOS} :

$$E_{\text{LOS}} = E_0 \frac{e^{-jk r_0}}{r_0}, \quad (5)$$

其中, E_0 为距离 AP1m 处的到达信号场强, $k (= 2\pi/\lambda)$ 为波数, λ 为波长, P_t 为 AP 发射功率, r_0 为 AP 与 MP 的距离. 对于非直达射线, 则由经过作用部分的反射和绕射特性, 迭代计算其到达信号场强 E_{NLOS} :

$$E_{\text{NLOS}} = E_{\text{LOS}}^1 \prod_{n=1}^N R_n \prod_{m=1}^M D_m \prod_{t=1}^{N+M} A_t e^{-jk r_t}, \quad (6)$$

其中, E_{LOS}^1 为由式 (5) 计算得到的第 1 个作用点相对于 AP 的直达射线到达信号场强, R_n 和 D_m 分别为第 n 和第 m 个作用部分的反射和绕射系数^[22,23], N 和 M 分别为反射和绕射次数, A_t 为第 t 次反射或绕射的扩散因子, r_t 为第 t 到第 $t+1$ 个作用点的距离. 将所有 n 阶以内直达和非直达射线到达信号场强进行叠加, 并由射线功率和法^[21] 可得 MP 处的接收信号功率 P_{total} :

$$P_{\text{total}} = \sum_{i=1}^l \left(\frac{\lambda |E_i|}{4\pi |E_0|} \right)^2, \quad (7)$$

其中, E_i 为第 i 条射线的到达信号场强, l 为射线数.

1.2 入侵检测

本文基于 Bayes 决策理论的核密度估计方法来实现对静默和入侵状态下 PNN 特征数据的训练¹⁾. 具体而言, 首先利用核密度函数估计不同状态的条件概率, 然后根据 Bayes 决策理论将具有最大后验概率的状态作为 PNN 输出^[24]. 本文采用的 PNN 中各层 (包含输入层、模式层、求和层和输出层) 神经元的计算过程如表 1 所示.

1) 考虑人体内水的含量大于 70%, 在入侵状态下将人体建模为具有一定高度的三维水柱^[25], 并由此计算 MP 处的信号功率.

表 1 PNN 各层神经元计算过程

Table 1 The calculation process of each layer of PNN neurons

Functional layer	Number of neurons	Calculation process
Input layer	Signal feature dimension d	<p>(1) Compute $z_k = \mathbf{x}_k^T \mathbf{x}$ ($k = 1, \dots, n$), in which $\mathbf{x} = (x_1/\sqrt{\sum_{j=1}^d x_j^2}, \dots, x_d/\sqrt{\sum_{j=1}^d x_j^2})$ and $\mathbf{x}_k = (x_{k1}/\sqrt{\sum_{j=1}^d x_{kj}^2}, \dots, x_{kd}/\sqrt{\sum_{j=1}^d x_{kj}^2})$ are normalization vectors of test sample and k-th training sample, respectively, n is the size of training samples.</p> <p>(2) Assign the connection weights ω_{jk} of the j-th neuron in the input layer and the k-th neuron in the model layer, and the assignment process is described in Algorithm 3.</p>
Model layer	n	<p>(1) Compute kernel density function $\varphi(z_k) = \exp(\frac{z_k-1}{\delta^2})$, in which δ is the smoothing factor.</p> <p>(2) Assign the connection weights a_{ki} ($i = 1, \dots, c$) of the k-th neuron in the model layer and the i-th neuron in the summation layer, in which c is the number of states. If $\mathbf{x}_k$ belongs to i-th state, then $a_{ki} = 1$, otherwise $a_{ki} = 0$, as described in Algorithm 3.</p>
Summation layer	c	Compute the conditional probability of $\mathbf{x}$ belonging to the i -th state $g_i(\mathbf{x}) = \frac{P_i}{N_i} \sum_{k \in \{1, \dots, n\} \cup a_{ki}=1} \varphi(z_k)$, in which P_i is the priori probability of the i -th state and, N_i is the number of training samples that belong to the i -th state.
Output layer	1	Computemax $\{g_i(\mathbf{x}), i \in \{1, \dots, c\}\}$, in which the i that corresponds to the maximum value of $g_i(\mathbf{x})$ is the output state of PNN.

Algorithm 3 PNN training

Input: $\mathbf{x}_k = (x_{k1}, \dots, x_{kd}), k = 1, \dots, n$ (n is the number of training RSS data; d is the dimensions of RSS characteristics);

Output: Connection weight between the j -th neuron in input layer and k -th neuron in model layer ω_{jk} ($j = 1, \dots, d; k = 1, \dots, n$) and weight between the k -th neuron in model layer;

1: $k \leftarrow 0, \omega_{jk} \leftarrow 0, a_{ki} \leftarrow 0$;

2: **repeat**

3: $k \leftarrow k + 1$;

4: $x_{kj} \leftarrow x_{kj} / \sqrt{\sum_{j=1}^d x_{kj}^2}$;

5: $\omega_{jk} \leftarrow x_{kj}$;

6: **if** $\mathbf{x}$ is corresponding to the i -th state **then**

7: $a_{ki} \leftarrow 1$;

8: **end if**

9: **until** $k = n$.

由表 1 所述 PNN 各层神经元的计算过程, 可知 PNN 训练目标即为确定具有最优分类性能的连接权重, 该训练过程如算法 3 所述.

为了保证每对 AP 与 MP 之间 RSS 特征数据的稳定性, 本文利用滑动窗函数^[26]对原始 RSS 数据进行分段²⁾, 并计算各分段数据的 RSS 均值、方差、最大值、最小值、极差值和中位值. 在此基础上, 利用该 6 种信号特征分别训练 6 个 PNN 结构, 然后对于每个 PNN 独立得到关于测试样本的分类结果. 最后, 根据投票准则^[27]完成对新采集 RSS 数据的多分类判决, 进而实现对室内目标的入侵检测

2) 每段 RSS 数据长度即为滑动窗宽度^[26].

图 8 实验环境结构图

Figure 8 Structural diagram of experimental environment

图 9 (网络版彩图) 各代种群的总体适应度变化情况

Figure 9 (Color online) The change of the overall fitness of each generation of population

表 2 每对 AP 与 MP 之间射线建模所需的平均时间开销

Table 2 Average time cost for ray modeling between each pair of AP and MP

Performance index	Ref. [18]	Ref. [12]	The proposed method
Time overhead (s)	6.03	7.25	3.41

与区域定位.

2 实验结果

2.1 实验环境

本文选用的实验环境如图 8 所示, 其中, 2 个 AP (即 AP1 和 AP2, 型号为 D-Link DAP2310) 和 3 个 MP (即 MP1, MP2 和 MP3, 型号为 SAMSUNG GT-S7568) 分别放置于 2 m 和 0.5 m 高处. 在每个 MP 处, 分别采集静默和入侵状态下来自各个 AP 的 5 分钟 RSS 数据.

2.2 结果讨论

2.2.1 GA 优化结果

图 9 给出了在不同 ρ_{th} 值条件下利用 GA 算法计算深度限制数为 3 的射线场强贡献率³⁾时每代

3) 在本实验环境下, 利用 GA 算法可得最优深度限制数为 3.

图 10 (网络版彩图) 关于不同 AP 的 RSS 热度分布图

Figure 10 (Color online) RSS heat distribution map of different AP. (a) AP1 measurement; (b) AP1 prediction; (c) AP2 measurement; (d) AP2 prediction

图 11 (网络版彩图) 关于不同 AP 的 RSS 预测误差 CDF 曲线

Figure 11 (Color online) RSS prediction error CDF curve of different AP. (a) AP1; (b) AP2

种群的总体适应度变化情况, 其中, 总体适应度定义为种群中染色体适应度大于阈值的个数 m 与种群规模 M 的比值. 可以看出, 随着种群代数的增加, 总体适应度整体上呈上升趋势且当种群代数达到 30 时趋于一致, 从而验证了 GA 算法在深度限制数自适应优化方面的可靠性和收敛性.

此外, 表 2 比较了在深度限制数为 3 的条件下传统二维射线追踪模型^[18]、三维射线追踪模型^[12]和本文方法关于每对 AP 与 MP 之间射线建模所需的平均时间开销. 由表 2 可知, 本文方法在时间开

图 12 (网络版彩图) 静默状态下不同 AP 与 MP 之间的射线建模结果

Figure 12 (Color online) Ray tracing results between different AP and MP under the silence scenario. (a) AP1 and MP1; (b) AP2 and MP1; (c) AP1 and MP2; (d) AP2 and MP2; (e) AP1 and MP3; (f) AP2 and MP3

销方面明显优于文献 [12, 18] 中方法, 其主要原因在于后两种方法需要遍历所有经过作用部分的射线路径组合, 而本文方法则利用 GA 算法快速优化深度限制数, 并通过剔除对 MP 处信号功率贡献较小的射线来降低数据库构建开销。

2.2.2 信号预测结果

根据图 10 给出的实测和利用本文方法预测得到的 RSS 热度分布图, 可知本文方法能够有效预测

图 13 (网络版彩图) 入侵状态下不同 AP 与 MP 之间的射线建模结果

Figure 13 (Color online) Ray tracing results between different AP and MP under the intrusion scenario. (a) AP1 and MP1; (b) AP2 and MP1; (c) AP1 and MP2; (d) AP2 and MP2; (e) AP1 and MP3; (f) AP2 and MP3

真实环境下的 RSS 传播特性. 此外, 图 11 比较了在深度限制数为 3 的条件下文献 [12, 18] 和本文方法的 RSS 预测误差累积密度函数 (cumulative density function, CDF) 曲线. 可以看出, 本文方法关于 AP1 和 AP2 的 RSS 预测误差 3 dB 内的置信概率分别为 66.76% 和 65.22%, 优于前两者的 43.62% 和 43.39%, 以及 59.81% 和 56.64%.

2.2.3 射线建模结果

图 12 给出了在静默状态下利用本文方法得到的关于每对 AP 与 MP 之间的射线建模结果, 图 12

图 14 (网络版彩图) 不同参数条件下入侵状态的成功检测概率

Figure 14 (Color online) Successful detection probability under different parameters. (a) Successful detection probability vs. sliding window width; (b) successful detection probability vs. smoothing factor

中, 不同颜色的直 (或折) 线代表不同的射线类型 (如直射、1 次反射/绕射、2 次反射/绕射、3 次反射/绕射、1 次绕射、1 次反射加 1 次绕射、1 次反射加 2 次绕射, 以及 1 次绕射加 2 次反射). 当环境中存在入侵时, 某些 AP 与 MP 之间的射线将受人体反射或绕射的影响而发生变化, 从而改变相应 MP 处的信号功率. 以某一入侵目标 (坐标为 (5.5 m, 14 m)) 对不同 AP 与 MP 之间射线建模结果的影响为例, 通过比较图 12 和 13 的射线建模结果, 可看出该入侵目标对 MP 处信号功率的影响是显著的. 基于此, 本文利用每对 AP 与 MP 之间的 RSS 特征数据训练 PNN 多分类判决器, 以实现室内目标的入侵检测与区域定位.

2.2.4 参数优化结果

滑动窗宽度^[26]和平滑因子是影响 PNN 训练性能的重要参数, 这两个参数的取值将影响 PNN 多分类判决器关于入侵状态的成功检测概率⁴⁾. 一方面, 若滑动窗宽度过小 (如小于 30), 则可能难以保证 RSS 特征数据的稳定性, 从而导致成功检测概率下降; 反之, 若滑动窗宽度过大 (如大于 30), RSS 特征数据可能对入侵目标所造成的射线变化不敏感, 从而导致 PNN 分类结果不准确, 成功检测概率下降. 此外, 若平滑因子过小 (如小于 1.5), PNN 分类隔离效果可能会过度细化, 从而导致训练不充分, 成功检测概率下降; 反之, 若平滑因子过大 (如大于 1.5), PNN 可能无法准确分辨边界不显著的不同状态, 从而亦会导致成功检测概率下降. 综上所述, 滑动窗宽度和平滑因子的取值不宜过大或过小. 基于此, 图 14 比较了在不同参数条件下 PNN 多分类判决器关于入侵状态的成功检测概率, 并由此确定最优滑动窗宽度和平滑因子分别为 30 和 1.5.

2.2.5 入侵检测结果

为了进一步验证本文方法的入侵检测与区域定位性能, 将图 8 所示实验环境进行 2, 3, 4, 5 和 6 区域划分, 如图 15 所示. 基于此, 图 16 给出了在不同区域划分条件下的入侵检测性能混淆矩阵^[28], 矩阵中, s, a1, a2, a3, a4, a5 和 a6 分别表示静默、区域 1 入侵、区域 2 入侵、区域 3 入侵、区域 4 入侵、区域 5 入侵和区域 6 入侵状态, 第 i 行第 j 列元素表示第 i 个真实状态被判决为第 j 个状态的概率. 显然, 混淆矩阵的对角线元素值越大, 入侵检测与区域定位性能就越好. 可以看出, 随着划分区域

4) 即正确检测出目标区域内存在入侵的概率.

图 15 多区域划分结果

Figure 15 Results of multi-region division. (a) 2 regions; (b) 3 regions; (c) 4 regions; (d) 5 regions; (e) 6 regions

数的增加, 虽然入侵检测性能整体上呈下降趋势, 但其对应的平均成功检测概率均高于 95%, 从而能够有效保证大多室内目标入侵检测与区域定位应用的性能要求^[29].

图 17 给出了在 4 区域划分条件下不同单一 RSS 特征数据所对应的入侵检测性能混淆矩阵. 对比图 16(c) 和 17 可知, 本文采用的联合 RSS 均值、方差、最大值、最小值、极差值和中位值 6 种信号特征构建 PNN 训练数据库的方法, 具有最优的入侵检测与区域定位性能.

最后, 表 3 给出了本文方法与现有 MA^[8]、MV^[8]、射线层析成像^[9] 和神经网络^[10] 入侵检测方法的性能对比. 可以看出, 本文方法在满足较高成功检测概率 (即 97.40%) 的同时, 还能保证较低的漏检和虚警概率 (即分别为 3.42% 和 7.96%). 此外, 由于 MA 和 MV 入侵检测方法仅实现对静默和入侵两种状态的区分, 故其单次检测平均时间开销较小; 而相较于射线层析成像方法, 神经网络和本文所提方法具有更小低的单次检测平均时间开销.

图 16 不同区域划分条件下入侵检测性能混淆矩阵

Figure 16 Intrusion detection performance confusion matrix under different region division. (a) 2 regions; (b) 3 regions; (c) 4 regions; (d) 5 regions; (e) 6 regions

图 17 不同单一 RSS 特征数据所对应的入侵检测性能混淆矩阵

Figure 17 Intrusion detection performance confusion matrix corresponding to different single RSS feature data. (a) Mean; (b) variance; (c) maximum; (d) minimum; (e) range; (f) median

表 3 不同入侵检测方法性能对比

Table 3 Performance comparison of different intrusion detection methods

Performance index	MA	MV	Radio tomographic imaging	Neural network	The proposed method
Missed detection probability (%)	14.46	14.26	7.08	5.23	3.42
False detection probability (%)	13.85	10.40	12.47	9.01	7.96
Successful detection probability (%)	—	—	95.8	94.5	97.40
Average time overhead for single detection (s)	2.35	2.46	9.77	6.57	6.62

3 结论

针对现有室内 WLAN 网络环境, 本文提出了一种基于自适应深度射线树的准三维射线追踪模型, 以对室内静默和入侵状态下的 RSS 传播特性进行建模, 该模型相较于传统二维和三维射线追踪模型具有更高的建模精度和计算效率. 此外, 通过联合 6 种常见信号特征对 PNN 多分类判决器进行训练, 保证了 RSS 特征数据的稳定性及其对入侵目标所造成射线建模变化的敏感性. 然而, 本文方法关于 WLAN 室内环境下多入侵目标的精确定位性能还受到一定限制, 故进一步研究工作包括: 在多入侵目标造成 RSS 传播特性愈加复杂的情况下保证对入侵目标数的分辨力; 在多入侵目标运动相互干扰的情况下利用目标位置状态的相关性来提高对目标的连续定位精度; 以及在复杂、时变网络环境下保证 RSS 传播特性对射线追踪模型的建模精度.

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WLAN indoor target intrusion detection algorithm based on adaptive-depth ray tree

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Abstract With the wide deployment of wireless local area network (WLAN) and general support of WLAN protocol by various intelligent terminals, intrusion detection with respect to an indoor target can be realized using the existing WLAN infrastructure. To this end, the adaptive-depth ray tree-based quasi 3D ray-tracing model is constructed to model the received signal strength (RSS) propagation property under indoor silence and intrusion scenarios. Then, the RSS mean, variance, maximum, minimum, range, and median are allied to construct the training database for a probabilistic neural network (PNN). Finally, after the training, this PNN is utilized to perform the multi-classification decision with respect to the newly-collected RSS data and to consequently achieve indoor target intrusion detection and area localization. The experimental results indicate that the proposed algorithm has a high intrusion detection rate and low database construction cost.

Keywords WLAN, intrusion detection, ray tracing, genetic algorithm, neural networks

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